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<b>(54) Title:</b> BIALLELIC MARKERS  <b>(57) Abstract</b>  The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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## BIALLELIC MARKERS

## RELATED APPLICATIONS

This application claims priority to U.S. provisional application Serial No. 60/030,455, filed November 6, 1996, the entire teachings of which are incorporated herein by reference.

## BACKGROUND OF THE INVENTION

The genomes of all organisms undergo spontaneous mutation in the course of their continuing evolution, generating variant forms of progenitor sequences (Gusella, *Ann. Rev. Biochem.* 55, 831-854 (1986)). The variant form may confer an evolutionary advantage or disadvantage relative to a progenitor form or may be neutral. In some instances, a variant form confers a lethal disadvantage and is not transmitted to subsequent generations of the organism. In other instances, a variant form confers an evolutionary advantage to the species and is eventually incorporated into the DNA of many or most members of the species and effectively becomes the progenitor form. In many instances, both progenitor and variant form(s) survive and co-exist in a species population. The coexistence of multiple forms of a sequence gives rise to polymorphisms.

Several different types of polymorphism have been reported. A restriction fragment length polymorphism (RFLP) is a variation in DNA sequence that alters the length of a restriction fragment (Botstein et al., *Am. J. Hum. Genet.* 32, 314-331 (1980)). The restriction fragment length polymorphism may create or delete a restriction site, thus changing the length of the restriction fragment.

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RFLPs have been widely used in human and animal genetic analyses (see WO 90/13668; W090/11369; Donis-Keller, *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 85-99 (1989)). When a heritable trait can be linked to a particular RFLP, the presence of the RFLP in an individual can be used to predict the likelihood that the animal will also exhibit the trait.

Other polymorphisms take the form of short tandem repeats (STRs) that include tandem di-, tri- and tetra-nucleotide repeated motifs. These tandem repeats are also referred to as variable number tandem repeat (VNTR) polymorphisms. VNTRs have been used in identity and paternity analysis (US 5,075,217; Armour et al., *FEBS Lett.* 307, 113-115 (1992); Horn et al., W0 91/14003; Jeffreys, EP 370,719), and in a large number of genetic mapping studies.

Other polymorphisms take the form of single nucleotide variations between individuals of the same species. Such polymorphisms are far more frequent than RFLPs, STRs and VNTRs. Some single nucleotide polymorphisms occur in protein-coding sequences, in which case, one of the polymorphic forms may give rise to the expression of a defective or other variant protein and, potentially, a genetic disease. Examples of genes, in which polymorphisms within coding sequences give rise to genetic disease include  $\beta$ -globin (sickle cell anemia) and CFTR (cystic fibrosis). Other single nucleotide polymorphisms occur in noncoding regions. Some of these polymorphisms may also result in defective protein expression (e.g., as a result of defective splicing). Other single nucleotide polymorphisms have no phenotypic effects.

Single nucleotide polymorphisms can be used in the same manner as RFLPs and VNTRs, but offer several advantages. Single nucleotide polymorphisms occur with greater

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frequency and are spaced more uniformly throughout the genome than other forms of polymorphism. The greater frequency and uniformity of single nucleotide polymorphisms means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest than would be the case for other polymorphisms. The different forms of characterized single nucleotide polymorphisms are often easier to distinguish than other types of polymorphism (e.g., by use of assays employing allele-specific hybridization probes or primers).

Only a small percentage of the total repository of polymorphisms in humans and other organisms has been identified. The limited number of polymorphisms identified to date is due to the large amount of work required for their detection by conventional methods. For example, a conventional approach to identifying polymorphisms might be to sequence the same stretch of DNA in a population of individuals by dideoxy sequencing. In this type of approach, the amount of work increases in proportion to both the length of sequence and the number of individuals in a population and becomes impractical for large stretches of DNA or large numbers of persons.

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## SUMMARY OF THE INVENTION

The invention provides nucleic acid sequences comprising nucleic acid segments of from about 10 to about 200 bases as shown in the Table, column 7, including a polymorphic site. Complements of these segments are also included. The segments can be DNA or RNA, and can be double- or single-stranded. Segments can be, for example, 10-20, 10-50 or 10-100 bases long. Preferred segments include a biallelic polymorphic site. The base occupying the polymorphic site in the segments can be the reference (Table, column 3) or an alternative base (Table, column 4).

The invention further provides allele-specific oligonucleotides that hybridize to a segment of a fragment shown in the Table, column 7, or its complement. These oligonucleotides can be probes or primers. Also provided are isolated nucleic acids comprising a sequence shown in the Table, column 7, or the complement thereto, in which the polymorphic site within the sequence is occupied by a base other than the reference base shown in the Table, column 3.

The invention further provides a method of analyzing a nucleic acid from an individual. The method determines which base is present at any one of the polymorphic sites shown in the Table. Optionally, a set of bases occupying a set of the polymorphic sites shown in the Table is determined. This type of analysis can be performed on a number of individuals, who are tested for the presence of a disease phenotype. The presence or absence of disease phenotype is then correlated with a base or set of bases present at the polymorphic sites in the individuals tested.

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## DETAILED DESCRIPTION OF THE INVENTION

## DEFINITIONS

An oligonucleotide can be DNA or RNA, and single- or double-stranded. Oligonucleotides can be naturally occurring or synthetic, but are typically prepared by synthetic means. The oligonucleotides of the present invention can comprise all of an oligonucleotide sequence presented in column 7 of the Table or a segment of such an oligonucleotide which includes a polymorphic site.

10 Oligonucleotides can be all of a nucleic acid segment as represented in column 7 of the Table; a nucleic acid sequence which comprises a nucleic acid segment represented in column 7 of the Table and additional nucleic acids (present at either or both ends of a nucleic acid segment of column 7); or a portion (fragment) of a nucleic acid segment represented in column 7 of the Table which includes a polymorphic site. Preferred oligonucleotides of the invention include segments of DNA, or their complements, which include any one of the polymorphic sites shown in the

15 Table. The segments can be between 5 and 250 bases, and, in specific embodiments, are between 5-10, 5-20, 10-20, 10-50, 20-50 or 10-100 bases. The polymorphic site can occur within any position of the segment. The segments can be from any of the allelic forms of DNA shown in the Table.

25 Hybridization probes are oligonucleotides which bind in a base-specific manner to a complementary strand of nucleic acid. Such probes include peptide nucleic acids, as described in Nielsen et al., *Science* 254, 1497-1500 (1991).

As used herein, the term primer refers to a single-

30 stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and an agent for

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polymerization, such as, DNA or RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not reflect the exact sequence of the template, but must be sufficiently complementary to hybridize with a template.

10 The term primer site refers to the area of the target DNA to which a primer hybridizes. The term primer pair refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with

15 the complement of the 3' end of the sequence to be amplified.

As used herein, linkage describes the tendency of genes, alleles, loci or genetic markers to be inherited together as a result of their location on the same

20 chromosome. It can be measured by percent recombination between the two genes, alleles, loci or genetic markers.

As used herein, polymorphism refers to the occurrence of two or more genetically determined alternative sequences or alleles in a population. A polymorphic marker or site

25 is the locus at which divergence occurs. Preferred markers have at least two alleles, each occurring at frequency of greater than 1%, and more preferably greater than 10% or 20% of a selected population. A polymorphic locus may be as small as one base pair. Polymorphic markers include

30 restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats,



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and insertion elements such as Alu. The first identified allelic form is arbitrarily designated as the reference form and other allelic forms are designated as alternative or variant alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the wildtype form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic or biallelic polymorphism has two forms. A triallelic polymorphism has three forms.

10 A single nucleotide polymorphism occurs at a polymorphic site occupied by a single nucleotide, which is the site of variation between allelic sequences. -The site is usually preceded by and followed by highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations).

A single nucleotide polymorphism usually arises due to substitution of one nucleotide for another at the polymorphic site. A transition is the replacement of one purine by another purine or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine or vice versa. Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Typically the polymorphic site is occupied by a base other than the reference base. For example, where the reference allele contains the base "T" at the polymorphic site, the altered allele can contain a "C", "G" or "A" at the polymorphic site.

Hybridizations are usually performed under stringent conditions, for example, at a salt concentration of no more than 1 M and a temperature of at least 25°C. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C, or equivalent

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conditions, are suitable for allele-specific probe hybridizations. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleotide sequence and the primer or probe used.

The term "isolated" is used herein to indicate that the material in question exists in a physical milieu distinct from that in which it occurs in nature. For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstance, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid comprises at least about 50, 80 or 90 percent (on a molar basis) of all macromolecular species present.

#### I. Novel Polymorphisms of the Invention

The novel polymorphisms of the invention are listed in the Table. The first column of the Table lists the names assigned to the fragments in which the polymorphisms occur. The fragments are all human genomic fragments. The sequence of one allelic form of each of the fragments (arbitrarily referred to as the prototypical or reference form) has been previously published. These sequences are listed at <http://www-genome.wi.mit.edu/> (all STS's (sequence tag sites)); <http://shgc.stanford.edu> (Stanford STS's); and <http://ww.tigr.org/> (TIGR STS's). The Web sites also list primers for amplification of the fragments,



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and the genomic location of fragments. Some fragments are expressed sequence tags, and some are random genomic fragments. All information in the websites concerning the fragments listed in the Table is incorporated by reference  
5 in its entirety for all purposes.

The second column lists the position in the fragment in which a polymorphic site has been found. Positions are numbered consecutively with the first base of the fragment sequence as listed in one of the above databases being  
10 assigned the number one. The third column lists the base occupying the polymorphic site in the sequence in the data base. This base is arbitrarily designated the reference or prototypical form, but it is not necessarily the most frequently occurring form. The fourth column in the Table  
15 lists the alternative base(s) at the polymorphic site. The fifth column of the Table lists a 5' (upstream or forward) primer that hybridizes with the 5' end of the DNA sequence to be amplified. The sixth column of the Table lists a 3' (downstream or reverse) primer that hybridizes with the  
20 complement of the 3' end of the sequence to be amplified. The seventh column of the Table lists a number of bases of sequence on either side of the polymorphic site in each fragment. The indicated sequences can be either DNA or RNA. In the latter, the T's shown in the Table are  
25 replaced by U's. The base occupying the polymorphic site is indicated in EUPAC-IUB ambiguity code.

## II. Analysis of Polymorphisms

### A. Preparation of Samples

Polymorphisms are detected in a target nucleic acid  
30 from an individual being analyzed. For assay of genomic DNA, virtually any biological sample (other than pure red blood cells) is suitable. For example, convenient tissue

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samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair. For assay of cDNA or mRNA, the tissue sample must be obtained from an organ in which the target nucleic acid is expressed. For example, if the target nucleic acid is a cytochrome P450, the liver is a suitable source.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by e.g., PCR. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., *Nucleic Acids Res.* 19, 4967 (1991); Eckert et al., *PCR Methods and Applications* 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4, 560 (1989), Landegren et al., *Science* 241, 1077 (1988), transcription amplification (Kwoh et al., *Proc. Natl. Acad. Sci. USA* 86, 1173 (1989)), and self-sustained sequence replication (Guatelli et al., *Proc. Nat. Acad. Sci. USA*, 87, 1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

### B. Detection of Polymorphisms in Target DNA

There are two distinct types of analysis of target DNA for detecting polymorphisms. The first type of analysis,

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sometimes referred to as de novo characterization, is carried out to identify polymorphic sites not previously characterized (i.e., to identify new polymorphisms). This analysis compares target sequences in different individuals to identify points of variation, i.e., polymorphic sites. By analyzing groups of individuals representing the greatest ethnic diversity among humans and greatest breed and species variety in plants and animals, patterns characteristic of the most common alleles/haplotypes of the locus can be identified, and the frequencies of such alleles/haplotypes in the population can be determined. Additional allelic frequencies can be determined for subpopulations characterized by criteria such as geography, race, or gender. The de novo identification of polymorphisms of the invention is described in the Examples section. The second type of analysis determines which form(s) of a characterized (known) polymorphism are present in individuals under test. There are a variety of suitable procedures, which are discussed in turn.

#### 1. Allele-Specific Probes

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., *Nature* 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe

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hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

## 2. Tiling Arrays

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in WO 95/11995. One form of such arrays is described in the Examples section in connection with de novo identification of polymorphisms. The same array or a different array can be used for analysis of characterized polymorphisms. WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles as described in the Examples, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference

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sequence in which multiple mutations are expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

### 3. Allele-Specific Primers

5       An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in  
10       conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows  
15       a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best  
20       when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

### 4. Direct-Sequencing

25       The direct analysis of the sequence of polymorphisms of the present invention can be accomplished using either the dideoxy chain termination method or the Maxam Gilbert method (see Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind et al., *Recombinant DNA Laboratory Manual*, (Acad. Press,  
30       1988)).

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### 5. Denaturing Gradient Gel Electrophoresis

Amplification products generated using the polymerase chain reaction can be analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., *PCR Technology, Principles and Applications for DNA Amplification*, (W.H. Freeman and Co, New York, 1992), Chapter 7.

### 10 6. Single-Strand Conformation Polymorphism Analysis

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., *Proc. Nat. Acad. Sci.* 86, 2766-2770 (1989). Amplified PCR products can be generated as described above, and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

### 25 III. Methods of Use

After determining polymorphic form(s) present in an individual at one or more polymorphic sites, this information can be used in a number of methods.



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## A. Forensics

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See  
5 generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). The more sites that are analyzed, the lower the probability that the set of polymorphic forms in one individual is the same as that in  
10 an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are biallelic because the population  
15 frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic  
20 analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of  
25 polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime  
30 scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a

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match of suspect and crime scene sample would occur by chance.

$p(ID)$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In biallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism is (see WO 95/12607):

- 10 Homozygote:  $p(AA) = x^2$   
 Homozygote:  $p(BB) = y^2 = (1-x)^2$   
 Single Heterozygote:  $p(AB) = p(BA) = xy = x(1-x)$   
 Both Heterozygotes:  $p(AB+BA) = 2xy = 2x(1-x)$

The probability of identity at one locus (i.e., the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID) = (x^2)^2 + (2xy)^2 + (y^2)^2.$$

These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(ID)$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:

25  $p(ID) = x^4 + (2xy)^2 + (2yz)^2 + (2xz)^2 + z^4 + y^4$

In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(ID)$  and  $p(exc)$ .

The cumulative probability of identity ( $\text{cum } p(ID)$ ) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus.

30  $\text{cum } p(ID) = p(ID1)p(ID2)p(ID3) \dots p(IDn)$



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The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(\text{nonID}) = 1 - \text{cum } p(\text{ID}).$$

- 5        If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

10        B. Paternity Testing

The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced.

- 15        Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in the putative father and the child.

- 20        If the set of polymorphisms in the child attributable to the father does not match the set of polymorphisms of the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child  
25        attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation can be performed to determine the probability of coincidental match.

- 30        The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him

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incompatible as the father) is given by the equation (see WO 95/12607):

$$p(\text{exc}) = xy(1-xy)$$

where x and y are the population frequencies of alleles A and B of a biallelic polymorphic site.

(At a triallelic site  $p(\text{exc}) = xy(1-xy) + yz(1-yz) + xz(1-xz) + 3xyz(1-xyz)$ ), where x, y and z are the respective population frequencies of alleles A, B and C).

The probability of non-exclusion is

$$p(\text{non-exc}) = 1 - p(\text{exc})$$

The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$\text{cum } p(\text{non-exc}) = p(\text{non-exc1})p(\text{non-exc2})p(\text{non-exc3})\dots$$

$$p(\text{non-excn})$$

The cumulative probability of exclusion for n loci (representing the probability that a random male will be excluded)

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

### C. Correlation of Polymorphisms with Phenotypic Traits

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the

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circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria). Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance

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(e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Correlation is performed for a population of  
5 individuals who have been tested for the presence or  
absence of a phenotypic trait of interest and for  
polymorphic markers sets. To perform such analysis, the  
presence or absence of a set of polymorphisms (i.e. a  
polymorphic set) is determined for a set of the  
10 individuals, some of whom exhibit a particular trait, and  
some of which exhibit lack of the trait. The alleles of  
each polymorphism of the set are then reviewed to determine  
whether the presence or absence of a particular allele is  
associated with the trait of interest. Correlation can be  
15 performed by standard statistical methods such as a  $\chi^2$ -  
squared test and statistically significant correlations  
between polymorphic form(s) and phenotypic characteristics  
are noted. For example, it might be found that the  
presence of allele A1 at polymorphism A correlates with  
20 heart disease. As a further example, it might be found  
that the combined presence of allele A1 at polymorphism A  
and allele B1 at polymorphism B correlates with increased  
milk production of a farm animal.

Such correlations can be exploited in several ways. In  
25 the case of a strong correlation between a set of one or  
more polymorphic forms and a disease for which treatment is  
available, detection of the polymorphic form set in a human  
or animal patient may justify immediate administration of  
treatment, or at least the institution of regular  
30 monitoring of the patient. Detection of a polymorphic form  
correlated with serious disease in a couple contemplating a  
family may also be valuable to the couple in their  
reproductive decisions. For example, the female partner

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might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified.

Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., US 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wildtype with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered. Each production trait was analyzed individually with the following animal model:

$$Y_{ijkpn} = \mu + YS_i + P_j + X_k + \beta_1 + \dots \beta_{17} + PE_n + a_n + e_p$$

where  $Y_{ijkpn}$  is the milk, fat, fat percentage, SNF, SNF percentage, energy concentration, or lactation energy record;  $\mu$  is an overall mean;  $YS_i$  is the effect common to all cows calving in year-season;  $X_k$  is the effect common to cows in either the high or average selection line;  $\beta_1$  to  $\beta_{17}$  are the binomial regressions of production record on mtDNA

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D-loop sequence polymorphisms;  $PE_n$  is permanent environmental effect common to all records of cow  $n$ ;  $a_n$  is effect of animal  $n$  and is composed of the additive genetic contribution of sire and dam breeding values and a Mendelian sampling effect; and  $e_p$  is a random residual. It was found that eleven of seventeen polymorphisms tested influenced at least one production trait. Bovines having the best polymorphic forms for milk production at these eleven loci are used as parents for breeding the next generation of the herd.

#### D. Genetic Mapping of Phenotypic Traits

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992).

Linkage studies are typically performed on members of a family. Available members of the family are characterized



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for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-

5 segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the

10 odds) values. A lod value is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $\theta$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson &

15 Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $\theta$ ),

20 ranging from  $\theta = 0.0$  (coincident loci) to  $\theta = 0.50$  (unlinked). Thus, the likelihood at a given value of  $\theta$  is: probability of data if loci linked at  $\theta$  to probability of data if loci unlinked. The computed likelihoods are usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod

25 score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod

30 scores for differing values of  $\theta$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See

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Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $\theta$  at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $\theta$ ) than the possibility that the two loci are unlinked. By convention, a combined lod score of +3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

#### IV. Modified Polypeptides and Gene Sequences

The invention further provides variant forms of nucleic acids and corresponding proteins. The nucleic acids comprise one of the sequences described in the Table, column 8, in which the polymorphic position is occupied by one of the alternative bases for that position. Some nucleic acids encode full-length variant forms of proteins. Similarly, variant proteins have the prototypical amino acid sequences encoded by nucleic acid sequences shown in the Table, column 8, (read so as to be in-frame with the full-length coding sequence of which it is a component) except at an amino acid encoded by a codon including one of the polymorphic positions shown in the Table. That position is occupied by the amino acid coded by the



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corresponding codon in any of the alternative forms shown in the Table.

Variant genes can be expressed in an expression vector in which a variant gene is operably linked to a native or  
5 other promoter. Usually, the promoter is a eukaryotic promoter for expression in a mammalian cell. The transcription regulation sequences typically include a heterologous promoter and optionally an enhancer which is recognized by the host. The selection of an appropriate  
10 promoter, for example trp, lac, phage promoters, glycolytic enzyme promoters and tRNA promoters, depends on the host selected. Commercially available expression vectors can be used. Vectors can include host-recognized replication systems, amplifiable genes, selectable markers, host  
15 sequences useful for insertion into the host genome, and the like.

The means of introducing the expression construct into a host cell varies depending upon the particular construction and the target host. Suitable means include  
20 fusion, conjugation, transfection, transduction, electroporation or injection, as described in Sambrook, supra. A wide variety of host cells can be employed for expression of the variant gene, both prokaryotic and eukaryotic. Suitable host cells include bacteria such as  
25 *E. coli*, yeast, filamentous fungi, insect cells, mammalian cells, typically immortalized, e.g., mouse, CHO, human and monkey cell lines and derivatives thereof. Preferred host cells are able to process the variant gene product to produce an appropriate mature polypeptide. Processing  
30 includes glycosylation, ubiquitination, disulfide bond formation, general post-translational modification, and the like.

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The protein may be isolated by conventional means of protein biochemistry and purification to obtain a substantially pure product, i.e., 80, 95 or 99% free of cell component contaminants, as described in Jacoby, 5 *Methods in Enzymology* Volume 104, Academic Press, New York (1984); Scopes, *Protein Purification, Principles and Practice*, 2nd Edition, Springer-Verlag, New York (1987); and Deutscher (ed), *Guide to Protein Purification, Methods in Enzymology*, Vol. 182 (1990). If the protein is 10 secreted, it can be isolated from the supernatant in which the host cell is grown. If not secreted, the protein can be isolated from a lysate of the host cells.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene 15 and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating 20 the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, *Science* 244, 1288-1292 25 (1989). The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

30 In addition to substantially full-length polypeptides expressed by variant genes, the present invention includes biologically active fragments of the polypeptides, or analogs thereof, including organic molecules which simulate

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the interactions of the peptides. Biologically active fragments include any portion of the full-length polypeptide which confers a biological function on the variant gene product, including ligand binding, and  
5 antibody binding. Ligand binding includes binding by nucleic acids, proteins or polypeptides, small biologically active molecules, or large cellular structures.

Polyclonal and/or monoclonal antibodies that specifically bind to variant gene products but not to  
10 corresponding prototypical gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide fragments thereof. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, *Antibodies, A*  
15 *Laboratory Manual*, Cold Spring Harbor Press, New York (1988); Goding, *Monoclonal antibodies, Principles and Practice* (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are tested for specific immunoreactivity with a variant gene product and lack of  
20 immunoreactivity to the corresponding prototypical gene product. These antibodies are useful in diagnostic assays for detection of the variant form, or as an active ingredient in a pharmaceutical composition.

#### V. Kits

25 The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific  
30 oligonucleotides are provided immobilized to a substrate. For example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10,

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100 or all of the polymorphisms shown in the Table.  
Optional additional components of the kit include, for  
example, restriction enzymes, reverse-transcriptase or  
polymerase, the substrate nucleoside triphosphates, means  
5 used to label (for example, an avidin-enzyme conjugate and  
enzyme substrate and chromogen if the label is biotin), and  
the appropriate buffers for reverse transcription, PCR, or  
hybridization reactions. Usually, the kit also contains  
instructions for carrying out the methods.

10 The following Examples are offered for the purpose of  
illustrating the present invention and are not to be  
construed to limit the scope of this invention. The  
teachings of all references cited herein are hereby  
incorporated herein by reference.

15

## EXAMPLES

The polymorphisms shown in the Table were identified by  
resequencing of target sequences from three to ten  
unrelated individuals of diverse ethnic and geographic  
backgrounds by hybridization to probes immobilized to  
20 microfabricated arrays or conventional sequencing. The  
strategy and principles for design and use of such arrays  
are generally described in WO 95/11995. The strategy  
provides arrays of probes for analysis of target sequences  
showing a high degree of sequence identity to the reference  
25 sequences of the fragments shown in the Table, column 1.  
The reference sequences were sequence-tagged sites (STSs)  
developed in the course of the Human Genome Project (see,  
e.g., *Science* 270, 1945-1954 (1995); *Nature* 380, 152-154  
(1996)). Most STS's ranged from 100 bp to 300 bp in size.

30

A typical probe array used in this analysis has two  
groups of four sets of probes that respectively tile both  
strands of a reference sequence. A first probe set

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comprises a plurality of probes exhibiting perfect complementarily with one of the reference sequences. Each probe in the first probe set has an interrogation position that corresponds to a nucleotide in the reference sequence. That is, the interrogation position is aligned with the corresponding nucleotide in the reference sequence, when the probe and reference sequence are aligned to maximize complementarily between the two. For each probe in the first set, there are three corresponding probes from three additional probe sets. Thus, there are four probes corresponding to each nucleotide in the reference sequence. The probes from the three additional probe sets are identical to the corresponding probe from the first probe set except at the interrogation position, which occurs in the same position in each of the four corresponding probes from the four probe sets, and is occupied by a different nucleotide in the four probe sets. In the present analysis, probes were 25 nucleotides long. Arrays tiled for multiple different reference sequences were included on the same substrate.

Multiple target sequences from an individual were amplified from human genomic DNA using primers for the fragments indicated in the listed Web sites. The amplified target sequences were fluorescently labelled during or after PCR. The labelled target sequences were hybridized with a substrate bearing immobilized arrays of probes. The amount of label bound to probes was measured. Analysis of the pattern of label revealed the nature and position of differences between the target and reference sequence. For example, comparison of the intensities of four corresponding probes reveals the identity of a corresponding nucleotide in the target sequences aligned with the interrogation position of the probes. The



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corresponding nucleotide is the complement of the nucleotide occupying the interrogation position of the probe showing the highest intensity (see WO 95/11995). The existence of a polymorphism is also manifested by

5 differences in normalized hybridization intensities of probes flanking the polymorphism when the probes hybridized to corresponding targets from different individuals. For example, relative loss of hybridization intensity in a "footprint" of probes flanking a polymorphism signals a

10 difference between the target and reference (i.e., a polymorphism) (see EP 717,113). Additionally, hybridization intensities for corresponding targets from different individuals can be classified into groups or clusters suggested by the data, not defined a priori, such

15 that isolates in a give cluster tend to be similar and isolates in different clusters tend to be dissimilar. Hybridizations to samples from different individuals were performed separately. The Table summarizes the data obtained for target sequences in comparison with a

20 reference sequence for the individuals tested.

From the foregoing, it is apparent that the invention includes a number of general uses that can be expressed concisely as follows. The invention provides for the use of any of the nucleic acid segments described above in the

25 diagnosis or monitoring of diseases, such as cancer, inflammation, heart disease, diseases of the CNS, and susceptibility to infection by microorganisms. The invention further provides for the use of any of the nucleic acid segments in the manufacture of a medicament

30 for the treatment or prophylaxis of such diseases. The invention further provides for the use of any of the DNA segments as a pharmaceutical.

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All publications and patent applications cited above are incorporated by reference in their entirety for all purposes to the same extent as if each individual publication or patent application were specifically and  
5 individually indicated to be so incorporated by reference.





WI-9651b	105	A T ---	---	TCTCTACATTCTATGGACAACCTOCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAAATCCTTTCTCT ACTTGTCCTCATGTACAATTTTCTGCTGCTCCTTCA/ATJGGGGCAGCTTGCAAGCCTCCCTTTAGAC ACCTCTACAGGTACAGCGACCATGCCCTACCTCCATGGCACTGCCAGGGGACCCCTTATAGGCCTCTG TCCTTAAACCTGTAATGGTATATTAATCCTTGGTGTGAATGTCCTC
WI-9651	139	T C ---	---	TCTCTACATTCTATGGACAACCTOCATGCCCTTTGCACATGCTGATCCCTCCTCCTGGAAATCCTTTCTCT ACTTGTCCTCATGTACAATTTTCTGCTGCTCCTTCAAGGGCAGCTTGCAAGCCTCCCTTTAGACACCT CT/CACAGGTACAGCGACCATGCCCTACCTCCATGGCACTGCCAGGGGACCCCTTATAGGCCTCTGT CTTTAAACCTGTAATGGTATATTAATCCTTGGTGTGAATGTCCTC
WI-7676b	309	A C ---	---	GTGACCTTCTGCAGCGTGGAGATGGACATCCTTGTCTGGGGACTTGGCCCTGCTATTATTTTGTG TATTTATGTCTTAATCTCTTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG GCCGGCTTCTCTTGGTGGCTGCTGGTTCAGAGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTGTGC TCCCCCGTCTCCTGAGGCGAGTATAGGAGAGAGAGCAAGGATTGAGT
WI-7676	139	C T ---	---	GTGACCTTCTGCAGCGTGGAGATGGACATCCTTGTCTGGGGACTTGGCCCTGCTATTATTTTGTG TATTTATGTCTTAATCTCTTCCACTGATGCATCCTCCAAAGGTAGATGGGAGGGTCTGTGTGAAGGG GC/C/TTGGCTTCTCTTGGTGGCTGCTGGTTCAGAGGGCAGGAAGCGTGTGGACTGCAGCTTCTGCTG GTGCTCCCCCGTCTCCTGAGGCGAGTATAGGAGAGAGAGCAAGGATT
WI-10072	105	G A ---	---	CATTATCTTGCTTGGGTCTGTTCACTTCTCTCTCTCCTCAATGAAGAGGATATTTAAGCATCAT CATCTGGCCCTTTTGGAGTTTGAATATTTTGTG/ATGACTCCTATGCACATGATAAATTTGTTA TGCTTGCTCTTATCTTATCTTTTGTATAGGAGTTTGGCCATGACCCCTTATGAGGAGAAAGGGA TCACCCCTTTTGGCTCTACAACCTTATAGATATTTAAATATCTTT
WI-9986	42	T C ---	---	TTGGTGTGAACCTCAGAAATATAGGAAATAAGACAATTTGAAT/A,CJGTACCCAGGAAACAAGAG CCCTGCACTTGACTCCAAAGGAGTTCTATTTCTGGCTGTTCCAGACTTTATTTGATCTTGAGAA GAGAACTGTTTCCCTCTAAATCAGTTTCATCATCTGTATCCAGGGTAGTACTCACAAGACATGTCA ATATCAATAGCATGCATATGGGGTGTGGATTCTTAGAACTTATTGCAATT
WI-7041	174	C A ---	---	GTCTATTGCAGGAGAAACGTCCCTTGGCACTCCCACTCTCATCAGGCCAAGTGGAGGACTGGCCAGA GGGCTGCACATGCAAACTCCAGTCCCTGCCCTCAGAGAGCTGAAAGGGTCCCTCGGTCTTTTATTT CAGGGCTTTGCATGGCTCTATTCCCTCTGCTCTGCTC/C/ACCACTTCTTTGGAGCAAGGAGATGC AGCTGTATTGTGTAAACAAGCTCATTTGTACAGTGTCTGTTCAATGAATAA
WI-7224	134	T C ---	---	ATAAACCTTGTGTATGATCACCCAACTCACTAATTAACAACCTTATGTGCTATCAGATATCCTCTCT ACCCCTCACGTTATTTTGAAGAAATCCTAAACATCAATACCTTTCATCCATAAAATGTCAGCATTT /C/JATTAATAAACAAATAACTTTTAAAGAAACATAAGGACACATTTTCAAAATTAATAAAATAAAG GCATTTAAGGATGGCTGTGATTATCTTGGGAAGCAGAGTGATTCATGCTAG

WI-10826	132	A C ---	---	TCTTATTTGCATTTACAGTAGCCCCATGAAGTAGGTATAACACGCTCTATTTAACATGAGAAGAT GGAGGCCCTTTCCAAATGGACTAAGTAATGTGTCTCAGGTTTCCTAATAAGCAAAGACCTGCAJVC JCCCTGGCTTCTGACTCCAAAGCTTATCCCTTCTCATGCTGTGCTGTCAGCCAGGACCCCATGGCGCA GAAAGCCAGCCTCTCCATCCCCAC
TIGR- A004S25	145	G A ---	---	AGATCTGCCATTAGTATTTATTCCTTTGAAGATACTTTGGAGATTCAITTTCTTGAGTGGCACTGCAT GCTCATTGAGTGAAACTTGTGGGTATAGAAATGGAAATGGAGAGTTTCAACACAGCTTTGCTGAAAC TGTACTTTGG[G/A]CTCCAGACTTCACTGTCTTAGGCATTGAAACCATCACCTGGTTTGCACTTCTTC ATGACTGAGGTTAACTTAAATGACTGAGGTTAACTTAAAC
WI-1021	24	A T ---	---	AAACACAGAAATCATCAAAGCAC[A/T]ATCTGTGTTTGAGATAAATGATAGTCTGAGTCACCTATG TAAGAAGTAACCTGAAATAGTAGGATAGTATTATCAITTCCTGTAAATAGATTACCTCTCAGCAAT TGGTCTGTTTTCATTCTATGGAACTCTCCGTAATTTTCAITTCATGTAATGGAACTCCCCATACTGT AATTGGACAGTTTGGTTCCAC
WI-4687	121	G T ---	---	TAGTATGTCACCTGCCATGGTAAGGACTTTGATCACTAGGAAATAAGAACACTTTGAATGGTCTTGTC TTTCAATAAAAGAGTGACATGATTGAACATGTGTTTAGATAAAGGGCACTT[G/T]GCAGGAGTGT TTAGGATGAAGAGAGAGATTAAAGGAAGATCAGGAAGAAAGTAGCAATGGGAATGAAATAAG GAGGCCCTGAGATCCACTGGATAATCTAAAACCAAGAGAAAGAACTTGAT
WI-4719b	107	T G ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTCTTGGGTGAGCGGATT ATGCTGACGCCATGGGTGTTTCATAAGTGACTTGAGAGTT/GI/ACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTTCATTCAACAATTCCTGCTATGCTTCTCAGATTGCAGAAATCAG TGCTCAAAATTCCTCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-4719	70	G A ---	---	TTCAATTCCTTCCAAATCCTTAGGAAATTTACATTATGGGCTAGTCTTGGGTGAGCGGATT ATG/AJCTGACGCCATGGGTGTTTCATAAGTGACTTGAGAGTTACTGTAGAGGCTACACAGAAATCT CTGTGAGGGGCATGTAATTGTATTTCATTCAACAATTCCTGCTATGCTTCTCAGATTGCAGAAATCAG TGCTCAAAATTCCTCCACTTGTCAACTTATCCTTAAGACATTTTTCACAGGA
WI-9484b	216	G C ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTCTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCTCTGCACTGCCAAGT TAAAGAAACCCCTGCTTGTGGAGAGGGAGGCCAGACAGGGAGGAATTCAGGGCATGTATGGCTC AGTCCCACTTCT[G/C]ACTGCAGAGTATAGGGACCAGGGTTCCAACTTT
WI-9484	178	G A ---	---	TCAACACGCTTTTATTGCCACTTCTGGCTCCCTCGTCCAGCAAGATTCTACCTCTTACCTGTAGG AATACTGAGCTCCGATGCAGGGGAATGGGTGGGGTGTACCACCTTCTCTCTGCACTGCCAAGT TAAAGAAACCCCTGCTTGTGGAGAGGGAGGCCAGACAGG[G/A]AGGAATTCAGGGGCATGTATG GCTCAGTCCCACTTCTGACTGCAGAGTATAGGGACCAGGGTTCCAACTTT



WI-7330	207	C T	---	---	AGGATGGAAGGAGACACGGGGCAGGAGAACTCTCTCTGCTAAATCGATAGGAGTCAGTTTGTCT TAAATGCTGACTACAGCCACTGACATGGTTGGCTGGAATTTCTCTTTAATTTGTGGCATATAGGTTT GTGACACAGAAGTCACTACTTTGGTGGCTAAGTTTACTAAGGAAATAACTGAAAGATTAAG TGAGAGC/TJTGAAAGAGAAATGATAATGCTTCCAACCTGAGCTGTACACAG
WI-9443	211	G A	---	---	TTAAACAGTTTCAGGTTGGTGAAGCAGAAAGGGATGTGATTACAAATTAATGAATCAGTCACCT GCACAAATTAATCTCTTTGGCATCATACAAACTGGGTTTATGGCAATGATGACATCATAGCATGA CCAACTCATGGAAGGCAGTCTAGAGTCCATCAGCTCACACCTGAGGGGAGGCACTGCAACCCA CTGACGAGAC/GA/CAGAGACCTTGGAATACAGATGACACCATGCCACTT
WI-7166	59	C T	---	---	TCTCTCAAAGAGAAACAAACCCCTAAGAGACTGAGTTCTGCAAGCATCAGTTCTA/C/TJGGAT CATCAACAAGATTTCCCTTGTCGCAAAATATTGACTATTCTGTATCTTTTCATCCTTGACTAAATTCGTG ATTTTCAAGCAGCATCTCTGGTTTAACTTGTGCTGTGAACAATTTGTCGAAAGAGTCTTCCCAAT TAATGCTTTTTATATCTAGGCTACCTGTTGGTAGATTCAAGGCCCCGAG
WI-7259b	189	T C	---	---	GCTTCTTCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCCAGAGAGGCGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCTGCAACAGCTGCAGGCTGCTCTCTCTCTGAGTTCTCTGGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAGT/CJTGCGGGGAGCAG AGCCAGCAGGTGGACAGGTGTTTGAGGGGCGCAACTTCCCTGGAGCTC
WI-7259	188	G T	---	---	GCTTCTTCCCAGGAAGCGGGTCTTGGCCTGGAACCTTCCAGAGAGGCGGGAGCAATTTTAGCC CCACCTGCTCCCATCTGCCCTGCAACAGCTGCAGGCTGCTCTCTCTCTGAGTTCTCTGGGCT GCGCAGGCTCCCTGGGAATAGAGCAAGACGTGAGTCTAACCTGGCCACAGT/CJTGCGGGGAGCA GAGCCAGCAGGTGGACAGGTGTTTGAGGGGCGCAACTTCCCTGGAGC
WI-7322	275	A G	---	---	GTACTTTAGGCTGTGAGGGTGGGCAATTAAGTGGTGACCTTGCAACAGGGTTTCTACAGATGAC CCTGTGAATCATATAATTAACCTGCATATATTTATAGCCAGTCACATTTGCCCTCTCACCCCTATATG GCCATAAAGTGCCTAAGCACTCAGGCTCCCACTCATCAACCCCTTTGACCAGAGAAAGAACACTC TGTTCTCTATCCCTTGTACATAGAGAGTTTGTATGGGCTCTGGCTG
WI-7685	46	T C	---	---	TCAGTTCTAGTCTCTGCGGCCACACAGAACTCTTTTGGGCTCT/CJTTTCTCCCTCTGGATCA AAGTAGCAGGACCATGGGAOCAGGTCTTGGAGCTGAGCTCTCACCTGTACTCTTCGAAATCCT CTTCTCTGAGGCTGGATCCTAGCCTTATCTCTGATCTCCATGGCTTCTCTCTCTCTCTGCGGACTC CTGGGTTGAGCTGTGCTCAGTCCCAACAGATGCTTTCTGTCTC
WI-563	87	G A	---	---	TGTGACCAATTGTTATTTAGAGGGTTTAACAATGGCCTGACTATCACCTGATGGTCGCCAGAAATTC CTGGGGAGGGCTCCCTTGA/CCTGATGATGCTACCTAAGTGCCTACTCTAACAATACTACTCC TGTGATGGGATCCTAAGCCAAAGCTGAATGAACATGTTCTAGCACTACAGAAATCCATACT GCCCTCAGTAAAGGCAATTTAATCTCTTTGGATAACCGAGGCACAT

WI-931c	191	C A ---	---	GACCAGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTATCCCTCACCAACACCTTCCAGTGCTTATTCTGTGTCAAAATGATCCTCT GTTGCTGCACTGTCTACTGTGTGATGGATTATATAATTATTGTCCAAAAAAGCC[C/A]CGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931b	81	A G ---	---	GACCAGGCACCAGAAAGCCACGGAAGCCACAGCCACTAGCCCTGAACCTTGACACCCCTGGAGTT TCTCTCCCTCCCTT[A/G]TCCCTCACCAACACCTTCCAGTGCTTATTCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCTACTGTGTGATGGATTATATAATTATTGTCCAAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-931	31	A G ---	---	GACCAGGCACCAGAAAGCCACGGAAGCCAC[A/G]GCCACTAGCCCTGAACCTTGACACCCCTGGGA GTTTCTCTCCCTCCCTATCCCTCACCAACACCTTCCAGTGCTTATTCTGTGTCAAAATGATCCT TCTGTTGCTGCACTGTCTACTGTGTGATGGATTATATAATTATTGTCCAAAAAAGCCCGAGCCTGG TACAGAAAAGGCATGGGAAAGATGTGTCAGA
WI-10870b	91	C T ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGG[C/T]ACCTACTTAGAGCAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCTGTATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCAACCTTAAATAACGTTGCCCCCC
WI-10870	103	G A ---	---	GGATGACTTACCCAATAGCAGGGTGGGTACATTCATGGGTAACAACACCCCTGGACTGGGATGGCAGA GACATCCACCTTAGCAAAGTGGGCACCTACTTAG[A/G]ACAGTGGAGTACCCTGAGTACGACCCCC TTAGCAGCAGAATTACAAGAAATCTTGGGACCTGTACTCTGTATACAAAATAAGGACATGGGTCAGC CTGAGCCACTCTTAAACCATGAACCATCAACCTTAAATAACGTTGCCCCCC
WI-7719b	281	T C ---	---	AGTTATTCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAAGTCTACAAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCCATTAGATCAAGACTACACGGTCTATGAGCAATAATGTG ATTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAAGCAA
WI-7719	163	A G ---	---	AGTTATTCTTCCAGATGACCAGCAGTAGACAAATGGATACTGAGCAGAGTCTTAGGTAAAGTCTT GGGAAATATTTGGGCATTGGTCTGGCCAAAGTCTACAAATGTCCCAATATCAAGGACAACCCCTAGC TTCTTAGTGAAGACAATGTACAGTTATCC[A/G]TTAGATCAAGACTACACGGTCTATGAGCAATAAT GTGATTTCTGGACATTGCCCATGTATAATCCTCACTGATGATTTCAAGCTAAA
WI-10396	72	C A ---	---	GCCTTGGAGTATATCTAAACTGTGGCCCTCCACTTTCATTTTCTTGAACATTGCTATCAACTGGGAA GAGT[C/A]TGTGACTTTATGCCAGTTTCCCTCTCAGATTTTATGACGGTGTGTTTTCTTTTGTTA TGCCATTTGAGGGATTGATGTTTCTTAAACTATGAAGTACTTGGCTGTCTCTCCATTGCTGTTCAGG TTAACAGCCACCATTGTAAACACTTTGT



WI-10673	94 C G ---				TCCCTTTATGCAACCAAGAGATATTTATTAACACCAATTACGTAGCAGGCCATGGCTCATGGGACC CACCCCGTGGCACTCATGAGGGGCGTTCAGGTTGGAACTATGCAGTGTGCTCCGGCCACACA TCCTGCTGGCCCCCTACCTGCCCCAATTCAATCTGCGCAATAAATCCTGTCTTATTTGTTTCATCTG GAGAAATTGAAGGGAGGTCAAGTTGTTGTCAATGATTTGTGTCAGAGAACCT
WI-7842	57 T C ---				CACAGCCATGCCCTTGAGGAGCCGGCCACCAGATGCTGAATCCCTATCCCATTCGTTCJGTATGAG TCCCATTTGCCCTTGCAATTAGCATTCGTCTCCCCCAAAGAAATGTGCTATGAAGCTTTCTTTCCT ACACACTCTGAGTCTCTGAATGAAGCTGAAGGTCTTAGTACCAGAGCTAGTTTTCAGCTGCTCAGAAAT TCATCTGAAGAGAGACTTAAGATGAAAGCAAATGATTCAGCTCCCTTATA
WI-7721	145 A C ---				CTGCCTCATCACGCCACTGGAGTCCACACTTTGAATTTGGGCAGCTACACGGGTCTGCCATGCTCTGG AGGAGCAAGGGGCCACATCCACCACCCAGCTGTACCCAGCCGGGCAGGTGCAGCCCTTCTCTCC TGCTCTGCJACJCTGACTCTCTTTTGAGGTCCCTGTATGTCTACCTCTGACTTCTGTGTTCCCTCTG TGCTGCTCTCATCCATTCCTCTTACTGGGGCCTGGGCTCTAGCCCA
WI-4767b	173 C A ---				TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGAAATTCATAAGAGTTCCT CAGGTCTGGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATGTTT CTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACA[C/A]AATCACTAAGGAATTCACCTAAGA CTCCTCTAACCCAGAGATTTTAACT
WI-4767	50 A G ---				TTCCAGTCTGTTTTATCCTTTTCATTGTCAAAAGATGCTCTTAGACTGA[G/A]ATTCATAAGAGATT CCTCAGGTCTGGGTAATCCTAGATCTTCTATATCCATTGAGTGTGATGGAGTTGGAGAGGGTATG TTCTTGCCCTTGAGAAATCCTAGAAAGCACAGGGATGACACAAATCACTAAGGAATTCACCTAAGAC TCCTCTAACCCAGAGATTTTAACT
WI-7718f	222 C T ---				ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAAATTACAAAGAA[C/T]CATGCAGGAAGGAAACTATGTATTAAT
WI-7718e	60 T C ---				ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGAT[C]GCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAT
WI-7718d	31 G A ---				ATTGCACTGAAGTTTTTGAATAACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAA GGATTACAGAACTGATGCCAAGGGCTGAGTGAGTTCACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAAGAGGTGAAATGAAGAAGGAAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTAAT

WI-7718c	91 C G ---			ATTGCACTGAAGTTTGTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCGTGTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAG ATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTC AAAAGGAACAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTATTAAT
WI-7718b	248 A G ---			ATTGCACTGAAGTTTGTGAAATACCTTTGTAGTTACTCAAGCAGTTACTCCCTACACTGATGCAAGGA TTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGATAGATG ACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAGTCAAA AGGAACAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTATTAAT
WI-7718a	42 A T ---	C	.	ATTGCACTGAAGTTTGTGAAATACCTTTGTAGTTACTCAAGCAGTTC, TGTACTCCCTACACTGATGC AAGGATTACAGAACTGATGCCAAGGGGCTGAGTGAGTTCAACTACATGTTCTGGGGCCCGGAGAT AGATGACTTTGCAGATGGAAGAGGTGAAATGAAGAGGAGCTGTGTTGAAACAGAAAAATAAG TCAAAAGGAACAAAATTACAAAGAACCATGCAGGAAGGAAACTATGTATTATTA
WI-7227d	99 G C ---			AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTTCATCTTTCAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAGGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTCAACCAGCGACTAATG
WI-7227c	291 G A ---			AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTTCATCTTTCAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGCTT GGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAGGGGACTGAGCTAAACAGTG TTATTATGGGAAGGAAATGGCATTGCTGCTTCAACCAGCGACTAATGCAAT
WI-7227b	93 G T ---			AGGGAATTGTGTTGCTCCTGGAGGAAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGCTTC CGTGGACCAATTTCATCTTTCAGACAAAGTTCCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAGGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTCAACCAGCGACTAATG
WI-7227a	24 A G ---			AGGGAATTGTGTTGCTCCTGGAGGAGGAGCCAGGCATCATTAACAAGCCAGTAGGTACCTGGC TTCCGTGGACCAATTTCATCTTTCAGACAAAGCTTTAGAGAAATGGACTCAGGGAAGAGACTCACATGC TTTGGTTAGTATCTGTGTTCCGGTGGTGTAAATAGGGGATTAGCCCCAGAGGGGACTGAGCTAAACA GTGTTATTATGGGAAGGAAATGGCATTGCTGCTTCAACCAGCGACTAATG
WI-7310b	234 A C ---			CCACAATGCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGGAGGTGGGAGACAAGAACCTCCG AAGAGGAAGCAAGAAAGCCGTACTGTCTATGTGTGTATCCTTCATCGAACAACTGATCGGAAACT TGAATCTGTTACTGAAATGAGGAGAGAGGACATGTGCTATTGAACTGAGCCAAACACACTGTAAAT ATCCACAGACTCCTCCCTGCCCATCCCA/CATGATCTTGAGATTTC



WI-7310a	64 T A ---	---	OCACAATGCCCTCTCCACGATGTCAAGGACTCCTGTCTGTCTGAGGTTGGGAGACAAGGAACCTT/A JCGAAGAGGAAGCAAGAACGCGTACTGTCTATGTGTGATCCTTCATCGAACAACTGATGCGAA AACTTGAATCTGTTACTGAAATGAGGAGAGAGACATGTGCTATTGAAGTGAAGCCAAACACACTGT AAATATCCACAGACTCCCTCCCTGCCCTGCCCATCCCAATGATCTTGAGATTTC
WI-7878b	162 A G ---	---	CCAGCAACACCTACACCTTGTCACTGCCCTGGGACTCCTATGATGGCCTGTGCTGTTGATAATAATCA GATCATGCCCAAGACGGGCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAATGCGTCC CTGAGGAGAAAATCTGGGAGGAGCTG[A/G]GTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTGT CTGTGGGAGGCCAGGAAGCTGCTCACCCCAAGATTGGTGCAAGGAAACTA
WI-7878a	51 C G ---	---	CCAGCAACACCTACACCTTGTCACTGCCCTGGGACTCCTATGATGGCCTGTGCTGTTGATAATAA TCAGATCATGCCCAAGACGGGCTCCTGATAATCGTCTTGGCATGATTGCAATGGAGGGCAATGCG GTCCCTGAGGAGAAAATCTGGGAGGAGCTGAGTGTGATGAAGGTGTATGTTGGGAGGGAGCACAGTG TCTGTGGGAGGCCAGGAAGCTGCTCACCCCAAGATTGGTGCAAGGAAACTA
WI-7381c	213 C T ---	---	CTCCACATTCCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTTCTTCTTCTACC AGCCCTGCAAGTTTCTCATGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGTTGAGATC AGATGTGGCCAAAGGAGGAGCTCTGGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAGACA AAAGGCTCTC/TGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381b	54 C G ---	---	CTCCACATTCCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTC/GCTTCTTCTCT ACGAGCCTGCAAGTTTCTCATGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGTTGAG ATCAGATGTGGCCAAAGGAGGAGCTCTGGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-7381a	53 C G ---	---	CTCCACATTCCCACAGGCTTGAGCAGAAATTTCTGAGACTGAAGGAAATCCCTC/GCTTCTTCTCT AOCAGCCTGCAAGTTTCTCATGACGCTCGGAGGAGCAGGCTGCAGGTTTCTGCTATGTTGAG ATCAGATGTGGCCAAAGGAGGAGCTCTGGTTCCAGAGAAATTTGCACAAAGTTCCCTCTGTACAGAG ACAAACGGCTCCGGCTCTCAGAGCATAATCCTTGGCAGGGCTCAGCAGG
WI-1017b	93 G A ---	---	AAATTGCTCTATTGGACCTCATATTAAATAAGAGCAATGAGAGCGAGGAAATTTGAACTCTCTC AGGTACTGACTGTGGACCCAGACAA[G/A]GATGTAGATTGTCACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAATAAGGAGATTAAATAACTCATCAC TGTTTTCAAATAAGGAGTGTGAGGTTTGTCCC
WI-1017a	92 G A ---	---	AAATTGCTCTATTGGACCTCATATTAAATAAGAGCAATGAGAGCGAGGAAATTTGAACTCTCTC AGGTACTGACTGTGGACCCAGACAA[G/A]GGATGTAGATTGTCACATTCAATCCTGAAACAAACCTG CCAGGCAAGTCTTCTTCCCATTTACAAATAAGGAGACAAATAAGGAGATTAAATAACTCATCAC TGTTTTCAAATAAGGAGTGTGAGGTTTGTCCC

WI-1795b	130	T C	---	---	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGTCTGGGTTCTCCAGACTCCTACGATTA AATTGTATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTGCCTTTCGAGAAAGAAAGT[C]C GTCTACCAATTTACCAAAATTCGTAGTACAATTAAGTATCTCTTGTATTCTCCCTAGGAGTCTAA AGTGAGCTGGGAAGGCAGGATTT
WI-1795a	47	T C	---	---	GAAGCAACCAGAAAGTATCTTTATCCCCATCTAGATTATGTCTGGGTT[C]CTCCAGACTCCTACGA TTAAATTGTATGCATGTGAACAACCTGATGAGGTACTTAGATCTCAGTGCCTTTCGAGAAAGAAAGTCTC GTCTACCAATTTACCAAAATTCGTAGTACAATTAAGTATCTCTTGTATTCTCCCTAGGAGTCTAA AGTGAGCTGGGAAGGCAGGATTT
WI-10616d	136	G A	---	---	CACACAAATTTGCAACACTTCAAGTGAACGCCCGACATCATCAGCCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAACGCTTTACTTCCACGCTCTCTCCATACGTAGGTCCTGGTCTCTCTATCACATTGCCA C[G]ATAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCAATTCCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616c	136	G A	---	---	CACACAAATTTGCAACACTTCAAGTGAACGCCCGACATCATCAGCCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAACGCTTTACTTCCACGCTCTCTCCATACGTAGGTCCTGGTCTCTCTATCACATTGCCA C[G]ATAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCAATTCCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616b	141	C T	---	---	CACACAAATTTGCAACACTTCAAGTGAACGCCCGACATCATCAGCCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAACGCTTTACTTCCACGCTCTCTCCATACGTAGGTCCTGGTCTCTCTATCACATTGCCA CGTAGC[C]TCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCAATTCCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-10616a	116	G C	---	---	CACACAAATTTGCAACACTTCAAGTGAACGCCCGACATCATCAGCCCCGTTAACGTCCAGGCCATGT CCCACATAGAGAAACGCTTTACTTCCACGCTCTCTCCATACGTAGGTCCTGGTCTCTCTATCACATTG CCAGTAGCCCTCCCTTCCCTTCCCTACAGGCCCTCTTCAGGGCCCCAGTCCCTCTGAGACTCCC ATGGATCAATTCCTGTTCTGTATCAGGCAGTGATTAACTCCTTTTGT
WI-1126c	52	G A	---	---	CTCTTATTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTG[A]ATACTAATAA AAACCCTGTAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAAAGAA AATTTATTCTCAAGATATAAAATAAATAATTTAATTCAGTTTCCTCAAAAGGAATATGAAATT TGTTAAATGCAATCCAGCTGTAACTTTTGGACTTGTCTTTATTCTT
WI-1126b	230	T C	---	---	CTCTTATTCTCTGGGCACTGCTTTCTTTGGGGCAAACTTCCAGTATCACTGATACTAATAA CCCTGTAAGTCTGCTTGCAATTTCAAGATTCAATATATATCCAGATTGTTTCCAGCAAAAGAAATT TTATTTCTCAAGATATAAAATAAATAATTTAATTCAGTTTCCTCAAAAGGAATATGAAATTGTT AAATGCAAAATCCAGCTGTAACTTTTTC[G]GACTTGTCTTTATTCTT

WI-1126a	97 T C ---			CTCTTAATTTCTCTGGGCACTGCTTTCTTTGGGGCAACTCCAGTATCACTGATACTAATAAA CCCTGTAACTGCTGCTTTCATTTTCAAGATTTCJCAATATATATCCAGATTGTTTCCAGCAAGAAA ATTTTATTTCTCAAGATATAAAATAAATAATTTAATTCAGTTTCCCTCAAGGAATATGAAATTT GTTAAATGCAATCCAGCTGTAACCTTTTGGACTTGCTTTTATTTCTT
WI-11183c	124 C T ---			TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAACTTGAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCCTGTCATAACA TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATATTGGT ATGTGGTGTAGAGTTAGTAATGGAA
WI-11183b	192 T C ---			TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAACTTGAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCCTGTCATAACA ATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATTCJATTGGT ATGTGGTGTAGAGTTAGTAATGGAA
WI-11183a	118 C T ---			TAGTGCTAATTTTGGAAAAGTTTGCTGATTTTAAAAATCTTTTAACTTGAAAATTTAGAGTAC ATATAAATAAATAAGACCAGATAGGTATTAATTCAGATGATTTTGGCCCTTGTCCTGTCATAACA TTTATGACATACAAATGACCAAAATGATGTTTTATGAAGTGTAGGATAGAGTTTTAAATATTGGT ATGTGGTGTAGAGTTAGTAATGGAA
WI-10770b	174 G A ---			GCTTGGTTGCTTAGTCTTATGTCAGTCTTGAGTTCTCCCTTCTGCTGGCCCTTTGTATTCA CCCATACCTCTATGCTCTGCTCAGACCAATTCCTCTATCTGGAGCGCTCTCTCTGACTTCTCTG TTCACCAACCTTCTTTTATTTCTCAGGACACTCA[G/A]TTCACATGCCACTCTCTGTCGACTGCTCT TTCACATCTTTCTGTGTCCTTTCC
WI-10770a	49 G T ---			GCTTGGTTGCTTAGTCTTATGTCAGTCTTGAGTTCTCCCTTCTGCTGGCCCTTTGTATT TCACCCATACCTCTATGCTCTGCTCAGACCAATTCCTCTATCTGGAGCGCTCTCTCTGACTTCTC CTGTTCAACCAACCTTCTTTTATTTCTCAGGACACTCAGTTTCACATGCCACTCTCTGTCGACTGCTCT TTCACATCTTTCTGTGTCCTTTCC
WI-9667b	82 C T ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTGCTCATGACACTTTTCAATCTCTGCTGTATCATGG TTATCACTGGACA[C/T]AGCCACCTCCCGAGCGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAGTCCAAACTTGCATTCT
WI-9667a	68 G C ---			GATGACAACTTCTGCTGTGACCCCTTAGTCTGCTCATGACACTTTTCAATCTCTGCTGTATCATG GCTTATCACTGGACACAGCCACCTCCCGAGCGCTTAGAACTCCATGAGTAAGGACCCCTGTCTA ATGTGCCGTTTCTCCTTATGGTATTACACACAGTCATAGGCATGAGTCAACTAATGGATCTTGGCT GTTTAAACCTTTTCTGTACCCAGTACCTAGTCCAAACTTGCATTCT



WI-10400d	189	A G ---			ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATAATTTATTCTAATTTT TCTTCCCTTACCTTTACTCTCCCAACCCAAATAACGTAAGTACCTATGTC/A/GTTGCCATGTAG TTTTTGGTTCAATTAAGCAATTAATCAAGGCGTTAATGCATTATG
WI-10400c	166	A C ---			ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATAATTTATTCTAATTTT TCTTCCCTTACCTTTACTCTCCCAACCCAAATAACGTAAGTACCTATGTCATGCGCATGTAG TTTTTGGTTCAATTAAGCAATTAATCAAGGCGTTAATGCATTATG
WI-10400b	165	A G ---			ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCTGCTG GTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATAATTTATTCTAATTTT TCTTCCCTTACCTTTACTCTCCCAACCCAAATAACGTAAGTACCTATGTCATGCGCATGTAG TTTTTGGTTCAATTAAGCAATTAATCAAGGCGTTAATGCATTATG
WI-10400a	46	T C ---			ACATTTTATTAGCAAAATCAGCAAAATAATAATAGAAAGTAATTGCAATTCAGACATCT GCTGGTTAACTGTTATAAGATGGTTTAGCACACATGTAGCACTTACTAACACAATAATTTATTCTA ATTTTCTTCCCTTACCTTTACTCTCCCAACCCAAATAACGTAAGTACCTATGTCATGCGCATGT AGTTTTTGGTTCAATTAAGCAATTAATCAAGGCGTTAATGCATTATG
WI-10809b	78	C T ---			AAAGGGCTACAACTAAGGCCAAACCATGAACGGTATAAGGAGGTAATGCAAGGGGAGACCC CACCTCTACCAIC/TTTAGAAAGGGCAATTCAGGCACATTCATGAGGCTTCATATACTGGTTAG CAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCCAAGTATGAGGCCACA GTGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-10809a	33	C T ---			AAAGGGCTACAACTAAGGCCAAACCATGAAC/TTGGTATAAGGAGGTAATGCAAGGGGAGAGA CCCCACCTCTACCACTTAGAAAGGGCAATTCAGGCACATTCATGAGGCTTCATATACTGGTTAGC AAACAAATGGAATGTATTAGCCCAAGGCAGGGTATGGACCAAAAGTGCCCAAGTATGAGGCCACAG TGAATATCCACCTAACGACCTTCTTGGATGATGTACACATGACATAGGCTTAA
WI-7038c	266	T C ---			CGAGCTTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGAAGACTGTCAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATTGAT CATTTTATATGAAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGAGTCC
WI-7038b	140	A C ---			CGAGCTTGGGATAAGCAAGGGGACCTTGGCGCTCTCAGCTTCCCTGCCACATCCAGCTTGTGTCC CAATGAAATACTGAGATGCTGGGTGTCTCTCCCTCCAGGAATGCTGGGCCCCAGCCTGGCCAGAC AAGA/C/CGACTGTGAGGAAGGGTCGGAGTCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAAATAAAAGATCCTGCAATTTATGGTGTAGTTCTGA

WI-7038a	31 G A ---			CGAGCTTGGGATAAGCAAGGGACCTTGGCGA/ACTCTCAGCTTCCCTGCCACATCCAGCTTGTG TCCCAATGAAATACTGAGATGCTGGGCTGCTCTCCCTCCAGGAATGCTGGGCCCCAGCTGGCCA GACAAGAAGACTGTGAGGAAGGTCGGAGCTGTAAACCAGCATACAGTTTGGCTTTTTCACATT GATCATTTTATATGAATAAAAGATCCTGCAATTTATGGGTAGTTCTGA
WI-3429b	64 G T ---			ATACGCTTCTGTCTGTCCACAGTGGAAACAGCAACCGAGGTGGCCAGGGTCGGCTCCACACA/GTJ CCCTCAGCCCCCTTCAGCTTTCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCCAGTCTCCTCTCCTGGATTGGATCTAGCAAGACCAGACGAGACGGTCCCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATTTCTTAAGACCAAGCACGGAGC
WI-3429a	62 C T ---			ATACGCTTCTGTCTGTCCACAGTGGAAACAGCAACCGAGGTGGCCAGGGTCGGCTCCACAICTJAG CCCTCAGCCCCCTTCAGCTTTCATGTGTCCATCGGTGACTCAGCACAGAGTTTCCAACTCATGTGA CAAAATACAGATTCCCAGTCTCCTCTCCTGGATTGGATCTAGCAAGACCAGACGAGACGGTCCCTAGAA TCCTGACTGTTAACAGCACTCCAGGCAATTTCTTAAGACCAAGCACGGAGC
WI-6786c	151 G A ---			ATTTAGGACAGTGAAAAAAGGGATTTATAATAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATAAAGAGTGAGTGACGGTGACCT GTGAGCCCCCATCTCTTG/AJTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786b	111 A T ---			ATTTAGGACAGTGAAAAAAGGGATTTATAATAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAAGGATAAAGAGTGAGTGACGGTGGA CCTGTAGCCCCCATCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6786a	106 A T ---			ATTTAGGACAGTGAAAAAAGGGATTTATAATAAATCTATGCCATCCAGGAGGTATGTGTCACT GTCCAGAACATCCTAGATGAAGTGGCTTCCCTTGGCGAAATJGGGATAAAGAGTGAGTGACGGTGA CCTGTAGCCCCCATCTCTGTGGGATAAGGTGTCCATTGTTCTTGGAGGGTGAATGCCACATTC TTTTGGCAGGGGACACTCCTTCTGGGTGCTCTATTGCTCAGTTTCATCATT
WI-6711b	226 G T ---			GGCTATTTGTAATGCTTGGTTATTTGACTCCAAATTTGAATAAGTATTTGGGAAGATCCCTCAGCT ACTTCCAAATCCCTTACATATCAATTTTACACAAAGCCCTAACCTTCAGTTCCAACTCACTGAAT TTCATATACCTCCATTATTAAATTCATATCATCATTCAGAGAAAGACAAACGGTGCCAACTGGGTT TGGTTGGTGCCTGCACACCCACA/GTJGGCAACTAAGTGTATCTCTAAA
WI-6711a	36 T C ---			GGCTATTTGTAATGCTTGGTTATTTGACTCCAAATTTGAATAAGTATTTGGGAAGATCCCTC ACCTACTTCCAAATCCCTTACATATCAATTTTACACAAAGCCCTAACCTTCAGTTCCAACTCACTCT GAATTTCATATACCTCCATTATTAAATTCATATCATCATTCAGAGAAAGACAAACGGTGCCAACTG GGTTGGTTGGTGCCTGCACACCCACAGTGGCACTAAGTGTATCTCTAAA

WI-10613b	172	A C ---	---	ATTGTATGCCAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTTGAGCCATA TGGTGAAAATTTAGAAAGTATTATTCTCTATATGTATATATACTACGTTTAAACATCAATGAATGTGATTT TTTGTCAACTTTTGACAAGGCCAGGCAATTTATTG[AC]GCCCTAGGAGGTTACTATAATTTAGA AAGGCTCTTACCTTCGACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-10613a	44	G A ---	---	ATTGTATGCCAAATCATAATACCCCTGCATTCTAGAAACATACAGTGTAAATAGAAATTTTGAGCC ATATGGTGAAAATTTAGAAAGTATTATTCTCTATATGTATATATACTACGTTTAAACATCAATGAATGTG ATTTTGTCAACTTTTGACAAGGCCAGGCAATTTTATTGAGCCCTAGGAGGTTACTATAATTTAG AAAGGCTCTTACCTTCGACTCTATAATTTTAAAGTCTCGGACTTAGGATGTAG
WI-7587c	133	A T ---	---	GCTCTAGTGGGAAACCTCAGGTAGTCCCGAAGATCTGTGCTTTCCAAACAAGTGACTACCCCTTGAAGC ACATCCCTTCTGGATCTGAAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA/V TJGGAATGAACCACTCCCTGCCATTCCCTATAAGAATATCCCAAGACCAGGCAATTTTGCCCTCT TTCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-7587b	81	G A ---	---	GCTCTAGTGGGAAACCTCAGGTAGTCCCGAAGATCTGTGCTTTCCAAACAAGTGACTACCCCTTGAAGC ACATCCCTTCTG[G/A]ATCTGAAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGAATATCCCAAGACCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-7587a	28	C T ---	---	GCTCTAGTGGGAAACCTCAGGTAGTCC[C/T]GAAGATCTGTGCTTTCCAAACAAGTGACTACCCCTTGA AGCACATCCCTTCTGGATCTGAAAAGAGCCCTTGGCTCAGGGCGTCTTTTCCAGCCCTGAGGAAA AGGAATGAACCACTCCCTGCCATTCCCTATAAGAATATCCCAAGACCAGGCAATTTTGCCCTCTT TCCACATGCCCCCATATGTCTGAGCCAAACTGCACCTGGGGCTGCCCTC
WI-10681b	103	T A ---	---	ATGACTCAGGTGACAAAAGAGCATGTCTTAGACCCCATTTG[AT]CTTACGCAAACTCAATCAGCCA ACAGAAAAGCTAAAGACATCCTTTTAAAGCC[T/A]AAAGACAGCCATTTTAACTCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGAGAAGGAGTGACGCTCTGTTAAAAG
WI-10681a	41	A T ---	---	ATGACTCAGGTGACAAAAGAGCATGTCTTAGACCCCATTTG[AT]CTTACGCAAACTCAATCAGCCA ACCACAGAAAAGCTAAAGACATCCTTTTAAAGCCCTAAAGACAGCCATTTTAACTCTAATTCG TAGTTTATGATTTTCTCAAAATTTCCCCACACACAGAAAGAACTTCAAGGTTAGGTTCTAATGTTA CCATTGCTAACACTATTGTCTTTGGAGAAGGAGTGACGCTCTGTTAAAAG
WI-7222c	126	G T ---	---	GCCTCTCAACTGTCTGGACCAAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGTTCCCTCCCTT AGACTCCCTAAGCCCGAGTGAGCTCAGGTGTCACCCCTGTTCTCAAGTTGGGGATGG[G/T]AATAA AGGAGGGGAATCCCTTGAAACAAGAACTGGGGATAGTTATATTTCCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGTAAGGTTGTATTTCAAGACTCGAATTCATTT



WI-7222b	255	GA ---	---	GCCTCTCTCAACTGTCTGACCCAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGTTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGGAATAAAGG AGGGGAATTCCCTTGAACAAGAAGAACTGGGATAGTTATATTCACCTGCCCTTGAAGCTTTAA GACAGTGATTTTGTGAAGTTGTATTCAAGACTCGAATTCATTTCTCA
WI-7222a	126	GT ---	---	GCCTCTCTCAACTGTCTGACCCAGGCTAGGAAAGGGCTGCTTGAGATGACTGTGTTCCCCCTT AGACTCCCTAAGCCGAGTGAGCTCAGGTGTACCCCTGTTCTCAAGTTGGGGATGGG(GT)AATAA AGGAGGGGAATTCCCTTGAACAAGAAGAACTGGGATAGTTATATTCACCTGCCCTTGAAGCTT TAAGACAGTGATTTTGTGAAGTTGTATTCAAGACTCGAATTCATTTT
WI-8054d	41	CA ---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCTCTTTC/TATCTCTCCAGTTCAAATG CTTGCACTCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCA CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGCCACCATAGCCACTCTGCT TCCTGTACATAACGCCGCTTCCCTGGCGTACAGAGATCCTTGCCCTT
WI-8054c	237	GT ---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCTCTTTC/TATCTCTCCAGTTCAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGCCACCATAGCCACTCTGCTCC TGTCATAACGCCGCTTCCCTGGCGTACAGAG(GT)AATCCTTGCCCTT
WI-8054b	148	TC ---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCTCTTTC/TATCTCTCCAGTTCAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAGCACAA TCTCTTTGTAG(TC)TTAGCCCTTTTCCGGAAATCGGCTTAGTTTGCCACCATAGCCACTCTGCT TCCTGTACATAACGCCGCTTCCCTGGCGTACAGAGATCCTTGCCCTT
WI-8054a	131	CG ---	---	AAAGATGACACTTAGAACTGGATCAGTGGCCCTTTCTCTTTC/TATCTCTCCAGTTCAAATGCTT GCATCTTTAATAGCCAGCATTCTCTTAGATCTGCAGTTGGGCTCAACGCACTCAAGCCTTAG(C/G)A CAATCTCTTTGTAGTTTAGCCCTTTTCCGGAAATCGGCTTAGTTTGCCACCATAGCCACTCTGCT TCCTGTACATAACGCCGCTTCCCTGGCGTACAGAGATCCTTGCCCTT
WI-10854b	152	GT ---	---	TTCCACAAAACCTCCCTGGCCGGGTGACTAAGATGAGAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACACGAGACGATAGTTAACGTCTGGTAAGTTTAT ACGGTGTGCGAGGCAACA(GT)GGAGAGGTACGGGAATAGTTCTACTTCTTGTGTTTTTATTCTTGIG TTTTAGACACAGGGTCTGCTGTG
WI-10854a	102	CT ---	---	TTCCACAAAACCTCCCTGGCCGGGTGACTAAGATGAGAGTGGGAGAACTGGATAGTTTAAATAA ATGTTTATATTTTACTTTAAAGCGAAGTTGAAACA(C/T)GAAAGACGATAGTTAACGTCTGGTAAGTT TATACGGTGTGCGAGGCAACAGGAGAGGTACGGGAATAGTTCTACTTCTGTTTTTTATTCTTGIG TTTTAGACACAGGGTCTGCTGTG

WI-9826b	127	G A ---			AATTTATATGTGAAGGTTAGCAAACTATGCCCCACAGGCCCATTTCTAGCCATGCTATTTTGTG TGCTGATGGCTGTTTGGTGTGTTTGCACGAGTTGAGCCATTGTGACAGAGGCTGTTATG/AJGCCTT CAAAGCCAAAATAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGTGATTTCTAGATATTTAA GGCAGAGAAGATCAGAAGTGTGAA
WI-9826	125	A T ---			AATTTATATGTGAAGGTTAGCAAACTATGCCCCACAGGCCCATTTCTAGCCATGCTATTTTGTG TGCTGATGGCTGTTTGGTGTGTTTGCACGAGTTGAGCCATTGTGACAGAGGCTGTTATTTGGCCTTC AAAGCCAAAATAAATTTACTCTCTGGCCTTGACGGGAAAGTTTGTGATTTCTAGATATTTAAAG GCAGAGAAGATCAGAAGTGTGAA
WI-15986	60	T G GTGGGTTTT	TTGTTTGTGT	TGACATTATAT AAACGTAAAA GAAATGT	CGGACACGTGTATACAAATACAGATCGTATGGGTTTGTGTGGTTTTTTTTTTT/GJTAC ATTTCTTTTACGTTTATATAATGTCAGCATTTCAA
WI-8655	29	A G AG	AACTGCAAAAT AGGAAACCAG	CCACTGGGGC TCCC	TTCAAGTAACTGCAATAGGAAACCAGAG/AJGGGAGCCCGGTGGGACAAATCATGGCTACCCC TCCCCAACAGAACAGGGGAGGAGGTGGCCCTACACCCCTTAT
WI-8170b	259	G A ---			GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGTAAGGTTAG CATTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCCATCAAAAGTGCAATCCTATCAATCAGAA ATAAGGTAAAGGGCCCTCAATGAATCTACGGGAAACATAACACAAGA
WI-8170a	204	T A ---			GCACCTCTCTCTGAGCAACAGGTACACTTTTTTCTCTAACATTGATCTATAACACACCAGAACCG TGTTTTAATAGCTGCTGATAAATGAACCTATTTTAACTACTCTACCAAGATGCTGTGTAAGGTTAG CATTGGTGGAGAGATTTACAAGGTTAAGATCATGTGTCCATCAAAAGTGCAATCCTATCAATCAGAA AT/AJAAAGGTAAAGGGCCCTCAATGAATCTACGGGAAACATAACACAAGA
WI-8172	136	C G GACA	CCTTTATTAAA ATTGTTTTCTT	GAAGAGAAAT GTAATACCTGT AAAGGTAC	CAGGATTCCTTAAGTCATCTTCCATCTCCAGGTACATGGTGAAGAGTCACCTGTTAAACACGAA ATCTAACCATTAACAAGCTTTTAAATCCTTCGGTAACCTCCCTTTATTAAATTTCTTTCTTGACAT A/C/GJAGTACCTTTACAGGTATTACATTCTCTTACCGTTTACA
WI-8183	56	G A TGC	TGAAATAAAA ACAAATTTCTGT	TGTGTTGAAAT CAAACCTGC	AGCAGGTTTGAATTTGATCCCTTATTTACATGAATAAACAATTTCTGTGTC/GAJGCAGGTT TGATTTCAACACAGTTGAATCTGTAAACCAAGCTGTTCTGTATGCAGGACAAATATCCACAAT ATTTAAACTGCAAGCACCATGC
WI-14149	83	CT ---			GCTTTATTGGGATTGCAAGCGTTACAAGGTTAAAGACAAAACCCCAAGCATGGGATTTGCCGGAAAT ATTAGCGTTAAAGGAG/CJTJGAGTTGAGTCAACACCGGG
WI-8712	44	G A G	CACAGGGAAG AGGTAGTGGA	CAGGAAGCCTG ACCATCTC	TCAACAATGACACTGTGTAAACAGCACAGGGAAGAGGTAGTGAG/GAJGAGATGGTCAGGCTTCCTG TTCCTTAACCAGCAGAGCCCGCAGCAACCTAGAACGCGCTCACCTAGCCTCTTAAT

WI-8827	22	C	T	TCCTGGGAG TTAGTGTTCAC	GCGATTAGGAT TTAGTGTTCAC	GGTGCCCTGGGAGACTATGG[C/T]AGTGAACACTAAATCCTAATGCCATGCATTGGAATTATT CCGACTATTACTTTCTTTAGTTCCTTTCTTATCCACCCAGTCTTCT
WI-8833	51	A	T	TCCTCCATGCC ATTCTCTG	CCTCACACATT ATAGGGGCA	CTCCGGCCTTTAAAGCTCTGTAGACTGTCTCTCCATGCCATTCTCTG[A/T]TGCCCTATAATGT GTGAGGGTATTACAATAGTCCCTATTCAAACTGCCCTGTGCATAAAAGGTCAAGCTATGT
WI-8377	63	A	G	GGGACTTAAC CTTTGGCCT	--- CAACAGCCA GGCAGG	ATTTTTAGCCATGTTGGTAAAGTTCAATTTTCAGTACATGGGTAAACACCCAGGCCCTTTCCCA/GJT TATATCCAGGTATGCTACAAAGTTCTTTAACTCTTATCAGAAGTTATTATTACTGTTTCCCTTAGAGAG GCTACCAAGGCTAAATTCACCTTAGTTGGTTGTCTAATGTCTCATTATTTATCCTGAAGCTCGTG GAGGACTTAACCTTTGGCCTTAGCTGCTGGCTGTTGGCTCTGCGCTGCTGTTTTTGGTTTCTT TCTCTTCTACTGGTCTTTCTTTGCTTTGCCAGCCACTATGCTGCTGT
WI-8850	21	A	G	CCCGGGCATTG AGGATA	AGTCTTCTGA GCTTCCAT	ACTTTTCTTGAGCTGAGCAACCTCATCTCTTTAGCTTCTGTTGATAACGCTGTTAATCCCGGG CATTGAGGATA[C/T]ATGGAAGGCTCAGGAAGACTTCTCTCAA
WI-8853	79	C	T	--- ---	--- ---	AGGTGACTGGAATCACAGGCACAGACTGAGGAAGACAGTCATGGTGAACA[A/G]JACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCCATATAA
WI-8865b	52	A	G	CACAGACTGA GGAAGACAGT	GGTAAGTCCGA AGCATGTTG	AGGGTGAAGTGAATCACAGGCACAGACTGAGGAAGACAGTCAT[C]GGTCGAACAACAACATGCT TCGGACTTACCAAAGGGAGAGTCGAGCTTTCCATATAA
WI-8895	32	A	C	--- ---	--- ---	GTGCCACAAACCTGGACACCAACCAACAGAAAT[C]CTCCCGTCTTTGAAATTTCCATTAAAGACA CAATGGGGTAATTATACCAGGGATGCTCCAATCGCTCTTC
WI-8456	93	G	C	--- ---	--- ---	CCTTTAAAGTCACAGTCAACTCGACTGTGGACTGATATATTGTGAATATAATAAACTCTTTCC AAGCTCCCATGCTTGGATGTCACA[G/C]TTATGTCAAGTTAATAAACAATTTCTAAGTCTCACTC TCAACTTCTGTGTTATCTTGCCATGGTCCAGTAACAGTTACACGGCAGACCAAGTTGTGTAGCAC TGGCATAGACGAGGGCTTCTCAAACTCCCGTCTGGTCTCAGTCACCCAC
WI-8496b	157	A	G	--- ---	--- ---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAAJGGTAATGTTGTATCAGTGCATATTCTAGAAA ATTATATCTCAAGTAAGTAACTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAGTCA AAGACACAATGCTGCCAATGCA[A/G]TTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTCT GTGGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-8496	41	G	A	--- ---	--- ---	TTTCATCATCAAAAGTTTCTTTCCATAGAAGAAJGGTAATGTTGTATCAGTGCATATTCTATGG AAAATTATCTCAAGTAAGTAACTAGCCTAGAAATCAGAGACAGCACTATGTCAAGCTAGTATACAAG GTCAAAGACACAAATGCTGCCAATGCAATTAGTATATAGAAATAATACGCAGCTGTTAGAAAAAGTC TGTTGCCAAGTGGGATAAAACAGTAGCAGTGCAC
WI-14153	28	A	G	GTGAGGAAG GCCAGC	AACGGCAGGA GGGA	CTGCAGGTCTATGTGCAGGAAGGCCAGC[A/G]TCCCTCTCGCGTTGTACCCACATCCACAGAGCA GCCCTAGTCCAGGTGCAGCCACTGCCACCCAGGCACACGGGAACAGGACCCATGCTGC



WI-12108	40 C T	TGAAAGGG TTAAACTCAA ATA	TTGACCTGGTA TAATGAAAGT ATTTC	TCATGTATTACTTTCTGGAAAGGGTTAACTCAAATATC[7]GAAATACTTTTCAATTATACCAGGT CAAGAAAATGCCACAGCCAGAAAATTTATTTTAA
WI-5989	29 G A	CACAGGCA	GGGTATAACAG AACCGTATGTA CG	CAGGCAACGTCACAAAGGTCACAGGCA[G/A]CGTACATACGGTTCTGTATACCCCATATATTAC CCCTTCATGTCCTAAAGAAGACATTTCTCTTAGAGATTTTCATTTTAGTGATCTTTTAAAAAAAT CTTGTTAACTTGCCCTCATCTTTTCTGGTGAGGACACC
WI-12201	61 C T	CCTGTCATG	CCGACCACATA CCTGGC	ATAGICTTTTAGCCCTTTTCTGGAGTGTATGTCCCAAGCCCACTGATCACCTGCATG[C/T]GCCA GGTATGTGGTGGGTGATGACGTGGTTTGAGCCCTCCACTGCTCGATAAAAGGC
WI-12018	31 A T	TCTGACTT	GGAGAGATGAC AGAAACAGAG AG	TTTTATCTGTCAAGCAGCAGCTCTGACTT[A/T]CTCTCTGTTTCTGTCTCTCTCCCCACATACCA ACTTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATAGGGGCTCTGGAAAATTAGAC AGTGAAGCATGTTGCAG
WI-14162	57 A G	CCTC	AGGGATCAA GAGAAAGGC	TTTTCGTTTGTATATGATCCGAATGCTTGAGAGAAACCTGGCTCGCTGCCTC[A/G]GCCCTTTT CTCTTTGATCCCTGAGTTGCTGAGATTAAAGATGAGTCCCAATGAGAGCTACCAAGATGTAGTCG AGCG
WI-15407	92 A G	TT	TCTTCTCTT TGAGTGTGG	AGCATGTAAGGAGCAGTTTATTGATTGGTATATTCAAGTTTCTAACCAAGCTGAAAATTCAAATA CATGCCCTTTAAGGATTAAAGTTTAA[G/C]CCACACTACCAAAAGAGAAAGATTTATATGATCACAT ATAAGCAATGGAATCAGCA
WI-12319	109 T C	AATT	GGAAGGCTG GTACATATTGG	TCTGATGTCAATTTATTGGCACAAAATTTATTCTGATACACATGGTGTCTAGACATGGCTACACTTTA TACTTTGTGCATTTAGTTGAGTATTGTTCTGCTCATAATTT[C/C]CCAATATGTACCAGACCTTCCC
WI-12326	25 G A	CA	AGGTTTGAAA TATGTATTAAG TACTTTGT	CTGACAGACTTCAAAGCAATTCAC[G/A]CTTCCAGAAATACAAAGTACTTAATACATATTTTCAAAC CTGTTTGCAATTTCAAACAAAGTTAGCGTTTGTAAATCAAAATTTGATAACCCGACTAAAAAT
WI-12361	63 C T	---	---	TAAATTCACACTGAAGATCTGGAGTATGGGGGGATATAGGAATTTCAAGCATATGTATTAT[C/T] TGAACATAATTTACAAAAGTGGAACAGTTGGAAGTACTTATAGGTAGACCTGAGGGTCTGTACC
WI-11305	87 C T	ATCACACCA	GACCTCCCGT GGC	ATACTGGTTTAAATCCATGTCAATGTAGTTTACAAAGGAAAGGACAAAGTACCTTTGTATAGAATAT ACAGACACAGCATCACACCA[C/T]AGGGCCACGGGAGGGTGGGAGACGACACTTTTCCCTGGG AAAGG
WI-11321	67 A G	TTTT	CATTGGGGAAT AGCTAAACCTT	ATTTTATATGAAGTTTCTGGTGAATCTTTTAAAGCAGGGAGGAAAATCCAATAAATTTTTTAA AGJAGGTTTAGCTATTCCTCAATGCTATTTAATACAATTGAGGTTAGGACGTTAAGTCTTATCAGA CTGTGACTGGAGCCCCG
WI-11324	40 C G	TGTGCCCA	ATCAAGCTTTG GGCTCT	AGCATACTGCATCTCCTTTATGGATAAATCATGTGCCCA[C/G]AGAGCCCCAAAGCTTGATGACAT TCTGTAAAGTTACACAAATGTATCTGAAGAAGTTATCTGTCTTGTCC

WI-11352a	69	T C G	AGCACAGCAC ATAGTGGAAA	GACCTCTCGTA GGACACTTAGC	TGACACATGGTTCTGTTTCCAGAAGGAGAGAGAGTCACTACATAAGCACAGCACACATAGTGGAA AGT[C]GCTAAGTGTCTCTACGAGAGGTGATCATATCCATAGAAAACAGCTCTCTTTTACTTTGCA CACTTA
WI-11371	84	C T G	CAGCTTGGAG ATTCTGATTCA	GCCCCGCTGA GCAC	TTAGCCCATGCTGTCATTTCGCAATCACCTGTGAACCTATGAAACTATACCTGCCAGGCTCAGCTT GGAGATTCTGATTGAGT[C]GTCCTCAGGGGGCTGGACATCCATGTTTGGGAAGAGTTGCGGGGT GATTCGATGCGTATAT
WI-11385	75	T C G T T T T	ACAGAAGACT TTCATATTCTT	GATTCATTCT AGTCATGGTCA TATTTT	CTTAAAGCATTATAGTTGGCCTGATGGTGACACAGAAAGACTTTCATATTCTTTGTTTTTAAAGTC TCTTCAGT[C]AGGAAAAGGTACAGATTTAAAATAATGACCATGACTAGATAGAAATCAGC
WI-11388	88	C A A A G T T C	TGTTTGAAATT ACACGTAAC T	TGCTTGTATC CAAGTTAAAT T	TCATGTGCCAGTTAGCTCAGTTGGTTAGAGTGTGGAGCTCATAAAATAAAGAATGAATGTTTG AAATTACACGTAAC T AAGTTC[C]ATTATAATTTTAACTTGGATACAAGGCATTGTTATGCTAAT
WI-11392	55	T G A T A A A T A C	GGTTATGTGT CTTGAACTTTA	GTACATTACG TGTTTTGTAAA AAG	TTCTATCATTCATTAAAATGGCAGGTTATGTGTTCTTGAAC TTTAATAATAC[T]GCTTTTTTACA AAACACGTGAATGTACTTTCTTGTGTCAGAAAGGGGAACACTGAGTCTCCGCTCTAGATCCATTAACTGT CATACTCTTCCCCAGA
WI-11396	52	A T T	TTTGTGTTTTG AAATGGTGT T	AGCTTATTTTC ATATTCACCCA TC	AAAGATAAGATGGCATTTGTTTCAGTTAATTTTGTGTTTGAATGGTGTGTTTATGATGGGTGAATA TGAAAATAAGCTTACCTCATCCACTCTAAAGGTAGTTGGTGAATTTTGAACCGTTGTCAAT
WI-11441	100	C A C A G C	TCCCCACCAAC CAGC	TGCCAGGGCCT TATTTG	CTGTACGTCTTCCCAGCTAAACCGTGAGTTCAGTATGTCTGGCAGCACGTCTGTCTTCTTGGTG TATTTCCATTACTGAATCCCCACCAACCAGC[C]A]CAAAATAAGGCCCTGGCACAAAAGTAAGCTCTCC ATTTTGTAGATGAAT
WI-11466	26	C T T T T A T T T T G C A	TGAGAAGCCA T T T A T T T T G C A	GTTTATTGTTA TAAAATGAC CTACAAC T T	ACTTTGAGAAGCCATTTATTTTGCAG[C]T]CTTCAGTCCAAAAGTCAACATTTTCAGAAATTTTT TATATAAGTTGTAGGTCAATTTTATAACAATAAACTTTCTATTATCTATTTATCTCTCACATACATTT CATGTATCCTG
WI-13364	35	A G ---	---	---	TTTTCTTTTGTGCTCTTTT TTTTAGTAGAAGC]A/G]GGAACAGTTGTCAATACTACCTTCTGTG TCCCCTGTTAGACAACATACCTTTCTTTTGAAATGTAAAATGTCA
WI-11276	41	A G A G C A G A C	GGCAGCCAGG AGCAGAC	TGTA CTGAGGA GOOGGTG	AGGCAACACTGCTTTATTAGGCGGGGAGCCAGGAGCAGAC]A]G]CACCGGCTCCTCAGTACACATT CCCCACCCCTGCCCTCGGTGCTCCCACTCAGGGCTGGCATGGAGGGGCGCAGCGTAGGTCGGAA
WI-12210	76	A G A	ACTGGGAAA CAACTATTGC	TGCTAGTTTGC ATATGTTTCC	ATTGGAAACAAC TTAATAATTTGCATCTCTACATATAGAAAGCTGCTTTGAATAACTGGGAAAACAA CTATTGCAT]A/G]GGAAAACATATGCAACTAGCATCATTGTCTCTAGA
WI-14186b	88	A G ---	---	---	AATGGTCTGGTTTATTGAGAAGCTGTTGGTCA TTTGATGGAAAGACACATACGGTACAAAATTACA GGTGGTTAGTTCATTACATG]A/G]TACAAATCATTAGAGTCTTTACAAAGTCATTAGAGTCTTTGGAT TTT

WI-14186a	52	C	A	GGTCATTTGAT GGAAAGACAC	AACAAACCA CCTGTAATTT GTACC	AATGCTCTGTTTATTGAGAAGCTGTTGGTCAATTTGATGGAAAGACACATA[C/T]GGTACAAAATT ACAGGTGTTAGTTCAATACATGATACAAATCATTAGAGTCTTTACAAGTCATTAGAGTCTTTGGAT TTT
WI-12234	66	A	G	GAGAACACTT GTGGGGCTT	GGACCTATCAG TCCATGTTTGA	ATTTTTTTTGGCTATAGGTCAGTGGTTCTAAACTTGAGCTTGCAAGAGAACACTTGTGGGCTT[A/ G]TTCAAACATGGACTGATAGTCCACCCAGATTCTAAGTGGTGGTGGTG
WI-12345	37	C	A	GTGGCAGGAA AAAGAGGAA	TTGCAGAGGGG TTCAGG	GGAACAGACCTGATCCACGTGGCAGGAAAGAGGAA[C/A]CCTGAACCCCTCTGCAAGTATTCTCT TTCCTGACCAGCTGGGCTTGCGCACTTTGTGAGATTGCAAAA
WI-13416	71	C	A	AAATTTTGG AAGTTTTTCAG AAA	AGTGTATATAG TTCAATGAATA ATTTCAA	GAAAGGCTGTAATTTTAAATTTTGGAAAGTTTTTTCAGAAAAAATAAAATGACAAGAACAA CATA[C/A]AAATATTGAATTTATTCATTGAACATAAACACTTAGCAGAGGAAGGACTTTTGAT
WI-12310	46	G	A	TTATCCCAAG TATAATTTTA AAAAGC	TGTTAAATAT GTTGGTCTT AAA	TTGAAAAGATGCTGAAATTTATCCCAAGTATAATTTTAAAGCT[G/A]TTTAGGACCCAAACATA TTTAAACATCTCTTACACATACAGAAATTTTCAGTTTACAATATTCAGAAAGGCATTTTCTTAAGCAG T
WI-12086	72	C	T	CCGGGAAAC TTGGATT	GGAGTCTCGG GTCTTGG	GAACCGAGCTTTATTGGAGCAAGAGTGTGGACACTGTTTACAACAAACGTTTCCGGAAACTTG GATT[C/T]CCAAAGACCCGAAGACTCCTCCAAGTTCTCACTGTAGTAAGTCAATTTGGGGCAGA ACAGGAACATGCCTTAGCT
WI-11549	102	T	G	GGCATAAAGT TCATAATATTC TTTTATG	GGAAAGTCTGT ACAAATCCCC	ATGCTTTCACAGGTTGATTTTGTAAAGAGTTTGTCTATCTAAATTTTCATATTTATGGCATAAAGT TCATAATATTTCTTTTATGATCTTTTAAATATCTG[T/G]GGGATTGTACAGACTTTCCCTC
WI-11585	79	T	C	TGGGTTTGCAA AAACAAA	CCATGCTTCAC TGATACTTC	TTAGAGGAAAGAAATAAAACACCGGTAATGGGAAATCAGTTCAGAGGTAGGAAGGAGCTGGGTT TGCAAAACAAAAT[C/G]GGAAGTATCAGTGAAGCATGGCCTAGAACTCAAGAGCAGGGGTAGAGT TT
WI-11604	68	G	C	---	---	TTAGTTGGTTTCCCTGAAACTTTATGCTGTTTATTTTAAACCAATAGGATGTTCCAGTTACCAGCATTT G/C]AGAACTAGGGACTTTTCCATGAAATATTAAGAGCTAAGGAATTTCTGACGCTCACCATTTC TTGTACTCTGCAGT
WI-11614c	108	C	A	---	---	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTGAGGCAT GTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAAI[C/A]ATATAAGTATTCGTCAGCTAG GGACTTCGT
WI-11614a	60	A	G	CCAGAAAGACT CAGCTGCTTG	AGGGTGGGAAC ATGCC	CAAAATCAAAAATTGAGGAGGCAAGAACAGAAAGTAAATCCAGAAAGACTCAGCTGCTTG[A/G]GG CATGTTCCACCCCTGGACTTGCCAACTTTCACTGTGAAACTGCAACATATAAGTATTCGTCAGCTAG GGACTTCGT
WI-11626b	83	T	C	---	---	TTGATTTTACTAAGGCTTCCACTGGAACATGAAGGTAGGGATAAGTGTACAGGATAATATACTCAG ATATTTTAAATAAA[T/C]TACTTAATAAAGAAATTAGCCATACCACATTGTTCCATTGCTAG AAGAACAATTGGCAATGA



WI-11626a	39	G A G	TCCACTGGAA CATGAAGGTA	GTGGTATGGCT AATTTCTTATT ATTAAGT	TTGATTTTACTAAGGTCTTCCACTGGAACATGAAGGTAG(G/A)GATAAGGTGTACAGGATAATATACT CAGATAATTTTAAATAAATTAATAATAAGAAATTAGCCATACCCACATTTGTTCCATTTGCTAG AAGAACAATTTGGCAATGA
WI-11627	23	T C	CCTTTCCTTCC ATTGTCTCTC	CATTTGCAACC CATCTCAAG	ACCCCTTTCCTTCCATTGTCTCT(G/C)CTTGAGATGGGTGCAATGGGAAGTAAAGCAAAAAGGG AGATGAGAAATACTGATGCCTTTTGTCTGGCTTACTTCCATTCGCATGTCAAGTCCATCCATG
WI-11636	61	A G T C C T	GGACTTAAAA AGATCTGCTTA	AGAAACTTTGCT AAATAATTTTAT GTAAACACT	TCAGAAATGTTGCAAGCAATACTATTGTAAAGGTGGACTTAAAAGATCTGCTTATCCTT(A/G)TA TATCCACATAACTCTAGTGTACATAAAATATTAGCAAGTTTCTGTGACAGGTGCTCAGTAAACAC TTTGACTCCTTTTGGTA
WI-11637	119	C G T	ATTGCTCATCT TACTCTGACCA	GACCCAGCAA AAAGAATGAT T	GTACCAATTTCTTATGGTGGCAATAAGCAAACTGTGAGTAAACGAGGGCAGCTGAATAAATTTACAG TATACAATATTAGAGAATATTATGTTGCAATTGCTCATCTTACTCTGACCATTC(G)ATAATCATCTTT TTTGCTGGGTCCAGGAOC
WI-11654	37	G C C T G	GCCAAAAGAC TATTCAGCAA	GGCTCTCCAG GACAGTTT	AGTAGAACATCAGTGCCAAAAGACTATTTCAGCAACTG(G/C)AAACTGTCTGGGAGAGCCACTCCAG AGCTATTTCTAAGACTTTCTGTGGTGTTCATCTACTCTCAGAGTTTCACACTCATATTTTCATATTTT ATTTTGGGTGTTGGGT
WI-11656	28	G A A A	ATTGATTTTAG AAGGAACTGC	CAAGGCTTGT CCTCAAGTAAA	ACCTGATTGATTTTAGAAGGAACTGCAAG(A/G)CTTTACTTGAGGACAAAGCCTTGCTGCAGTTGTTT AAATGTCTGAAACAATCAGATTTCCAGCCTGGAT
WI-11680	55	T C ---		---	ACAGATACTTTTCCACGGCAACATTTCTGAAATGAAGCTTTGATTCTCCCTTTT(G/C)TTGCATAAA GGCTGGGAAGGTGGTTTGGCCAGACCGTACATCTTTT
WI-11696	47	T C	TTATCACAGC AGGGGACAG	GGCATTAGAGA AGCCAACTT	GTCCAAGAACAAAGATACTTTGACATCTTTATCACAGCAGGGGACAGT(C/J)AAGGTTGGCTTCTCTA ATGCCCACTCTTGTGTTTCAGAACTCTTCCACTTCGCC
WI-11702	69	C T C A G C A G	GAATAATACT GAAATAACCA	AGAACAACCT AAGCAAAATTAT ACTGAAA	TTACATGTGTCAATGGTGACATACTTTCAATAATTAATAAATCGAATAATACTGAAATAACCACAGC AG(C/T)TTTCAGTATAATTTGCTTAAGTTGTTCTAGAAACACTGCTAATTTTGTTCGTCAGAG
WI-11706	60	C T	TGGCTGGAATT TTCTCTTCTT	ATCACCAAAG AACAAATTCCA	TGCTGATTCAGCTTCTACCATCTGGCTGGAAATTTTCTCTCTTGTGTACAATTTATTG(C/T)GGCTG GAATTTGTTCTTTGGTGATTTGTCCCTTGCTGCT
WI-11709	105	T A	AGAAGCTTGC TTCAGTTTGC	TCATTTCTTCT AATTTACGGG A	AATATCATCTCATATCAGGCATGTTTATAAAAATGAGAGATTATGTCTTTTGGCATACTTCATC TTCTTCAGGACACAGAGAGAGCTTGCTTCAGTTTGC(T/A)GTCCCGTAAATTTAGAGAAATGAAT GGCCAGATGGATGGAAA
WI-11710	103	C A C A G I C T T C A	GCACCTAGCCT CAGICTTCA	GTGTGGAGGAG GGAGGAG	TTATTACCATCAACCTGTCCCGAGCTTTCCAGCACAACAGCCAGCCACACTCTAGACAGCCCTTCAC TCCAGTCCATTCTGGCACCTAGCCTCAGTCTTCA(C/A)CTCCTCCCTCCACACACTCCTTC

WI-11715b	123	C T	AGGCTGGCTGC AGCTT	TCCCATCCTG TGGCT	AGAAATGGAGCTGTTGGGAGGGAGCATGCACACAATGTAAACAGACAAATGCATTACAACCTGTGG TGTAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGCTGGCTGCAGCTTCTJAGCCAC AGGATGGGACTGGGGAAGA
WI-11715a	49	A C A A A	GCACACAATG TAAACACAGAC	CATTACACCAC AGTTGTAATGC A	AGAAATGGAGCTGTTGGGAGGGAGCATGCACACAATGTAAACAGACAAJNCJTGCAATTACAACCTG TGGTGTAATGTGGCCACTATGAATCCCTATGTATAGAGGAAAGAGGCTGGCTGCAGCTTCAAGCCAC AGGATGGGACTGGGGAAGA
WI-11727	43	G C T C A A C A	AACAATCCTT AAACAACATA	CCTGTGGTTG TGTTGCAG	CTGGATTCCTATACCTAACATCCTTAAACAACATATCAACA[G/C]CTGCACACAAACCACAGGC AAATGAAACACAGATGCCCCAGACAGCAGCAGCCACCATGGCACACAC
WI-11728	16	C G ---	ATCTGTGGTTT ATCGCTG	---	TTTTATTATCAAACT[C/G]CAATTCCATTTCACAAATGTAAGTTATCATCAGCTCCCCATCCACTTT CTCCCATCTTCTTATCTCTTCCACCCCTACACTTCTCTCCCTACACCCGGGTTCCAAA
WI-11758	61	A G T G C C T G	GCCTCACAAA GTATTTTCTAA	TGATTGGCOCT GTGGTCTA	TTTTCTCTCTTTTAAAGTCGCTATACTAACTAGAAAGGAGATCTGTGGTTTTCGCCTG[A/G]TAG ACCACAGGGCCAATCACACAGCTTCTGTAGAGAACATGGAGAGTGCCAAAGATCACCATCA
WI-11295	37	A G A A T A T A A	GGCTCACAGA GCAAGGGAA	AAAGTGCTCA TCTGTGAACCTC T	CCGGCCTCACAAAGTATTTCTAAATATAATTTGCT[A/G]TAGAGTTCACAGATGAGCACTTTTCA CATTAGGTGATATGCAACAATCACTATTGGCTCAGCAGGAAACAGACTTTT
WI-11773	93	T C ---	GGCTCAGAGA GCAAGGGAA	---	AGCACATGATATTCTGCCTGGAGTTTCTGTAGCTCAGCAACAGCAGAGTCAGAGATTAAGAAAT ATTTATTGCCCTCCTTTTTTCCCCCT[C/G]GTGATTGTTAATTAGGGAGTCAAGGCCAAGTTATC
WI-11282	42	C G G C A A C C T C T G	CCCAACTTACC AAACCTCTG	AAACTCAGA CTGTAAATTTT GTGTG	CATGACAAACCTCTTTATTTAATGGGCTCAGAGAGCAAGGAA[C/G]ACACAAATTTACAGTCTGA GTTTGGCGCAGAGACCCCTCTCCACCTTTTTCATGCTGTGTGTACACACACACTGTCCAAGCCTC AGA
WI-11790	28	A G A A C C T C T G	TCATCTAATCT GTGAGGTATTT	CGTAGGCGAG GCTAAGC	TAATTCACCCAACTTACCAACCTCTGT[A/G]GCTTAGCCTCGCCTACCGTACACATGCTCAGAGCAC TTACATTAACTACAATGGGCAAAATCATCTAACACAAAGC
WI-11879	61	C A A G T A T A C A	GTGAGGTATTT AGTATACA	GATAGTTGAAC CTCTTCACTTT ATAAAA	TTTTAATCCCAAAGCTTACAACCATCTTTTCATCTAATCTGTGAGGTATTTAGTATACAG[C/A]AGT GATTTCTCTCTTCTTTTATAAAGTGAGAGGTTCAACTATCCAGACAGTCCCATCTA
WI-12469b	91	C T A A G T T T A A A	GTTTTTAATGT GGTATTAGAA	CAATTTTCAGA TTGTCTATAGC AAAC	TTTACTAATTTCCATTCTCCCTTTTATAGTTTTTAATGTGTTATTAGAAAAGTTTAAATTACAT ATGTGGCTTATATTCTATTCTA[T/C]TTTGACAGCACAGTTCTTCAAGTTTGCTATAGACAATCTGA AAATTGGGTTCTGAAC
WI-11906	52	A G A T C T G A A	TGTTATAACAT CAAAGAAAGA	TTAATTTCTGC AGTTCCCTCA	ACATTTGAGTAGGAATGACTTTGTGTTATAACATCAAGAAAGAAATCTGAAT[A/G]TGAGGGAACCTG CAGAAATTAAACTTTCAGTCTAATCTCAGAAATGCCAGAGTAAGATGAACCCCTTTACAG

WI-11909	78 A G	TTTGTGTTGGG TGGTCAAG	CCTCTCTGAG ATTTTCTGAAT AG	GCAGTTCTCTGAAAGACAATGGATTGTGGAGCATACTGAAGACTATTCCTAAATGGCTATTTGTGTG GGTGGTCAAG[AG]CTATTAGAAATCTCAGAGGAGGACAAATGATAGTCACTGCAGCCAGCTCG GACTGGCTTGCAAGAGTC
WI-11806	60 T G	CATGAAGAGT GGCAGTTCA	TCCTGTAAAGC CAATTTTATAT ACTAATAA	AAAAATACCATTTAGCATCAATTTGCCCAAGTTTGGCAGGCATGAAGAGTGGGCAGTTCA[TT/G]GTT TTATTAGTATATAAAATTTGGCTTTACAGGAAGCATTATGG
WI-11946	31 C A	---	---	CCCTAGTGAATACAAACCTTTTGTCTCTGGAGAC[CA]CCAGCTAGTCTAAGAAACTTCCTAGGCTGAG CTCTCTTGGGAATCTAAGATAAAGAACTGAGATCCTCTGGGAAGAGGAA
WI-11965	65 T G	TGAAGATCAG ATCTCTGGTTT ATTT	CAGCTGTGGTG AATGTTGAT	ACAAAATTCACAAGTACAACACTGCTTATTTTCTTGCTTGAAGATCAGATCTCTGGTTTATTTAA[TT/ G]ATCAACATTCACCACTGAGCTGAAGAAATTAACCTGAACCT
WI-11027	90 T A A	TGCCCTACTAC GCTTTTAAAA A	TGAGGAAATGT GTTACAGTATT TTTATT	ACCTATTTTGAACCTGCAGAAAGGGCAGGACAAACAAATCATTCTCATAGATTTTCTGGGAAATAT TGCCCTACTACGCTTTTAAAAA[TT/A]AATAAAATACTGTAAACACATTTCTCTATTTCTTTACGA ATACTTTCTTTTGATATTGCAAAATTTCTATGGCATACAGAGGCACCTCCTCAATGCCCTG
WI-11049	95 C T	---	---	TTCTGCTGAAGATCACAACAAATTTCAACCTCTGTGTTTCAAAATAATTTAAGGATCTTGTACCTTT GTGTTTATTTTCTGTTTCAACTAAGGA[CT]AGACTTCAGAAAGGCATAGCTTCCCTTGTAAACGTTTTT AAACATCTTTTTCATTTGTAGGAAGGAACATTTTCAAAAGCCCAA
WI-15488	69 C T	AAAAGGACAG CCAGATATCA AC	TTTCCATCTTA TTTTCATTTCTG TAAC	CAACATTTATCAACATGGTAGGAAAGTTTCTCACTCTGCACCTATAAAAGGACAGCCAGATATCA AC[CT/]GTTACAGAAATGAATAAGATGGAAATTTTAAACAAATTG
WI-13654	49 A G	AACAGTTAAT GAAACACATC CGT	GGCTGGTGAAA TGATGTCAT	TGCTCAATTTAATGTGATAATCTCCAACAGTTAATGAACACATCCGTA[AG]GTATGACATCATTT CAACAGCCAGCTACTTCATGTGGCAGAAAGGTAACTTTTCCCATTTTACAGACAAACCCAGT
WI-11070b	135 C T	---	---	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATATGGAAAGGAGCTAGGACAAATTTCTTGCTT TCAAGTAAATTTGTGACTGAGCAGAAATCAGCCAGCTATCTTGGGTGCAGAGAGGTACTCCAAGTA C[CT/]GTGGGGTTCTGATGACTTCCACGGTCACTGGGATCCAAACAGAGGGAA
WI-11070a	110 G T	CAGAAAATCA GCCAGCTATCT T	TTGGAGTACCT CTCTGCACC	ATGAGACCCCTGCTTTGAACGTTAAACGTTTGGAAATATGGAAAGGAGCTAGGACAAATTTCTTGCTT TCAAGTAAATTTGTGACTGAGCAGAAATCAGCCAGCTATCTT[GT/]GGTGCAGAGAGGTACTCCAA GTACCGTGGGGTTCTGATGACTTCCACGGTCACTGGGGATCCAAACAGAGGGAA
WI-12020	121 T C	---	---	AATCTTTTATATTTCCAGCTGTTGAGACAGTATTTTGGGGCTGATGTTACCTCTAGCGGCGAAACC AGAGCCAGCTATTAGCAGCCAGAAAGCTACAGTAATTGAATACATGACCATTT[CT]CTCTTTTAGC ACGTTCTTTGTTCTCCTC



WI-11076b	142	G A ---			CATGGTTCTGCCAGCTTACAGGAAGCATGGTCTGGCATCGGCTTATCTTCTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCAATGTACATACCCAGAGCAGGAGAGAGAG AAAGAGAG[G/A]AAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-11076a	106	T C AGGCA	AAGGGGAGC	TCCTGCTCTGG GTATGTGAC	CATGGTTCTGCCAGCTTACAGGAAGCATGGTCTGGCATCGGCTTATCTTCTGGGAGGCCTCAGGAA ACTCTGAATTATGGCAGTAGGCAAGGGGAGCAGGCAATGTACATACCCAGAGCAGGAGAGAG GAGAAAGAGAGGAAGTGCCACACATTTTAAATGATGAGTTCTCTCAAGGAACCTCACTCACTGTCAT G
WI-14263	49	T C GGCATATTCA	CGCAGAAAA	GGTTATTCAAA AATTAGTATGG GACA	ACCTTTAAAGTTTCTCCCACTACTCCCGCAGAAAAAGGCATATTCAAT/CTGTCCCATACTAATT TTTGAATAACCTAACTCTCCCTTTGTTCTACTAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-14267	28	T C ---		---	AATTATTGCTGAAATTAGGAAGGAGCA/CTGTGAATGGGAAGGGGAGGTTAGAGAAGACAGAG ATTTAAAGAGCAAGTACCATTTTCCAGTATAAACTCGTA
WI-13892	50	G A TAGAAC	CTTTTCATTT TGCTTTTAA	TGATGATGTCA TATACTAAA ATCAAAG	GATTTGTTTTATTCACTCTCGCTTTTCTATTTTAAATAGAACAI/G/A/CTTTTGATTTTAGTA TATGACATCATCATGAATTTTCTCTTACTTTGTATTAGGCTCCACCTCAGTAGTTTGACAA AGGTAGATGAGTTCA
WI-15288	108	C G TTCCCTCTCTC	CATGAGAGGA	AAAAGCTTCTT TCCCTTGA	ACCTCTTCTGATGACACTTGACCTGTAAAGGGTCTAGAGAGAAAGAGTAGTACTCTACTTTGCG TACAATTCAGGATGCGAGGCATGAGAGGATCCCTCTCTC/GTCCAAAGGAAAGACTTTTGGC
WI-13951b	88	G C ---		---	AATAATGGAAGAGGTGAACAAGTAATGAACAACAGACACCCAGATCAGAGGAAGATG GCCTTCTTGTTAATTCTGGAGCA/G/CTTCAAGCAGCAATATTACTGAACACTTGCTATGTGCTG G
WI-13951a	39	C T CAAA	GGAGTGAACA AAGTAATGAA	TTCTCTGATC TGGGGTCT	AATAATGGAAGAGGTGAACAAGTAATGAACAAC/CTJAGACCCAGATCAGAGGAAGAG ATGGCTTCTTGTTAATTCTGGAGCAGATTCAAGCAGCAATATTACTGAACACTTGCTATGTGCTG G
WI-13264	25	G A TTGCCCAT	AAAAGGCTC	GGAGGGAGAG ACGGAATA	GAGACCAAAAAGGCTCTTGCCCAT/G/ATATCCCGTCTCTCCCTGACTGACCCAGTGTCTT ACAATGAAACATCCCTCAGCCCCATGGCATGGTGATCCCTTCTCTTGGATCTGTGAATATAACCA ACTGTCTTGTCATGGC
WI-13960	39	A C TGATAGA	AGCAAAAGGA AGTTAAATAC	CATGAAAGGA CAAATTTGCAT C	TTATTTGTCAATAGCAAAAGGAAGTTAATACTGATAGA/AC/GATGCAAAATTTGTCTTTCATGCA TTTGTGGAGCAAGTACTAATTGTCTCACTGTCAATTCCTCAGAGGTTGAGCCCTAGATGAC
WI-15843	62	C T CAG	ATCTTATAAC AAGAAGCCTT	CTCTGGCTCAG ACTTGCTCT	AACTCTTATTGTTAGCTAGCCCCAGTGACTTTATGCATCTTATAACCAAGAACCTTCAG/CTJAG AGCAAGTCTGAGCCAGAGGTTTATCACACTTTGTCTCAGGGTCCACAGGAACAGGCTTGGCT

WI-13983	52	G A	TCTCTCCCACT CCTTAAACCT	CAATACTCTCT TAGCCAGTGG	TTGTGTATCTGATTCCGAAACATAGAAATCTCTCTCCCACTCCTTAAACCTTG/AJCCACTGGGCTAA GAGAGTATTGTACAGAAATATGCACCTCACTGACTTAACAGAAATTAGAACATCCAGGCACTCACTGAGA
WI-13850	51	A G	AATCTCAGGG TCACAGCTTTA TT	TGTTCCCTGAC AATGTTTGTA	CATGAATCTCAGGGTCACAGCTTTATTTATAGATTTTAAACACAGCCATTAGTTACAAACATTGT CAGGGAACATTTACAAGATAAATAAGATGGACTTGCGAGGTGTAAAAGATTACACTTCA
WI-15295	27	G C A	TGTCAGTTTGA ATGTATTCCCTG	TGAATAGTTGG CAAAGGAAA	AGATGTCAGTTTGAATGTATTCCCTGATGCTTTTCCTTTGCCAACTATTCAATTATGACCATCTTTTC CTCGTCAAGTGACCTGCCATCATCACAAGAAAGGCCCGGAAATATGAGTGAGACTCA
WI-14284	55	C T	---	---	ATTCAAACAATCCAGAACAGGTTCTCACACTTTGAGCCTTTAGTGCAAAAACA/C/TTATGCCAT GCGGGAATAAATGCTTATCCAGTGGAGCGCTCCCTGATGCATTGA
WI-14288	85	G C	CCGCTGCTATT CCCAGAT	GGTCTCTTCC ACCAAATCTT	ATGACCAGACCAGAACCCCTGTTCTATATGAAGACAAACAGGTGCCCATACTTGGGTGGAGGGATA CCGCTGCTATTCCAGATG/CJAAGATTTGGTGAAGGAGACCATGACAGATGACAAACGG
WI-13522	33	C T	TGATGTAGTTA CCCCACTAAT ACAAC	CATAATATTG AAGTCAGTGGT TCTC	TTTATTTGATGTAGTTACCCCACTAATAACA/C/TJGAGAACCACTGACTTCAAAATATTATGAGAG AAAATTACTCCAGGGAATTTTGCAGAGAGATAATA
WI-13529	42	T C	CACAAACATT TATTGAACAG TTACCA	TCTATACACTT CTCACTCTCTT GCTT	AAATATGATTCCATCCACAACATTTATTGAACAGTTACCA/T/CJAAGCAAGAGAGTGAGAGTGT ATAGAGGTGATTTAAGAGTGTCTCTGCTCGAGGGTTTATAGTCTAACAGGGGAACAACCTCTC A
WI-13859	84	G A	---	---	TTATTTGTCAGAAATTTCCAGAATCAGAGTCTCTACTGGGCAAGTAGAAAAATAGAAAAGTTTACTAC TTTGAAAAGGAAACTAT/G/AJACAACAAGTATATATTCAGGAAAGGCACTCCTAGAACTTGAGCA ACA
WI-13536	29	T C	---	---	TGAAAGGATACAGAAAAAAGTCCAGGAGT/CJGAAAAAGGTGGATAGCGTGAGTAGAGGAGAAAT TAAGCACCAAGCTTCCAGTTGCTCTCTCCAGTGCCATTACATGGAGTACACTTAATTTTCTCAGCA
WI-13373	52	G A	---	---	TTTTATTGTTTGGTAGAAAAACAGGCTCTTTAACACTGAATAAACATCTCAC/G/AJAACCTGTCGCTC CTAGATTACAAAAAGTCAAAACCAATTTCTTTGACGCCGGGCCCTTGAATCTGACATTCAAGTCAC CGTAATAGAAACCAGAGCT
WI-13477b	61	A G	---	---	TTGGTTTTTAATACCTCTTGTGGATAAAGGACATTGTTTTTTCATTAGCTTGTCTTCAA/AJGAC AGAGAAATAAGATAAAATTACCTTAAGAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCAGTT
WI-13477a	32	A G A G G	TTAATACCTCT TGTTGGATAA CAATG	GAAGACAAGC TAATGAAAAA CAATG	TTGGTTTTTAATACCTCTTGTGGATAAAGG/AJG/CATTGTTTTTTCATTAGCTTGTCTTCAAAGAC AGAGAAATAAGATAAAATTACCTTAAGAAAAATTAATAGAAAAATTAAGGGAACATGTACCAAGGTGG TTTTAGACTCTCTCAGTT

WI-14297	86	A	T	G	AATGTTGGGT ACTTTTCCAA	TGTGCACATTC AGAAACATTTT	CTGACITTTATTAGCATGCAATGCAATTTATTCTGGCAATAAATTAATATGTGCAGTTATAAAAAAT GTTGGGTACTTTTCCAAAG[AT]AAATGTTTCTGAATGTGCACACTAGATAATATGCAGAAATCCTTT AAACAGTCGACT
WI-12229	89	T	G	AAA	CATGTGCACA AAAAGAGTAA	ACATGTGAATT GTCCCAAAAA	TCCATGTAATAATTCTCAACAGAGAACACTATCTTTAAATGAAGGATTTACCATTAAGAAATCAACA TGTGCACAAAAAGAGTAAATTT[G]ACCAAAAAATTAAGATTTTGGGACAAATTCACATGTTT AAAAAT
WI-13582	43	C	A	AGACTGGGA	TGCAATCTAG	TCTGGGCAGTT AGATTCCA	AAGGCTGCCCTTACTGGACCAATGCAATCTAGAGACTGGGA[CA]JTGGAATCTAACTGCGCAGAG AAATCAAGACCGATGGTGTGAAATCTGGGCAGCTTCAAAATTTCTGCCTCCTAAACATTTTCAC CCAAATTTTCATTATTGCC
WI-13857	28	A	G	---	---	---	TCTGAGTTGATAAAATGCTTTTCTGAAC[AG]TACATTTTAGGTATCTGGCACAATTAACCAAAATGT CTGCCCATTTTGTAGCTTTCATACAGTACAGATTTTCATTGATGTGCTGCCACATCTG
WI-15809	77	T	G	TGTAATGCC	TGGTTTTCTGT TGTAATGCC	TAAGTAGCTA ATTCAATGTTT GTAAA	GTTTTAAGTTGCAGAGATGTGAATGGTTTACAATCTGAAGCTGAAGTTCAATCTTTGGTTTTCTGTT GTAAATGCC[TT]GTTTACAAACATTGAATTAGCTACCTTAAGTATTGAAGAGCTTCCATT TTAATCAGTCTGTGTCAAGAAGAAACAGGACTTGATCAAGCTTCAGCCCTCACCACTCTATCAGCA TAGCAATTTTAAGGATCAGAGCTTTGTTTACATTTGTCTAAACCAAGAGAGAA[AT]JGGAATCA ACTCCACAGATCAACATGT
WI-15892	123	A	T	---	---	---	TCTTTTATCCAAAGATGGGAAGCGCATTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACTCTA GCTGCAGTAATAC[TT]G]GCATCCCATCCACTCTTCTCTCTTTTGTACTGAAACTCTTCAAGAACT GCTGAATGTCTCTCTC
WI-15801b	81	T	G	AA	CATACTCCACT CTAGCTGCAGT	AGAAGAGTGG ATGGGATGC	TCITTTATTCCAAAGATGGGAAGC[G/A]CATTTTTCATTGGCTTGAATGAGAAAGCTTCATACTCCACT CTAGCTGCAGTAATACCTCCATCCACTCTTCTCTCTTTTGTACTGAAACTCTTCAAGAACT GCTGAATGTCTCTCTC
WI-15801a	24	G	A	AATGGGAAGC	TTTATTCCAAG AATGGGAAGC	TCATTCAAGCC AATGAAATG	GCTCGTAATGAGACAGAACGCTACAATCTGTTCAACACTGGCTGGACACTGCAGTGATT[C]JAGGG GCAGGTGGGCAGGGTGGGCTCTGAGCCGAGGACAAATGTCCATGGCAGAGCTTCCAGAA
WI-13763	59	T	C	GCAGTGAT	GGCTGGACACT GCAGTGAT	CCCACACCTGC CCCT	TTTTTTTTTGGTGAGTGTTTGTCTTCAATAAAGAGCAGAAAGAAACC[TT]AJAGACAAAAGATGTT CTTACACACTGAGCTTTACACAGTCACCCAAACATTGATAATTTGCTTTTCCCGAGGGCAAAAGA GAGTCTCCAGAAACC[C]
WI-13578	48	T	A	AACC	TCAATAAAGA GCAGAAAGAA	CAGTGTGAAG AACATCTTTT GTC	TCCAAGGAAAAAGAAAGAAACCAATCAGTGAGAAACTCAAGAAATGGATGGCTGAGGGAG[G/A] GAACAGAGGAAGCGCACTGGGCTGGGACTGAATATGGACAGTGATGGTGGTCTCTACTCTCTT GAGGTCCCT
WI-13789	62	G	A	AGGGAG	TTGGATGGCTG AGGGAG	CAGTGGCTTC CTCTGTTC	---
WI-13594	66	G	A	AGC	TTTTTAACACA GATCACAAA	CCTTTGGCCA GTACTTTT	AATAACAAGTTTAAGTTTCGAGCTGCAATGTTGGCAATGCAGGTTTTTAACACAGATCACAAAAAGC[ G/AT]GCACAAAAAGTACTGGCGCAAGGACAAAAATATGCTAAGAAATTAGGCCAACAGCTGC



WI-15825	40 C T	---	---	GTTTCTCCACCTACTCCGAGAAAGGCATATTCAA[C/T]TGTCCTACTAATTTTGAATAA CCTAACTCTCCCTTTGTTTCTACTAAGAGAGGTTTCTTTTGGCTACAAGTAACA
WI-13367	84 C G A	CCACACTGAA GACTCACCAG	TCCCACCCCA OCT	GTCTCAGTTTCTGTAGGCTGTAAATTTTCAGTTTAAACAAGTTTCTTATGTGATTTGTGGCCACACT GAAGACTCACCAGAA[C/G]AGGGTGGGTGGGAATACTTAATCAATAATTTGTGGAATTTACCCGAT GAAATCCAGTTATTCTT
WI-13600	26 G T	TTAATGAGCC AAGCATCCAT	CATATTGAAAA TTGTTACTAGA TGATGG	CTCAGTTTAAATGAGCCAAAGCATCCAT[G/T]CCATCATCTAGTAACAATTTTCAATATGCACATTATAT TATAGTGGAAACAAGAATACGGATTGTGTAGGGAAGAGCATAGAGGACCACCATCAGCAACCCCTCT TGATCCCTTCTCTAACC
WI-13602	89 G T	TCCATTCTGGA GACAACACA	GCATACCTCAT GACAATAATTA ATATTAAT	GATAGGAAAGAAGAATGAAGTCAATAGTCTTTAGCAAGCCAACTAGCTCAAGGAATAGACAGCCC CTTTCCATTCTGGAGACAACACA[G/T]AAATCTATTAATATTAAATATTGTCTATGAGGTATGCACCT GCCCC
WI-13650	76 A T	AAAGATTAC AATATTTCACT TTTAAAC	CAGGCTAGGAT ATGAAGAGTA GTTTT	GCATTAACATTTAAAAATTTCTGAGGGATATTGATGAGAACTATGATGAAAGATTCAACAATAATTTAC TTTTAAAC[A/T]TAAAAAACTACTCTTCATATCCTAGCTGATGACTTAAAGTTACCGG
WI-14319	83 C T A	CAATTCAGG CACAAAGCTA	CCAAATCATCT ATATTGTTGCA TG	TGTTTTGATTGAAGAAACATCTCTAAAAATACCATCTGAGTGCAAGATAAAAGGAATAGCAATT CAAGGCACAAAGCTAAG[C/T]ACATGCAACAATATAGATGATTTGGGGTGGGACAGTACAGAAATT
WI-13528	80 A G AAA	CAATACATT GCATTTTCCTA	CATGATACCAC AGTTTCTCTG AA	ATTGGATACATGCTTTTAAAAATGGTAGCTTTTAACTGTAACTACATATTGCAATTTCTCTAAAA AAAGAAAGACATTT[A/G]TTCAGAGAAACTGTGGTATCATGCGAGGAAAGCAGAAAAAAATT
WI-13909c	93 A T	---	---	ACTTAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCAGTGAAGTTTCATCTTCTCAGACT CTCTTCAAACTCGAATATCTTTTTC[A/T]GAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-13909b	80 G A C	TTCCTCACACT CTCTTCAAACT	GCAGTGGGTAC TAGCTAGACAT CTC	ACTTAACTGGCTTATCTTCACGGTAATCTATTCTGTATTTCAGTGAAGTTTCATCTTCTCAGACT CTCTTCAAACT[C/G]AATAATCTTTTTCAGAGATGTCTAGTAGTACCCACTGCAACATCTCTCAA
WI-14323b	86 C A	---	---	TTTTATTGAATTCCAAATGTAGCAAATCATTAAACAATAATAAAGGGACAGAAAAATTAAG AATCAACATCATCTCTGGAC[C/A]ATGGGAACCTTGAAAAAGGCATGGCAGTGGAGACCAGTAACTA
WI-14323a	78 T C	ACAGAAAAAT TAAGAATCAA ACATCA	GCCTTTTCAAG GTTCCCAT	TTTTATTGAATTCCAAATGTAGCAAATCATTAAACAATAATAAAGGGACAGAAAAATTAAG AATCAACATCAT[C/T]CTGGACCATGGGAACCTTGAAAAAGGCATGGCAGTGGAGACCAGTAACTA
WI-15389b	104 G A AAA	AGATAATGAA ACATCTGCGA	GATGAGGTGAT TCCCACACTT	AAATTGACAAATCAACTAGCTTGCTTTTGTGCTTTTGGGAAGACTACCATATTCAAAATTTATTATGT AATACACTCATCCAGATAATGAACATCTCGGAAA[A/G]AAGTGTGGGAATCACCTCATCTGTGTC

WI-15389a	33	G A T C	AATCAACTAG CTTGCTTTTG	TTGAATAATG GTAGTCTTCCA AA	AAAATTGACAAATCAACTAGCTTGTCTTTTGTCTG/AJTGGGAAGACTACCATTAATCAAAATTTATT ATGTAATACACTCATCCAGATAATGAACAATCTCGGAAAGAGTGTGGGAATCACCTCATCTGTGTC
WI-15747	88	T C A G T G T T	TGCTTCATTT AAACTAATTT	CATAATTCACC AAAAGTTCATA TAATTT	TGTAATCTGCTTACAGTCTTTGCAAGACAGACATATGTTTTTGCATAAAGATATAAATTTGCTTCAT TTAAACTAATTTAGTGTCTTT/CJTAAATTATATGAACCTTTTGGTGAATTAATGAACGTGTACCAAAC C
WI-13752b	117	C T ---		---	AAGAAAAGCACATACATTTCCAGAAATTTTGGAAAAGTTCACCTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTCTCTCGTTAAGTGTCTGGATATACCTTGGCTTGACAC[C/T]GGACACCTTTTACG GAGGGATTCCGGACAAC
WI-13752a	106	T C A G T G T G G A	CCTTCTCGTTA AGTGTGTC	CCCTCCGTAAA AGGTGTCC	AAGAAAAGCACATACATTTCCAGAAATTTTGGAAAAGTTCACCTCTGCAGCAGCTGAATGGCAGATGGT CTCTGCGATGAGTTCCTCTCTCGTTAAGTGTCTGGATATACT/CJTGCGTTGCACCGACACCTTTTACG GAGGGATTCCGGACAAC
WI-14339	102	T G T T A C	CCCAATCAAA CAGTACATGA TTAC	TCCAGATTTCT GGAAACCG	AATCATTAAATGAATGTTCCAAACACACCCCTTCACTGGGCTACAGGTAATTTCACTGGGATGGAAG CAGATGAACCCACCAATCAACAGTACATGATTACT/GICGGTTTCCAGAAATCTGGATAC
WI-13744	115	C T A A A C T G A A	TGGTGTCTGAAC	AATCAGGAAA GATAAGCACAA GC	TGGATGGATGGATGAGGCCACCTGTGTTCAACAAAACACGTAATGGAACCTTCATGCAGCTTTAGAT TTCCCTTGCCCGAGCTAGGAGCTTGTGTATGTGTGCTGAACAAACTGAA[C/T]GCTGTGCTTATCTTTC CTGATCT
WI-14061	68	C T ---		---	CCTTTGACTATATTGTTTTTCCAAAATAGGACTATGTGTAGAAGAGAGCCCCCGTACATACCTTAT [C/T]AACCATTTTCACCACTTTGTAAATCTCATCTTCTGGTCTGGATACTCAAAAACAGAT
WI-15719	69	A C C A T T C A G C	ACCTTTTCATC CATTACGC	TGACTTTGGC AAGAGTTTTAA ATT	TTACAGTTGGATTAAACACTACACACTGAATATACTGAATTAACCTTCAACCTTTTCATCCATTCAG C/A/CJAATTTAAACTCTTGCCCAAGTATCATGAACCTACGAAGAGGAGATAAGAGATCTGATC
WI-13810	106	T C A A C T T	CTCTAAATCG ATACATCCAA AACTT	GAACTGATGCT TGCTGCTAACT	TAATCCATCAATCTAAATCACACATACTAGATCAAAACAGAGTACCAGATGCTTTATTTTGCA GGTATTAAATTGGTTCTCTAAATCGATACATCCAAAACCTTT/CJAGTTAGCAGCAAGCATCAGTTCTTC
WI-15736a	27	G T C A C A	ATTTTATTCAC ATTAAACTTG CACA	GTTCTTTGATA TGTTGCTTAGT TTT	GGATTTTATTCACATTAACTTGACACAGTTAGCAAAAATCAAAACATAAAACTAAGCCACA TATCAAGAACAATATACAATAGAGATTGAAATTTCTCAATAGCATTGGAAGGATTTCATAAATA TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGACACAAAATGAAC AAGTGC[C/A]TAGTGACACATAGCTGTCAACACAGATG
WI-13785d	72	G A ---		---	TCAAACTGCACACTATAAAGTGTCTTAAATGCAGCAGCAGGAGATGTGAAGAC[C/A/C]CAAAATG AACAAAGTGTAGTGACACATAGCTGTCAACACAGATG
WI-13785c	56	A C ---		---	

WI-13785b	40 C G ---	---	TGTTGTGACAG CTATGTGTCAC T	TCAAAGTGCACACTATAAAAGTGCTTTAAATGCAGCAG[C/G]AGGAGATGTGAAGACACAAATG AACAAAGTGCAGTACACATAGCTGTACACACACAGTG
WI-13785a	27 T C TGCTT	---	AAACTGCAC ACTATAAAAG	TCAAAGTGCACACTATAAAAGTGCTTT[C/J]AAATGCAGCAGCAGGAGATGTGAAGACACAAATG AACAAAGTGCAGTACACATAGCTGTACACACACAGTG
WI-13793	88 C G ATAGG	---	GGATTTTACAT TCAGCCTAGAT	AGAAACCAAGTATATCATAGGCAATAAAATAGTTTTACCCCATTTGATACACATAAGGGATTT TACATTCAGCCTAGATATAGG[C/G]AGTAACAATACTCTCTGCCATAAATCTATGACTTG
WI-13794	52 A G TTTCTTTCTC	---	TTCTCACCCCT TTTCTTTCTC	TAGTCTCTACAAATTCCTTCAATCCATTTTCTCTCACCCCTTTTCTTCTC[J/G]TACAAGGTTAAGA GCCCATTTCTCAACAACAACAACAACAACAATAGAGCAAT
WI-15729	35 A G GTGTAGACTGC	---	CTTTGAACCAT GTGTAGACTGC	TCATTTAAGTGCACCTTTGAACCATGTGTAGACTGC[J/G]GGCACTTTAGAAAGAGCTGAGACTGAA AAGTCTGTCTTGACTTCCAGGAAGGTAGTCCCTGTTTGCAGCCCGGGCCTGCTCATTTGTTA
WI-13424	66 G A C	---	TGAGGTTTTTC ACCCTATTCTT	GTCCCTTGCACAAGTCTCCCACTGGTTTGGAGTTTCCCTTCTGAGGTTTTTACCCCTATTTCTTC[J/G] JTAGACCTGGGGAGAAAACACATGTGTAGTGGCTCAGGACATGAGGCAGGCCGTTTCAACAAGAT GCTGGCTAAGCGGCTTC
WI-14065	29 T C AATT	---	CAAGCTGAATC TGGGATCTC	AACTGTCTTATAAAGGTCAGAGGCAATTT[C/J]GAGATCCAGATTCAGCTTGTCTCATAAAAGAT TCAACTTCAAGTAGCACAAATTTCTGTCTGCTTTAATCTGAACATTTCTTGAAGCACGAA
WI-13446	22 G C TCACTCATCA	---	AAGGGAATCA AAATCAGAAG	TGCCATGTTCTTTCACTCATCA[G/C]CCTTCTGATTTGATCCCTTCTGCTCTGTAATTTTTTCTTC TTCCCTTTTAGGGCCTAGTCTGTTTGAATACTGTTTGTAGAGATGTGAGCCCTTTACTTTTTT CTGACTGCCTAATT
WI-13725	56 A C TGGGTGOC	---	OCTGTGTCTC GGCC	TCACACAAAGGCATTTGGAATGTCACCTTACACATGGTGAGCACATATGGGTGCC[J/C]GCCCGAG ACAGCAGGATAAGTTTCACAAACTTGACCAGGCAGGTTAGAACAGCAAGCATGGTTTCAGGATG
WI-15702d	107 T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAATAAAGGCTTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCCTGTAAACAAAT[C/J]ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702c	101 T C ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAATAAAGGCTTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCCTGTAAACAAAT[C/J]ACTAATGGGTTCTTTGAACAAATAGTTT TGA
WI-15702b	90 C T ---	---	---	CAAATGTTTTATGAAGAGACTCCGAACAAATAAAGGCTTTTCAAAAAGGGGGTAAAGGGGTGAGG AAAGCATGTGAGAGAACTGTAAACCCTGTAAACAAAT[C/J]CTGTAAACAAATACTAATGGGTTCTTTGAACAAATAGTTT TGA



WI-15702a	48 G C	AACAAATAA AGGCTTTCAA AAAG	CCTCACCCCTT TACCCC	CAAATGTTTATGAAGAGACTCCGAACAAATAAAGGCTTTCAAAG[G/C]GGGGTAAAGGGGTG AGGAAAGCATGTGAGAGAACTGTACCCTGTAAACAATACTAATGGGTCTTTGAACAAATAGTTT TGA
WI-13831b	113 T C	---	---	TTTTTTTTATGGATGCACGTGTTACATGTTTATTTAGCGAAGGTGACTTGGAAAGGAGATTACACAT ACTTCCACTGTATCCTCCGGTAAGTTTCCTTCTCTCTGTAGATTCCTCCATGTTACAGTCAAC TATAAACATGGCTCA
WI-13831a	56 G C	---	---	TTTTTTTTATGGATGCACGTGTTACATGTTTATTTAGCGAAGGTGACTTGGAAAG[G/C]GAGATTCA CATACTCCACTGTATCCTCCGGTAAGTTTCCTTCTCTGTAGATGTCTCCATGTTACAGTCAAC TATAAACATGGCTCA
WI-13806	62 G A	---	---	TGATTGAGCTTAGAAAGGAAGTCATGTTGAAATCAGAGAGAGGCCAAACTAGGCCCTCAGGT[G/A]C CCATTAAGCATGCTGTGAATGCAAGGAAAGCTTAAAAAATTTTTTAAGGGTGACTCCAGTAAA CAT
WI-14372	86 A G	---	---	CACATTTTCAGCAACAAATCGAGGTGCAACAGGGTTTATTTACATTATATTAATTAAGTGGATTT TTTGTCAAATAAATAGGGA[AG/TTTCTCTTTAAATAACCATCTCCTCATTCTATGGCCAGT
WI-14373	95 A G	---	---	AGGCTGTTTTTGAGGCTGAGGACCCCAACATGACAACGTAAAGACTGTAAACCATGTGTCATGTGAGTT ATGAGCTAGGAACCCCTGGACGAAACCA[AG/C]ACATATACAATCATCTCCACCTCCCAACGCCCTT ACTTTCACAGCCTCTGCA
WI-14078	61 C T	AAAGAAGTAA ATTAGGAAGA GCAAGA	TGTGTGCATGT CTCTTACTGC	AGAAACCGAGAACTCAAAGAACCACATGGTGTATCAAAGAAGTAAATTAGGAAGCAAGA[C/T]G CAGTAAGAGACATGCACACAAATCGAAACAAGGGCATGGAGGAAGGACTTTAGATGGTCACG
WI-14083	47 C T	AGACTTGAGA GCTTAAACA ACACT	GCCTACTGGAC CTCTAAACTAG TGA	TTGCTACATAACACATTACTCCAGACTTGAGAGCTTAAACAACACTCTTATTTGTTATTTACACAG CTCAGTAGTTAGAGGTCAGTAGGCTTGGCTGAGTTGTTTGGCTTAAGGCTTTACAAGGCCAA
WI-14085	31 A G	CATTATTTTC ATGTGTAAGA AGAAAA	CAGTCATGTTT ACGTGCTAGTT	TGCATTTATTTTCATGTGTAGAAGAAAAAC[AG/TTA]ACTAGCACGTGAACATGCTGATGGATAC ACGGCTCAGCACGAGGCTAAAGTCAGAAAGTGAGTGAAACAAAAATAGCATGTTGATTAAGTGAAA TAACAGAACAGGAGGCCCTT
WI-12169	121 G C	AATAAAACTT CCTATTTTCTT TTGCTT	GGGTTCTGAGG TGAAAGAAAA A	GTCAAAGGTTGGCAAAATTTTATTTCCACTTATCAAGAACTTACAAAATATTTTGTTCATTTCTAAA TTTTACACCTTATTGCTAAGTTATAAAATAAACTTCTATTTTCTTTTGTCTT[G/C]TTTTTCTTTCA CCTCAGAACCCCTTA
WI-15705	50 A G	GGAGGGAGAT TTTAGACTGA ATC	AGCTGTAGTCG TCAAATACTCT AGAA	TTGTTTTTATTGGGAGAAATGAAGGAGGAGGAGATTTTAGACTGAATC[AG/TTTCTAGAGTATTT GACGACTACAGCTCCTCTCTCTTTGTACTACGGAGACCCCTGCTTATAGCCCCCAACAGGAAATCCTCA TCTGCGGTTGCCAGACAG

WI-14379	102	C T	TCTATTAAACA GGGTTATGTCA CACC	ATCATCTGTTT TGAGGTTGACA	TTATGCTGTTGTTTCTACTGGTGGTCTGCTCACTAATATCCATCCTAGTATGATTTCTTT TACTTGTGTTCTATTAAACAGGTTATGTACACCC[C/TTGTCAACCTCAAAACAGATGATACT TAAATAAAACAAGCAGAAA[C/A]CCACCATTAAACAGGAGACACTGCAGAGGCTTATGTACA ACAGTGTCCCGGAGGCTGGCGCAGGACTGCCACTCACTCCAAAATTTCTTTGGAGCAGAG
WI-14102	22	C A	---	---	ACCGCAGAGCTGCTGATTTAA[A]GJACAAAGCTCTGGATCTCTGCAGGGCTGGGACCAGCTGC AGTGGGGCTCCGGCAGCTGCTCTCTCTCCAGGACTCTTCCACCAOCC
WI-15937	24	A G A	CGCAGAGCTG CTGTATTTAA A	GCAGAGATCCA GACGCTTGT	TGAACTGAAACGTATTTCTCTCC[A/C]ACACCGTAGAACTTAAAGCCGCAAAAGACTCACACCC ACCACCTAGCGCGGCAAAAGGAAGTTTCAGGTGATACAAAGATGCTCTGCCATCACACCTGAAGGAT GGTT
WI-15944	24	A C A	AACTGAAAC GTATTTCTCTC A	GGCCTTTAAGT TTCTACGGTG	ATGTTTTATGATCAATCCAAACATACAGTACAGGGAAGGTGAATGAGTAAGAAAATAATCAT ATTTAAGTCCCGTTAACACTAAGCC[A/G]TATTATTCAAATGTGTTTCAAATACTCAGCCAGAT CACCAAAGCTCAGTCACTAC
WI-14124	92	A G	---	---	...
WI-14125	88	C T	GGTTGACCTG CATAGATTTT	GGAATGGCATG GCCAC	GACAAAGAGGCAGTTTCTGTAGTTCCAGCAGGGCCAGAGCAGTTATCAGAACGGTGGTTTGACCT GCATAGATTTTGTGACGACTA[C/TTGTGGCCATGCCATTCCTGTAAAGTGAAATTAATGAACA
WI-14136	120	G A	GCTTTCTCAAC ATGCTTTCACA	CTTGTTCTGTC TCTTTGGCC	GTTATTTTCTCACAGTTCTGGAGTTAGAAGTCTGAGATGAGGATATCACCAGCATGGTTAGTTCT GGTGAGGACTCTCTGGCTTACAGCTGGCTGCTTTCTCACCATGTCTTCACAT[G/A]GCCCAAAGAGAC AGAACAAAGCTCTCTGTT
WI-14138	23	C T	TGTTGGCACCA GAAAAGCT	CAGTATGTACA GTGACATAACA TAGAACA	TTGTTGTTGGCACCAGAAAAGCT[C/TTATGTTCTATGTTATGTCACTGTACATACTGTAAACAAGACT GCATTAATATTGTTTCTTATGATTTGTTCAATG
WI-13551	74	G A	TCCTTCAGTAG TAGTATATTCA GACAATC	GCTCATTTCTT TTAGTGCTAAG TAATATT	GGCAGGTTTATTCATAAATTTCAAACCTTGGAAAGCAACCAAGATGCTCTCAGTAGTAGTATTCA GACAATC[G/A]AATAATTACTTAGCACTAAAGAAATGAGCTATCAAGTCAATGAAAGACATGCAGG AACCTTAAATGGATATTACT
WI-15953b	59	C T	---	---	TTTTTTAAGAGTGTCTTCACATCATTTATATTGTATTGCACACAAAACCTTTTAACTC[C/TTGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGAGATAGAAGCCTTCTTCAGAATCA CCTCCC
WI-15953a	26	T G A T	TTTTAAGAGTG TCCTTCACATC	TCATCTGTTCT TGTTGTTTTTG A	TTTTTTAAGAGTGTCTTCACATCATTTGTTATATTGTATTGCACACAAAACCTTTTAACTCCGTCAA AAACAACAAGAACAGATGAATAAGGAAGCCAGTGCTTTTGGAGATAGAAGCCTTCTTCAGAATCA CCTCCC



WI-14631	82	G A ---			---	TGAATCAATGGACAGTTTTGCTCTGTTTATGTAACCCCTCACAGCACTCTGCATAGTCGGCTTTCTGTCTCTTTAAAC[G/A]GCTCTGTTCCCTCTGCCAAACTTTTAGGATTGGGCTCCTCAGGGCCTTGCTCTGA
WI-6053	24	A G ---			---	ATCACCCGTGTCTAAGAACAACI[A/G]TCTTCATGTCCAACTCATATCCCGGGACTTTGTCAACTGCAGTACACTTCTGCTGCAATTGAACCTGCTTCTGAGGGAAGCTCTAGAGGCCAGGTAAGGGGTGCAGCAGTGAGGGGTATATCTGGCTGGCCAGTTGGAACCAAGGAG
WI-15964	99	T A	GCTCTCTGTCC	CTGGAGGTA	GACTTCTCCAC	CAGAAACCTCTTCTGTGTATTAAGCTGATGCTAAAGTCAGAGCAGTCCAAAGGCAGGAGGCTGCCTTGGAGGTAGTAAGCTCTCTGTCCCTGGAGGT[A/G]CAAGAGGGTGGAGAAGTCTTGGCAAG
WI-12075	103	G A	AGCAGCTGGG	GGCAC	CCCTTCTTTC	CAGCTAAAGGATCACTGCAGCTAAATACAGATAGAGAAGCAACAAGCCAGGCAATATCCCATCAGAGACAGTGACAAGAGCAGCTGGGGCACGGGGAGGC[G/A]GAAGGAAGAGAAAGAGGGGAGGAGCCT
WI-12179	96	G A	GGAGGTACGG	TGGAGGTCA	TCGAATGACCC	TAATTTAAACACGCCCTTCCACATAGTGCCTGAGGCATCTGCACATTTTCCTAGAAGGACATGATAGTGATGTGGAGGTACGGTGGAGGTCA[G/A]GCATCTACAGGGTCAATCGAGGAGGAACAG
WI-14651	49	C G	CAAGAATCAT	TCTCATTTAA	GGAGATATTGA	CACAAATAGTGAATATCTGAGCAAGATCATTCTCATTAAATTTGTC[G/A]AATAAGTCAGAAAGATCAATATCTCCCTGCTTCAAAATGACACTCCCAATTTTACAGAGGTAAACCACCTGTTA
WI-14666	105	T A			---	AATGTGGACTTTCAAACAAGGGTTTAAACTAATCTAATACAACCTTCTACAACACATTCACAGGCATATAACAAGAATTATTTACAGGCAGCTAATGTATTAAAT[A/A]AACCATGAAAAGAAAACCTTG
WI-13473	31	CT			---	ATCTAGATGTCAGCAAAATGGGCTGAGACTGTC[T/G]TGTCTGGTAGATGCAGTGTTGTATGTTTCTACTATTACAAAATTACAGAAATATGGCTTCGCTTTGTGCAATGTTTATATCACAGTC
WI-13967	103	A C	AAAAGACTAC	AGATACAAGG	TTGTGTTTICA	AATTTAATAGCAGCTCTGTGTTGTGATTTTAAAGAACAAGATAAAATATGTCAATTCAGCAGTCATTTAAAAATAAAGACTACAGATACAAGGAATAAAA[A/C]CACTTTTAGGAGATGAAAACACAAA
WI-14408	60	T A G	GCAGACACAC	TATTACAGGCT	TTAATTGTGTA	TTAATATTCAGCAAGTTATTGCAACAGGTTGAAAATGCAGACACACTATTACAGGCTGTT[A/J]AAAGTAACAATGAGTTTACACAATTAAATATTACACATACTTATGGGATTTGTTGAATGA
WI-13683	47	C G			---	TTTTGTGTTAAGAACAGCATTTTGAAAATAAACCTATCTGCCCATG[C/G]TTTACAGCCCTTTTAAATTTGTAATATTATATAGTCGTTTATGGTACATATTGATTGTC
WI-13910b	63	CT	CACCATGGCA	CGTCT	CATTGAGATAA	TTAGAAAAGTATAAAGCAACACAACCTTTTGGGAAAGCACCATGGCACGTCCTTTGTGCTA[C/T]GTGATAAGTGCTTTATCTCAATGAAGCAACCCCA
WI-14635	22	G A			---	ACATGGCAGATACAGAGCTGTC[G/A]TCTTGAAGACCACCACCTGACCAAGGAATGCCACTTTTACAAATCATCCCCCTTTTCATGATTGGAACAGTTTCTGACCGTCTGGAGCGTTGAAGGGTGACCCAGCACATTGACATGCACAAA



WI-16002	59	T C	GATAACATAA AATGATCATG AGAAATTC	GCATCTCTC TTTGACTTTT	CCAACATTTAAACCTATGACTGGTCATTGATAACATAAAATGATCATGAGAAATTTCA[T/C]GTTA AAAGTCAAGAGGAGATGGCTAATGCATGCTGGCT
WI-15361b	101	A G A	CCCACCTTGAAC TCAAGTCATC	AAACTAAAC CTTTGTGCGTA AAA	GTGGAATTTTATTAAAGCCATCAAAATTTCTTCACACTCAATACTGTTGAACAACAAGATAACACAT CTTCTTGCTCATCCCACTTGAAGTCAAGTCAATCA[AG]TTTAGGCACAAAGGTTTTAGTTTTCTCGG GAAATCAAGTTTAAACCA
WI-14759	73	T C	GCGTTTGACTT GTGOGG	TCCACACTGC OCC	TGAGTTACAACAATGAGCAACAAGTTAGAAAATTTGGTTTATTCAAACTTCCTAGCGTTTGACTT GTGCGG[T/C]GTACTCAAATGGGGGCGAGTGTGGACGGGAGGATTGCAACCAGAGTTCATACTG CAA
WI-12535	50	A T T A T	CTAGGAGGGTT GAGGTGTAGA	GCTCCACGAGA AGAGAGGAA	TCCCTAACATTTTTCAGGTGTGACTAGGAGGTTGAGGTGTAGATAT[AT]CTTCTCTCTCTCTC GTGGAGCCTTACTGAAGACAGGATCGCGTTCTTGTGTTATCAGCTGAGAAGGGCAGTCTCGCATC TTAAAGACCTGCOCTOC
WI-13805a	112	G A G G G A A	AAAGGCACAC GGGAA	CTCAGCCTGOC TTGACC	TTCCATTCAATATGCTTGGCTTTACCAATTTTATAGCTATTGGGAGGCAGGAAAGGGAATTTTGGC CCAGAAACCATGAGATTGGGTGAGAAAGGCACACGGGAA[G/A]GGGTCAAGGCAGGCTGAG AGTCACATTTCCAGACCTC
WI-12340	18	T C ---		---	ACACAATATAATTCATTT[C]CGAGTGATTAACCTATTTGTTGTTTAGAACCAACAAACTAC AAGAAACATTTTCAAAACCTTTTTTTCAGGCTGA
WI-14808	52	T A C T A C C C T G T	ACCCACCACA CTACCCCTGT	GAGGCATCACA ATGTTAAGATT TT	CTTTGAAACACTTTAAGCAACAGTTAAAAAGTACCCACACACTACCCTGTT[A]AAAACTTAAAC ATTGTGATGCCCTCTGCATCAATTTTAGAAAAACAAGAAACACAACTGAAGGCCCATGTA
WI-14816	29	A T ---		---	AGTTAAAAAATCGAGTCAGCATTTATT[AT]AAAACTGGACACGCTTCTATATTGCAAGCTCAT TCAAATGCATTTATTTTGTATCCCAAGCCCTGAAACATGAAAAAATATTACTAAAGGAATGTTG ATTACCAGCTACGACTTC
WI-12542c	71	G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTATCCATGTGAGGGCTCTAGATC ATG[G/T]TAGGTGATTGATACAAATACGATCCATAA
WI-12542b	70	G T ---		---	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTATCCATGTGAGGGCTCTAGATC AT[G/T]GTAGGTGATTGATACAAATACGATCCATAA
WI-12542a	45	C T T T T A A A	GCTATTAGGC AAACTGAACA TTTAAA	TCTAGAGCCCT CACATGGAT	CCGTGTTTCATTGAAGGCTATTAGGCAAACTGAACATTTAAATGTCTATCCATGTGAGGGCTCTAG ATCATGGTAGGTGATTGATACAAATACGATCCATAA
WI-12173	57	C T C A A A A A	GGATACAGCA GTAAAGAATA	CCACCTCTAGA ATGTATGCTCT ATAA	CACCTAAATCATTTCTAGAAACTGGGGATACAGCAGTAAGAATACAAAAATCCTGC[C/T]CTTATA GAGCATACATTTCTAGAGGTGGGAAAGAGGCAATAAATA

WI-14836	28	T C	---		TCITGGAGGGATAGAGGACAGAGTGTTC/CJGTTGATTTTCGTTTCGGTTTCAGTTTGGTTGTCATT GGTTTTGTTTTTGGCTAATTTTGGCCCACTATAAAAGCAGTGGCCACCCAGAGGCAG
WI-14856	60	A T A A		TGGTGACAG GAAAATACCT CTTTTACAAA CTTT	ACATTTCCCTTATGATAGCAACAATAATATGATGGATGGTGACACGGAAATACTTAATTA/TJTA AGTTGTAAAAGTAGCAACAATAATTGAGTATATACTATAAGTGATAGAGGATGATATATGAAAA GGCTATAAAAAGCTCCAAA
WI-14863	61	G A	---		ATGGCAATTTACTTTATAGCAATGAACAATAATTTGTCAAGGGCAATAATTTTGTCTG/G/AJAG TTAATAAGTTAATATCTTTTACCACAAAGCTAGAGGTCAACAGTACCACCTATTATTGATTGCCACT ACCTGGC
WI-14867	46	T C A		GACATTCCAA GGCTCTCTAAG T C A	TTTTAATTAACGTAAAAGGCAGGACATTCGAAGGCTCTCTAACA/T/CJGAGTGTCTGCAGCCCCA TTCCGCTTTGAGATGTGAATGTGTAAACCCAGGGTGA
WI-14733	98	G A A		CCAAATTGAC AGATAATTCTGC A	ACGGAGTCGTCTCTGATGTATTCTTTGTCAAAAATGTTTGGCTGATTCTAATCATGAAGAACAATT AGAAAAATCCAAATTGACAGATAATTCTGCA/G/AJAATAAATGGCCTGACCTCATCAAAAACATCA ATGTCATGAAAAACACAAA
WI-14898b	79	A C	---		TTTTGTACCTATTCCCTGTTTCAGTGTCATGTACAGGAAGAGTTGTCTCATI/CJAGGTGCCACTAAGG ACTTCTCCAT/CJAAGCTGCCTGCTGTGCACGTTGCCCTTTGCTAACCCCTGGTGTCTGCATCT GCCTGTGTTCTGTCTT
WI-14898a	50	A C CA		CATGTACAGG AAGAGTTGTCT A C CA	TTTTGTACCTATTCCCTGTTTCAGTGTCATGTACAGGAAGAGTTGTCTCATI/CJAGGTGCCACTAAGG AAAACCTTCTCCATAAAGCTGCCTGCTGTGCACGTTGCCCTGGCTTTGCTAACCCCTGGTGTGCATC TGCTGTGTTCTGTCTT
WI-14907	48	G A G G A C		GGCACACATT GGACTCTGAC G G A A T	TGGTATTTATTTCCGACATTACTGTAGAGGCACACATTGGACTCTGAC/G/AJATCCCTTGCAGCAG ACATTTGTGAAGCTGCTGTGGCGCACACCCATCAATCAGTGACTCTGCTGCAGAGGGGCCACATG CACGATGCTCACGTGTG
WI-14911	52	G A C		CCAATACATT CAGTTCCTGGT A C	CTAGAATCTGGGAAGTCCAAGCTCAGTGCACCAATACATTCACTTCTGGTC/G/AJAGGTCTTTTC CTGGTTTGACAGACAGATACCTTGTGTATCTC/CACATGGCAGAGAAAGAGAGTAATCT
WI-14913	88	C A	---		CTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCGCAATTTC TAGTGATAGTAGAGGACTCA/C/AJCTGTGCACGTGCACCTTTTCATATACAGATCAACCAATCCAAAC CTACACCTCCAACCACT
WI-14914	66	G C A		CTGGACACAG TTTTCTCTAGC A	ATTTCCTTGATTGGCTGTGTAAGCCTGTGAAGTCAATGCACATCTGGACACAGTTTCTCTAGCA/G/ CJGAATTTATTGTCTGGGCTTGATGGCTTTCACAGC
WI-14926	49	T C	---		GTTTATTTCAAAATGACACATCCAGATTGAAATGGGCACTTAGCGAA/T/CJACTTGTGGACCACA AGACTGTCTGAGAACATGTTCAAGACAGTTTCAATAAAAATTTCTCTTAATCAGGTCCA



WI-16083	89 C T	ATGTTTAAACA CAAACATATC AAGGAT	TGAAAAGATT CCAGCC	GCATCTTTATACACAGAACTCATTATGTCTTAATCATCTTAAATATAATAAGCATGTT TAACACAAACATATCAAGGATCTTGGGCTGGAATCTTTTCCATTCTATAGAAAAGCACTAACCATC CATTAAAGCAG
WI-14930	55 C T	GGAGGAGTCC CTCATGGAT	CACAACCAACC AATACCGC	CAGTTCTGTGTTCTGGAACAGCTCTCTTTCCACAGGAGGAGTCCCTCATGGATCTTGGCGTATTG GTTGGTTGTGGTGAATTTGGGAGCACGAGGAGGAGCAA
WI-14946	47 T C	---	---	TCAATACTGAAGGTGTCAAAGTGTCTATTGCCCCCAGACATAACATTCCTCTAAATCATCTCTA GATCAGGAGTGCATAAGGACCATTAAGGCTCATTACACACAGTACTTTATGGAAGGATT
WI-15987b	80 A G	---	---	ACATTAAACACAGCACAAATTAAGGGGTCCCAACGAGGTGGTAGTGCTTCCACTATGTGAGGACAC TAAGAAGATGTCATGATGAACCAAGCTGCCGTGCTCTTAACCTCTCAGC
WI-15987a	32 C T	CACAATTAAA GGGTTCCAA	GGAAGGCACTA CCAACCTC	ACATTAAACACAGCACAAATTAAGGGGTCCCAACGAGGTGGTAGTGCTTCCACTATGTGAGGA CACTAAGAAGATGTCATCTATGAACCAAGCTGCCGTGCTCTTAACCTCTCAGC
WI-14948	56 T C	AGGGAACCTG CTAACTTGTCA G	GATGATCTTAC ATCAGTTGTTG GA	GAATAAGTTCTTATTGCCGTTCTTCAGGGAACAGGGAACCTGCTAACTTGTGAGTCTTCCAACA ACTGATGTAAGATCATCTTCTGACCATAGCGAACCTGTAAAGGCTTGTCTTCCCTCCAGCTGA
WI-16100	52 A G	CAAAAAGCTA TTTCTCTACAC TTGA	ACAGGAATGTC AGAAAACAGT ATATTAC	TTGTGTTAAATTCATCAAGGAATTGACAAAAGCTATTTCTCTACACTTGACAGGTAATAATACTG TTTCTGACATTCCTGTTATCAACTCTCTGAAATC
WI-14958	83 A G	AATAATTTAT CTCTTTCTTTT CAAGGG	AATGCATTCAT TTGGGTTTTT	GTGATTGATCTGTAAATTTGGGATTATTTATTCAACTCTAAATTCAGATGAAATAATTTATCT CTTCTTTTCAAGGGAGGAAACCAATGAATGCATTTTCAGTTTCTCCAGGCTTTGAACTGC AGCAGAAAATTCAGGA
WI-14976	35 C T	GTTGATTTGCT TCGTTCAAAG	TCAAACATAAT CTTCCATTCTA AGC	TATTTTAAATGGTTGATTGCTTCGTTCAAAGGCTTGTAGAAATGGAAGATTAGTTGAGGAG GGCAGGTTTGGGGTAGGCTCAGCGGGCATAGTGCCACAGAAAGATGCCATCTCACAOCTGGAG ACGTCCATGAGCACTCG
WI-14981	31 G T	TCAGTGGTGT TATTGGATTTT	CACCTCTGACA TAATACTTAGC ATAAA	TAATTGATTCAGTGGTGTATTGGATTTTGTGTTATGCTAAGTATTATGTCAGAGGTGGAGAT AAAGAGGAAAAGAAACAAGTGTGGCTCTCGCATCAACGACCTGATCTTGTACAGGAAGTTTTTGA GAGCTCACAAA
WI-14992	80 C T	TGCATTAAAT GAAGCTGCAG	GCTATGTGCTC AGCTTTIOCT	TGATTACATTTTAAATCATGCTACCGCCATCTAAGCCAAATTC AACACCACTCTGCATTA AATGAAGCTGCAGCTTJAGGAAAGCTGAGCACATAGCACCCCACTGATCGGAAAGAAACGTA
WI-15002	72 T A	---	---	AAATCTCTTCTTTCACACACAGATGAACCTTTAATAAATTACAAATGCACCTGAAATGCCTTCTTGA TTTCCCTAATTCAGTTTAGGCTCAAATGGCTCTCTCAAGGCTGGACCTCAAAGGCCAGTT
WI-15000	90 G A	GACAGAAAA GACTCAGACT GTCTAA	GTTTCTAGTTC TGCACAACTT CA	TCAAGCCAAATATCTGCAACAATAACATGTATTGAAAGGTATAGAAATAACAGATGGATAGACAG AAAAAGACTCAGACTGTCTAAGTATG/ATGAAGTTTGTGACAGAACTAGAAACAAATCCACCT



WI-12323	68	G A	CACAATACTT CATGTACCTAT GAAATAA	CACTGGACATA TTCCCTACCTG	ATTTGTTGATGTTGGTTAAATCTTATCTCTTTTATACACAATACTTTCATGTACCTATGAATAA G/AJACAGGTAGGGAATATGTCCAGTGCACAAACAGAGGACTCACACCTGTGCATAGACAGCAAC
WI-14683	91	A T	AAGGACGAT TTAGTATCTAA AAACA	GGCATGTCCCA GTGTTTT	CATAAGTTGCATTTATTCACGTCACGCCATCTAAAGCTACTGTGTACAGTAATCAGGACTGGAGAA GGGACGATTTAGTATCTAAACA/AJTCAAAAAACACTGGGACATGCCCTGAATTGCAAGT TGGAGTTCGTAAGAATCTAC
WI-13470	100	C A	CCTGCCCTTAT ATTGGAATTTT T	GGGAGACCATG GGTCTCT	ATTTGTTGTTTATTAGCACCTGAATTTAGGCAAGAGAAACAATTTCTACCTGAAGACTCCATGCAGT CAATTTCCCTGCCCTTATATTGGAATTTCTA/C/AJAGAGACCCATGGTCTCCCCAAGTGAGGAAGCC AGGCACTCAGCCCTTC
WI-14712	38	T A	TGAATGCTTCC AAGTACAAAT CA	TGAAAGTATGT TGTATATGGTA TTGTGA	TTTGGTGCTACTTTGTGAATGCTTCCAAGTACAAATCA/AJCTACAATACCATATACAACATACT TTCAATCACAACTCAATATAAAATAACCTACAAATCACATTGC
WI-13712	40	A C	TTTACTTTGTT GTCAATTTTAT TCTATTG	CCATAAGGTCT CACACTTTTCT TAT	TGGATACCCCTTTACTTTGTGTCATTTTATTCTATTG/AJATTATAAGAAAAGTGTGAGACCTT ATGGCTTCTGCTTATTGGCAATATGCAATATAATATTGTGTGTTGTTAAATTTATGCAT
WI-16163	35	C T	TCTGGTGATGC AATTGAAATA A	GCTGCCAATTA CATTAACTTAC AA	TCTAAGATTTTACTCTGGTGATGCAATTGAAATAIC/TJATTGTAAGTTAATGTAAATTGGCAGCATT GCCAAAGTTTAAAGGACTATTCTTTAAACAAGACAGTGTCTGACATTTATTTTCAGGT
WI-13453	88	T A	AATGCACAA ATCTTGCTCT TC	TCAGATTTTAA CATCTCTTCT AGCA	TTTTTTTATTTGCAATTTGAGTGTCTTATTATATTGGGAATTCAGTGATATTACATTTGTACAAT GCACAAATCTTGCTCTCTCT/TJTGCTAGAAAGAGATGTAAATCTGACCTAGTTGAACAGTCTT AATGAACTCATTGTCCAT
WI-16167	58	T C	CGCACTCTAA ATTAGAGATA GATTTT	TGCTCGTGGTG AATAAGATG	CGGATATAATTATGTACCGCACTCTAAATTAGAGATAGATTTTCTGATATACATTT/CJCATCTT ATTCACCAGGACACACACGACAGTAGAACAGTTCACACCTGATAAATTGCACAAGATG
WI-14482	17	G A	---	---	GCAGAACCAATTAATAIG/AJATCTGCAAGTTTCCCCAAGAACTCTGGAACCATAGTGCCTAAT GCCCTTAAATCGATACTAAAGGAGAGAGATAAAAGGACTGCTTGATGTGACAGTCACTGGT
WI-15069	81	T C	---	---	TGTAGTTCTTCAAAAGACATGTTGGCAGATAGCCAGGCCATACTATGTGTATTTCCAGTATCATGTAC GCACTAAAAAAT/CJGTGTGCTTGTGCTGCTGTGAGTGAACCATTTGCTTAAGATAAA
WI-16156	97	A C	TGAAGATTAA CCAGAGTCGC	AATTGTGTGCA TTTTGAAGAGA	ATCTGGTATTTGTGTATCCCAACAAGTATACAGATACTCTATAAACCAACCCACCCCTTCAATA TTACACTAATGAAGATTAAACCCAGAGTCGC/AJCTCTCTTCAAAATGCACACAATTAAGACG
WI-15012	59	G T	GCAGCAAGAT TACATCAGTA ATGT	CTCCAAATAGC CTAGAGTATAG TAAGGT	CATGGCAGCAAGATTACATCAGTAATGTATAATAACAGCTTTTTCATTGAAGCTTTTG/TJACCT TACTATACTCTAGGCTATTGGAGTGTCCCCAC

[illegible]

WI-15182	49	C A	GCACAACCAG GGCAAAATA	GCATGGGTTAA TCCAGCA	GAGACTGCCCTGTGACACA ACTAGCTAGCTGACAAACAGGGCAAAATA	ATGCTAATGGTTACCTTATTAGTAATCATGGTCCCTCATAGCATGGTCCAGATCCG	GAGACTGCCCTGTGACACA ACTAGCTAGCTGACAAACAGGGCAAAATA
WI-15198	38	T C	GGGCOCTTGGC ACTATG	ACTATCCGTC AGCAGAGTAG	GTGGACCTCTACAAGTACCATGGCCCTTGGCACTATGTCCTACTCTGCCCTGACGGATAAGTTGGC ATATGGTTACAGATTGCTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCTT	GTGGACCTCTACAAGTACCATGGCCCTTGGCACTATGTCCTACTCTGCCCTGACGGATAAGTTGGC ATATGGTTACAGATTGCTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCTT	GTGGACCTCTACAAGTACCATGGCCCTTGGCACTATGTCCTACTCTGCCCTGACGGATAAGTTGGC ATATGGTTACAGATTGCTGTCTACACAGTCCAGTTCCCTAGAGACTAGTCCGACTCTCTT
WI-12601	42	T C	CATTATTGAG TATTCTTGCTT TGAT	GTTGTAGTCTT ACATGCTTACG TAGAC	TCAAGTGGTAAATAGCCATTTATTGAGTATTCTTGCTTGAATTCCTACGTACGTAAAGCATGTAAAGACT ACAACATTACGACCCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAAACAAATTTTGTCATTACAGAT	TCAAGTGGTAAATAGCCATTTATTGAGTATTCTTGCTTGAATTCCTACGTACGTAAAGCATGTAAAGACT ACAACATTACGACCCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAAACAAATTTTGTCATTACAGAT	TCAAGTGGTAAATAGCCATTTATTGAGTATTCTTGCTTGAATTCCTACGTACGTAAAGCATGTAAAGACT ACAACATTACGACCCCATCTCTTCAAGAGGAAGTCTGGTATTATGGAAACAAATTTTGTCATTACAGAT
WI-14510	104	A T	TGGCAAAATA TGCATAACAA AA	TTGAAATGGT TAAACTGGCA	ATGTTGAGAGTAATATGCCCTACATAATTTAGTGTAAAGTACACCCCCAGATATTTTGGGGAAGAG TTGTTTGCTTTTGTGGCAAAATATGCATAACAAATATTTGGCCAGTTTAACCATTTTCAAGAGT	ATGTTGAGAGTAATATGCCCTACATAATTTAGTGTAAAGTACACCCCCAGATATTTTGGGGAAGAG TTGTTTGCTTTTGTGGCAAAATATGCATAACAAATATTTGGCCAGTTTAACCATTTTCAAGAGT	ATGTTGAGAGTAATATGCCCTACATAATTTAGTGTAAAGTACACCCCCAGATATTTTGGGGAAGAG TTGTTTGCTTTTGTGGCAAAATATGCATAACAAATATTTGGCCAGTTTAACCATTTTCAAGAGT
WI-15239	57	T C	CATTTGCAAT AAACACCATC A	GGACCTTATCT GTGGACTCAGG	CAGTGTGATGACATTTCAATGGGAAAGATTGTGCAATTTGCAATAACACCATCATTTTCCTGAG TCCACAGATAAGGTCCCGGAGAGGGGCTTCCCTCTCTCTGCTGGTGGTTGACGTTCCAGGAGT	CAGTGTGATGACATTTCAATGGGAAAGATTGTGCAATTTGCAATAACACCATCATTTTCCTGAG TCCACAGATAAGGTCCCGGAGAGGGGCTTCCCTCTCTCTGCTGGTGGTTGACGTTCCAGGAGT	CAGTGTGATGACATTTCAATGGGAAAGATTGTGCAATTTGCAATAACACCATCATTTTCCTGAG TCCACAGATAAGGTCCCGGAGAGGGGCTTCCCTCTCTCTGCTGGTGGTTGACGTTCCAGGAGT
WI-12634	52	T C	GCATCATATG AACTGTCTAGC AGT	GGACAAATTGT AAACATAGCT AATAGC	ATGAGTTTATAAAGTGGAGACAGCGCATCATATGAAGTGTCTAGCAGTATTATTCCTATTAGCTA TGTTTACAAATTTGTCCTGAAGGGTCTAGATGTGTACACCCAGAAAGTGGTGAATTCCTGA	ATGAGTTTATAAAGTGGAGACAGCGCATCATATGAAGTGTCTAGCAGTATTATTCCTATTAGCTA TGTTTACAAATTTGTCCTGAAGGGTCTAGATGTGTACACCCAGAAAGTGGTGAATTCCTGA	ATGAGTTTATAAAGTGGAGACAGCGCATCATATGAAGTGTCTAGCAGTATTATTCCTATTAGCTA TGTTTACAAATTTGTCCTGAAGGGTCTAGATGTGTACACCCAGAAAGTGGTGAATTCCTGA
WI-15249	34	T C	GGGCTTGACAC AAAGTTCTAA AA	GGAAAGCCAG AGATTTTAAAC AA	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTTTTCCTTAAATCTCTGGCTTTCCTGGCTGG TGAGGAGCACAGGCTGGGGTCTTCAGGTATCCACTGGTGGCCCGCATCTGTTCCTCCACTCCCCAG	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTTTTCCTTAAATCTCTGGCTTTCCTGGCTGG TGAGGAGCACAGGCTGGGGTCTTCAGGTATCCACTGGTGGCCCGCATCTGTTCCTCCACTCCCCAG	TTTGCTTGAAGGGCTTGACACAAAGTTCTAACTTTTCCTTAAATCTCTGGCTTTCCTGGCTGG TGAGGAGCACAGGCTGGGGTCTTCAGGTATCCACTGGTGGCCCGCATCTGTTCCTCCACTCCCCAG
WI-12159	28	C T	AAGACACCGT GCAAATGC	COCTCTCTCA GTGCACCTT	CTGTCCGGGAAGACACCGTGCATTAAGTGCCTTAAAGTGCACCTGAGGAGGGGAGGTCTGTGACTC CCAAACCCCTCGAATATTTATGAATCTAAGAGTCCAGACGAGTTCATCCACGGAGATCTGC	CTGTCCGGGAAGACACCGTGCATTAAGTGCCTTAAAGTGCACCTGAGGAGGGGAGGTCTGTGACTC CCAAACCCCTCGAATATTTATGAATCTAAGAGTCCAGACGAGTTCATCCACGGAGATCTGC	CTGTCCGGGAAGACACCGTGCATTAAGTGCCTTAAAGTGCACCTGAGGAGGGGAGGTCTGTGACTC CCAAACCCCTCGAATATTTATGAATCTAAGAGTCCAGACGAGTTCATCCACGGAGATCTGC
WI-12648	41	A G	CCTAGTGGCAT TAAGGATGC	TTGCTACTAAA AGTGGACATCC T	TCCCCAGATTGTATGGAAATGCCCTAGTGGCATTAAAGGATGCAGGTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACCTACTCCATGTTAGGTGCTTACTTGGATTATCTCATTAAACCCACA	TCCCCAGATTGTATGGAAATGCCCTAGTGGCATTAAAGGATGCAGGTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACCTACTCCATGTTAGGTGCTTACTTGGATTATCTCATTAAACCCACA	TCCCCAGATTGTATGGAAATGCCCTAGTGGCATTAAAGGATGCAGGTAGGATGTCCACTTTTAGTAGC AACCGATGTTAATTCACCTACTCCATGTTAGGTGCTTACTTGGATTATCTCATTAAACCCACA
WI-12684	64	G T	CATGCTGTAA ACAGCTGTGC	GGAACAACAA AGCCTAAATGG	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTAGTAACCATGCTGTAAACAGCTGTGCIG/ TCCATTAGGCTTTGTTGTTCCATTTAGAGAGCACAGGAGAGGAAATTTAGCATAATTTCTT	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTAGTAACCATGCTGTAAACAGCTGTGCIG/ TCCATTAGGCTTTGTTGTTCCATTTAGAGAGCACAGGAGAGGAAATTTAGCATAATTTCTT	ATGAGAGGTAAGTGTCAACAGTAGGCTTAAATATTAGTAACCATGCTGTAAACAGCTGTGCIG/ TCCATTAGGCTTTGTTGTTCCATTTAGAGAGCACAGGAGAGGAAATTTAGCATAATTTCTT
WI-15260	75	G A	AAAGGATGAA GCTAATCATG GA	TCTCTCCAGGG AGCTTGC	TTTATAAGCTGAATGAAAGAGGTCGACACAGCGGACACTGTCTATAAGTGGAAACAAAGGATGAAGCT AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGATGAGCTGGAGAAATTA	TTTATAAGCTGAATGAAAGAGGTCGACACAGCGGACACTGTCTATAAGTGGAAACAAAGGATGAAGCT AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGATGAGCTGGAGAAATTA	TTTATAAGCTGAATGAAAGAGGTCGACACAGCGGACACTGTCTATAAGTGGAAACAAAGGATGAAGCT AATCATGGA[G/A]GCAAGCTCCCTGGAGAGACAGGGACAAATCAAGATGAGCTGGAGAAATTA
WI-15325	39	T C	CATGTGGCTGG GAGGC	CCTTCCACCAT GATTGTGA	AAGGTTAATGGACTCACAGTTCCATGTGGTGGGAGGCTTCCTCACAATCATGGTGAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC	AAGGTTAATGGACTCACAGTTCCATGTGGTGGGAGGCTTCCTCACAATCATGGTGAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC	AAGGTTAATGGACTCACAGTTCCATGTGGTGGGAGGCTTCCTCACAATCATGGTGAAGGCAAAA GGCACATCTTACATGGTGGCAGTCAAGAGAGATGAGAGC
WI-13936	123	C T C	AGTTGGCATTG AATAGCCTAT	TGAAACTCCCA CATGGAGTT	TATTTGAGTATTTCCATCCATGGCGCTTCTCAGTCCCTATACATTCTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCCAGAACCTATGACCTGTATCTTCAGTTGGCATTCAATAGCCTATCIC/TAACTCCATGT	TATTTGAGTATTTCCATCCATGGCGCTTCTCAGTCCCTATACATTCTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCCAGAACCTATGACCTGTATCTTCAGTTGGCATTCAATAGCCTATCIC/TAACTCCATGT	TATTTGAGTATTTCCATCCATGGCGCTTCTCAGTCCCTATACATTCTCCAGGGTTGAGGTAGTCTACCC CCATAGGTTCCAGAACCTATGACCTGTATCTTCAGTTGGCATTCAATAGCCTATCIC/TAACTCCATGT



WI-14528	62	T G T A A A T	TTTTAACTTTT TCTGGATGGTA	CTCGATTAGCA CTTATTATAAA AATTAAAA	TATGCTTTATTGAAGAGAAATAGGCTATTATATATTTTAACTTTTCTGGATGGTATAAAATT/GJTT GAATTATAAATTTTAAATTTTATAATAAGTGCTAATCGAGACATCACTGGGTATAATTGA
WI-15347	74	C T A A T T T	GACTTCAAAG GAAAAGAACA	TCACTCCCCCA AGTCCTTIG	TATTTCTTTCGGTTTCGGATGCAAAACAAAATTTTAAAGAAATGTGACTTCAAAGGAAAAGA ACAAATTT/CJCAAAGACTTGGGGAGTGAAGGCAGAGCCTGGTGCAGATGGACGAGGTCTGCAGA CG
WI-14546	95	C A G G A C T C A	CCAATTTCTAG TGATAGTAGA	AAGGTGCACGT GCAGG	GTATTTCTGATGCTTTGACATCTGGGGCATTGCTGTCTCTAGAGAGACTACTTCTCTGGGACCAGC CAATTTCTAGTGATAGTAGAGGACTCA/C/AJCCCTGCACGTGCACCTTTCATATACAGATCA
WI-15353	37	G A ...		...	TTTATTGGCTGTCTCTGTATAACAAATGTGGTGAACAC/G/AJTCTTAATTCAGGACATCTTCCACCTTG TTTTGGCTTCCAGTTGTACTGCAAGACCAGTGTGAGGCACATAGGCTGATTAATCAGTGG
WI-14580	100	G A G T C T T G C A	CATTCCCATCT GTCTTGCA	CCGACCAAGAT CCTOC	AGAAATTTTCTCTTTTAAACAGGACAAGTAACAGATTACATCAAACTTCAGAACTTCTCAATAC CTAGTTATTATACACATTCCTCATCTGTCTTGCA/G/AJGGAGGGATCTTGGTCGGCTTAACA
WI-8540	73	T C G G C T T A	GGCCTGCAATT GGCTTA	GCCCTTCTTTT TCAGGCAC	CCAGCTGGAGGTGGAATAAATGCGGCAACCACAGAAAACACACAGCTACACAGGCCTGCATT TGGCTTA/CJGTGCTGAAAGAGGGCCGACCTCTTGATAAAGAAATGICT
WI-8039b	97	T C ...		...	AAGTAGAACACAATAAGATGGCTCAAAATATCAGAAATGCACATCGCACATCAGAGTAAATACTG TTTGGTAAACCTTGTTCAGTT/CJAATATGTATGTGTCCGTGCATGTGATTAATATCCTTCT TACCACAGTCACCCCTAAGAACCAAGCTTAGGACTAGGACACACACCAATGCAGAAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATGATTTAATGCCGAGCCGACACCCACA
WI-8039a	87	T C ...		...	AAGTAGAACACAATAAGATGGCTCAAAATATCAGAAATGCACATCGCACATCAGAGTAAATACTG TTTGGTAAACCTTGTTCAGTT/CJAATATGTATGTGTCCGTGCATGTGATTAATATCCTTCT TACCACAGTCACCCCTAAGAACCAAGCTTAGGACTAGGACACACCAATGCAGAAAAGAGCAGGGA GACCAGACACTCTGGTTGAGATGATGATTTAATGCCGAGCCGACACCCACA
WI-8044	107	C A ...		...	CACAACTTCAGAAAGTTTCTGCAATGTGTCTTCTGTCTGTCTAAAGATTTGAGCTTTGACTAT ACGATTTCCACACTGAAGGCATTATAAGGTTTCTCCC/C/AJAGTATGGATTCTCTGATTAATA AGCCCCGAATCTGGCTAAAGGCTTTCCACATTCAAGACATTTGTAAGGTTTCTCCAGTGTGGAC TCTCTGTTGTGCACAAGAATGGAATTCGGCTGAATGCTTTCCACACT
WI-8550	32	G A A T G C A A C A A G	GGGAACATCA ATGCAACAAG	TTTGTGGCTTG AGTTTACAAAT T	CTTACTACATGGGAACATCAATGCAACAAGTA/G/AJAATTTGTAACTCAAGCCACAACTTAGTTA ATAATCATGTTAAGGGACATTGCCAAAGAGCAACTGATGCTCAGTGAA
WI-8057	87	T A ...		...	TATTAGATAAAACCCCTTTGTTCCGATTCAGGATGTTAATTTGCTTCTTTAACTCTGTGACTTTT CCTGGTTCAAAGGACAGT/AJGATGGACAGCAGCAGAGGAGTGGGGTCTGAAAATGTAATCTTT GTGTCAAGGCACTCTGTGGCTCACAACCTGCCCTGTGTCAGAGGATGCTGCTTCCAGCCCTAAAG ACACTAGGGCTTTTCAATGGACGGGTGTTGAAGCAGCAGATGGTAAGG



WI-6192	91 A	GACTGCTAAG GATTTAATTG GAT	TGAAGTGTTAG ATGGCTAAGTA TTAAA	AAGAGGAACAAATTAGCTCAGTCCACATGATTGGCAGTTGGCATAATTCTAGTGAAGCAAGTGTCT GACTGCTAAGGATTAAATTGGATTAATTTAATACTTAGCCATCTAACACTTCAAGCATAAC
WI-6194	105 T	CACATGGCAA TGATAATAAA GAAA	TCTATCCTCAG AGTGTAGTCTG CA	AAGTGATGTGCTCACAATAACATTTCTCAAACTCAAACATCATGCTTGAAATATCACTGAACCTT GTCACCAAGAAGTCACATGGCAATGATAATAAGAAATTAATGCAGACTACACTCTGAGGATAG AGCTCTAAGAGTAAACAAATGGAATTTGGAAAAAATAGGAGTAAA
WI-6213	164 CT	---	---	CATATGCTGCTTTATTTCTGTAAGGATACACTGAAACGTTAGATGATAATAGCTAATGACAGAATGT AGAAATGAGGCATCAGCTTCTTAACCACTCCTACAAGAAATGTTAGTATGTATTGTCATTACATGTTT ACTTTTGATAATTGCTCATTATACATATGTC/TATATAATAATGTAATAACAGTAAGTAGGTGATCC TGCAATTCAGGTAAGCGGTAGGTGGAATCCAGATTTCTCTTGAGGAAA
WI-6217	131 CT	---	---	CGGGTTAAGAAATACCTTTAAATTTAGGTAATAAAGCTCAAGGAGGTGGGCTGTCATCTGTGGTG TCAGTCTTCTGGCCCCCTGGCTGTGTCAGTGTGCTCCAGGCTTGACAAGCAGCTCATTCAAGC/T GGCCACCATGGCCCTAGGTGCTCAACAAGTCCAGCAGCAATCATGGCTTCTCGTATATCTGATCC AC
WI-6238	175 GA	---	---	ATAGTCTTTATTTGTCAACGAAGGCTACACGGGATCACTTCTGGTTTGTATGCTTTTTTTTTC TAGAAGGTATCTACATCTGCATTTATTTACAGCCTTGTGTTGTTATTTACACAGTCAAGATACAGTGTTA GAAACACAAAAGTGTGAGAAAAAACTTCTCAAAATTTG/AJTTCCAGACTTCAGGAAAATGATT TCCACATGGTAAGGCCAGAGTCTCCAGTGTGGTTCATCCAGAAAGCAGCTTG
WI-6272	86 CT	GCATTTATTCA GGGAAACTT TAA	CTGTTTTTGA GAAGACAAAG AA	CTTGATTAATCAGGGCTTTGGGTCATAGGGGATTAGTCACTGTCAAGTCATAATAATGCATTTA TTCAGGGAAACTTTAATC/TTTCTTTGTCTTCTCCAAAACAGCTGCTGGAACACCTCAAATTA GGGATGTTTCATCTAAACACCTTTACTGAACTTGTATCTTGGGCCAGAGGAGGTTCTTTACTGTAG CAGAGGACTTAATGCAATGCCTATTGGGCAATAAATGAATACTTGATGCATTCATACAGGCAAGAA TCCCAGCATCCAGAGAAAGCTGTGTCTGCG/AJCTGCAAAAGCCATGGCTGCAGACATCAGGGAAGCT GGTGAGTTCTAGTCTCGCCTCTCGATTTCCTGOCAGCAGTCTTCTCTCTCTCTCTCTCTCTCTGCCC TCTG
WI-6303	98 GA	CCCAGAGAAG CTCTGTCTGC	CAGCCATGGCT TTGCAG	ATGCTTTTGATGATTCTAATTATTGCCCTTTTTCAGAGCTCTGCTGGTAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCCAGCGTGTGTCATGCTGCTGCCAATCAATCACTGTAAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGTAGTGTCTCTGTT CTTCCCTTTACATTTCTTTGGGGA
WI-6315b	193 CT	---	---	ATGCTTTTGATGATTCTAATTATTGCCCTTTTTCAGAGCTCTGCTGGTAAAGTGGGTGCCATACA AACAGTCCCTTTTCAAGCCCAGCGTGTGTCATGCTGCTGCCAATCAATCACTGTAAATGTCCATTGTCCA AACAGGTCAACCGTTGTCTCCATGAAAAACTGGATAAAGAGTTGCTGATAGT/CJAGTGTCTCTGTT CTTCCCTTTACATTTCTTTGGGGA
WI-6315	187 TC	---	---	CTTCCCTTTACATTTCTTTGGGGA

WI-6375	28 A G A A	GGTTTATTGCA TATGGAAATC	AATGTGAGATC TTTATTCTAAC CTTTTT	AAGGTTTATTGCATATGGAAATCAATAGAGTATCTTTTACAAAAAGGTTAGATAAAGATCTC ACATTTGTAAAGGCACATATGAACATTTTATAGCAAGCACAAAGGCGAGTGAGACATCAACAA TTGTGCTCAACAGATGAAATTCATAACCTTGTGTTTCTGATAAGACAAATTCACAAATCAAT TACAACAATGTGCTTATCAGCTCCCTCCACCCCTATATTTTAAAT/AJGCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409b	112 T A ---		---	TTGTGCTCAACAGATGAAATTCATAACCTTGTGTTTCTGATAAGACAAATTCACAAATCAAT TACAACATATGTGCTTATCAGCTCCCTCCACCCCTATATTTAATGCAACTGACAGTTTGAAG GACACCAAGACAATAGGGCT
WI-6409a	73 A T ---		---	CTAATAATCCTGGGCACATGGATTCCAAGAGAGATTTTGCAGCAGATTTTATTATAGTTACTTAA CAGCTAAATAAAGGGTGTATTAACCTTACTTACAGAGTCACTAAATAATGGAGGGGAAAGGAA GAGTAGGGCTAATCCAGTAGAGACTGAAGCTG[GT]TATCAACCTTCCCTAAGCATCTGTCTGGTCCG CAGC
WI-6523	165 G T GCTG	GCTAATCCAGT AGAGACTGAA	AGATGCTTAGG GAAGGTTGATA	TCTCTAGCCCTATTAGGCTACACTGTAGTCACTTCTATGAGAGCAAGGGAACAGGAAGATGGGC TCTGGAGTCCAAACAGGATGTGACGTCCCTGGTAGTCTCTCTTTTACACAACTTTTCCCTGAGA ACTGTCCCAGTCAGGTGGACCTTCACAACAACGACAGCTAAACCTCTGAGAGAAAC[C/G]CTG ACTTTCAGAAAGCATAAAGCTGAGAAAAA
WI-6554	195 C G ---		---	ATTGTAATTAATAATTACATGGGCCCTATTTATTAAGGACATGTGTAAATGTTCCACTTTGTTTAA IC/T]AATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558b	68 C T ---		---	ATTGTAATTAATAATTACATGGGCCCTATTTATTAAGGACATTTG/C]TGTAATGTTTCCACTTTGTTT AAACAATTACAAACATGTGGCTTAAATAATGTACAGATCAATGTAAACAAGTTTGAAAAATGGCG
WI-6558a	42 G C ---		---	AACCAACAACAACTAAGAAATGGGAAAGAAATGGCAGGTGAAGAACTCTTTTCAGAGAAATAA AGTTGTCATA/T/C]AGCAATGGATGTGTGTCAQAACATACTGCCAATAAAGTTTAAAGAAAAAGGA ACTCAATGAAGTTACTGTTATATAAAACAGGAGCTCACAGCAGGGATGTAAAGAGTTAATGGAAGAT ATCGTGAGCCAAAC
WI-6629	75 T C GTCATA	TCTTTTCAGAG AATAAAAGTT	TGACACAGCAT CCATTGCT	CTGCCCTGAACCAATCAGATTTAGTTTAAATCAATCAATCAAACTCCAGCTGTTTCTTGTCTTT TTACTTAGCAAAAGGAAACTTTAGTGAATGCTACTTGACAAGAGAAAGTCAATTTCTCAAGCACA T/C]ACCCAACTTGAAGGTGATTGAACCCAAAATAATGGTGGGAAACACCAATGAGGTGGAGGA ATGAGAAAGATGTGTGGCCAAAGCTATCTGTTATATTTTGAATGTTGCCAAT
WI-6644	134 T C ---		---	TGCTAACACACCACCATTTAAGGAGAGTACTAGGAAAACTACCAACACAGCATGTGAAACAGT TGGGCACGGTGTAAAGGGCACAGACTCTGGAGCCACAGC/C]TGGCTAATACACTGCAATATTTTA TGTTTAGCAAATTATAGCTGGTGTGTATAACCAGAGAGCGGTATCTGG
WI-6690b	106 C T AGCCACAGC	CAGACTCTGG	ACATAAAATA TTGCAGTGTAT TAGCC	

WI-6690a	28 T C	AAACACCACC ATTATTAAGG AGAG	GCTGTGTTGG TAGTTTTTCCT	TGCTAACACCACCATTATTAAGGAGAGT/CJACTAGGAAAACTACCAACACAGCATGTGAAAC AGTTGGGCACGGTGTAAAGGCACAGACTCTGGAGCCACAGCCGGCTAATACTGCAATATTTTA TGTTAGCAAATTATAGCTGTCTGTGTATAACCAGAAGAGCGGTATCTGG
WI-6770	53 A G	CAAACCCCAA AACATCACA	GCTTTGGAGT GTATAATAGTA TGAATAA	GATGTTTAATGACACAGATCTTCCAAAGTAATCCAAACCCCAAAACATCACA/A/GJAATTATTCAT ACTATTATACACTCCAAAGCAAATACTTCAACTGCAATCC
WI-6686	151 A G A	GCATTCTTCCA AAAACAAAGA	CCTTGTAAGTG ACTATTCCAAT GTT	ATTCTGTAGGCAAAGGTTTCAGCAATCAGCTAGCACTAATCTTGACCAATGGGTGAGTCAGCCTCA TCACAGAGATTTTTTTTTTAATTAGATGAATTTACATTTAAACACATGGTAACTCCAAGCATTCT TCCAAAAACAAAGAAT/A/GJAACATTGGAATAGTCACCTTACAAGGAC
WI-6761	32 C A G	GATCTAACAG CTGCAGAATG	AAAAGCTGGG AAGGAAGAAG	CCTGAGAGGCAGATCTAACAGCTGCAGAAATGG/CJCTTCTTCCCTTCCAGCTTTTGTGAACAAAC AATTCTCCTAAGGCATCAGAAAGCACTGAGTGCAAAATGGGTGTTTCAGGTACAAAGTCTC
WI-6844	225 T C ---		---	TAAATACTGCCAACTAGCATTAGTCCACTCTTGCCATCATTAAACAAAGGTAATTTCTCCTTG GTATTTTCAAATGATGCATTATACAATAACGAAGTTAGAACTTAAATGCACCCTGATTAAATTATG TAACTGGTAATTTGTTTTTAAAGCATAATAATTGGTTCCTTTCATATAAATGGAAATTTTAA TATTTCTCTGATAGTCTGAGGTT/CJATCATTATGAGTAGTGCAAGTGTG
WI-6824	112 A G ---		---	CGGTTTTGCTACACTTAATGGGTTTTTTTTTAAGGATTTTTTTCAGGTCTTGTGCAACATCAA ACAAAGGTACTGAGTACTCCACAGGTACAGAGTGTGCTGCCAA/A/GJACCTTAGAAAAATTACAT GACACGGAGAAATGGCCTCTTGCTCCTTGAAGAGCTTACAGTCTAGGATTTGACAACTCACAGT CTTAGAACTGGCAAAGTAAGGCAATTTCTTCATCCCTAGAGCTATTGTG
WI-6889	139 T C AATTC	GAAAAATGAG ATGCAGTTAA	TCACCTTGTGG CTTTTAATTAT TCT	GTACAAAAAAGCTGAGAAGGCCAACATGGAAGTGTCAAGAAAAACATTTCTGATAGTACGGACAA AAGAGCTCCTTCAATCAAGAGGTTACATATTAGTTCTCACCATGTAGAAAAAATGAGATGCAGTTA AAATTC/CJAGAAATAATTAAAGCCACAAAGTGAAACTGTTGTTCTGGGCCCTATGTTGTAGATT CTCT
WI-6911	216 T C ---		---	TCCCAGCTCATATTTATTTGGGCACAGAGTGGGCACTCAAAATATCTGATGAACCTTGATGAACGTGAA AAGAGGTCTCCTTAACAAGATATCATCTCCGAAGAGAGAGTCCCAACCATATAAAATGTATGAT CAAGTCCCAGAAAACTTTGCCCTCCCAAGGAATGTGTTCTAATTTGGTTTCAAGCACACTGGTTCC CACTTTTACCACCTT/CJCATGACATTGGACAATAGTACTACTCTTTTCTAC
WI-9413	112 G C ---		---	GCCAGTCTAGTAAGTCTCTAGGACATGACCAGACAGAGCCCTGTTCTATATGAAGACAAAC AGGTGCCCATACTGGGTGGAGGATACCGCTGCTATTTCCAGAT/CJAGATTGGTGAAGGAG ACCATGACAGATGACAAACGGAACAGTTTCTCAAAAACAGAGGTATGA
WI-9557	74 C T ---		---	AAAAGCTTTAAAAAAAAGTGGTGCTATCTTTAGAAAACACTTTTCAGCAAGATCAAGTAGCCCCAGCT ACAGCCT/CJTTGGTGATCTTAACCCCTCTCCTTT



WI-9617	37	G T	---			TGCTCTTTTATTACAGTTTCAACAACACACGCCGTG[G/T]TGGCACAGTCTACCAAAGTGCCCGCAG CGCCACGCTTGGCCGGAAGGTCTCATTTCTGTCCTCTATGGACTGATTGAATTTGGGATGGCCAG CTCAGAAATGTTCCACGTGGGGGCACTCTGTGGCAGAGAGGCTAGCCCTTGCCACACTGGCAOCCA AAGAGTTGCACGATGCAGCTTGCAAGTGGTCCAAAGCCGGTGTGCTGTG
WI-9657	121	T G	---			AATGCTGGAGAAACATCAACATTGAGTTGACATTTGTTTGTGAAGTATAGCTACCATCCACTAT CATGAAATTTTGTTCATTACAAATGATAGAAAGCCAGATTCTCAAAATAAAGT[G/G]ATAATTCCTT TGTAATAATAATGTTTATAAATGTTTATGAAGCTCATTACATTATCTTTTTTAAAAAAGTAAAAA TTTTAGAACATATGACGCTTTTCATAAATTAATGCTTTTGATATAGATTTGAGG
WI-13119b	114	G C	GCTGGGA		CCTCCCAAGTA	AAAATTAAC CAGGTGTGGTG T
WI-13119a	51	C G	---			CAGGCTTGTCTGTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACTCACAGTAGCCTCAAOCTT OCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGT[G/C]ACACCACACCTGGTTAA TTTTTTAATTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAAC CAGGCTTGTCTGTCTCCAGGCTAGAGTGAGGTGACACAATCAAGACT[G/G]ACAGTAGCCTCA ACCTCCTATGCTCAAGCCAGCCTCCCAAGTAGCTGGGACTACAGGCATGTGACACCACCTGGTTA ATTTTTTAATTTTTGTAAAGATAGGGTCTCACTATGTTGCCCGTCTCAAAAAACAACCAACTAA C
WI-13112	71	C T	AGCTTTT		TCATAAAGAC TACAGACTTA	ACAGGAATCTGAAAGTTACCAAGGCAATTTTCCCTTTTAGGATCATAAAGACTACAGACTTAAGCTT TTTT[C/T]CTTTTCCATATAATACACAATAATTTCTAAATATCCTTAAAAAAGAAATATAAATAGT TTCAGTATGTTATGTAGAGTCACATACTATGGCAAAAATATTTTATTAAATGAGGGAATAGGCCAAT TT
WI-12988	36	C A	CTCAGTACAA		TGGTACGTGCT	TGTTAACATTTTTATTGGTACGTGCTCTCAGTACAA[G/A]AACAGCATCAGTAGTGACACTTTGAT AAAAAGGAATTTTAGCTTAGTAGAAAGAAAGCCCAAGGTGAGAGTAAATGAATATGTACAT CTTTATGGAACCTGTTTGTGTGACCATCTTTATCTTCCCTGTGTGATGAGATGTATGCACACACAAGT AAA
WI-13020a	108	G A	CTTT		CTAATAGTGG AACCCTGAGA	TGCTATTTCATGACAGACACGTGAGACAAATATTCTTATTTTACAGATGGAAATAGACCCAGACATTA TTCAGTACTTTAACCACTAATAGTGGAACCCCTGAGACTTTA[G/A]ATCTGCAAGGGTTTAATAAT GCAATATCACATATAATTTCCATTTTAAACACCATAATTAAGTTTCCATTTTCTTAATAGAAAATGA TAAAAATGTTTCCCAATAT
WI-12837	87	A G	AAAGTCCA		CCATATACAT ATATCAAGGT	TGTATAAAAAATCCAACTTGTTCACAAGTACATATGTCCCTATGATTTTATGCATACATCCATATAC ATATATCAAGGTAAAGTCCA[G/G]TACAAAAAACAGCATTTCCCTATGGCCAGTGTCTACAGAAAGT AAGACTGTGCAAACTTTATCGTATAGTCAATGAGATTGCACACTAAGGCAGGATGAGGCAGAAAGCA AGTTGTGTTT



L42611b	50	G C	---				GTCCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCTGTGCTGCTCTGCTCTGCTCTAG TCTTCCCTGCTCTCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTTATTCACCA CTGGAGCTTCACCTTTGTTAC
L42611	34	T C	---				GTCCTCAGGCCCTTCTCTGGCTGCAGAGCCGCTTCTCAGGTTGCCTGTGCTCTGCTCTGCTCTAG TCTTCCCTGCTCTCGAGGTAGAGCTGGGTATGGATGCTTAGTGCCCTCACTTCTCTCTGTCTATACCT GCCCATCTGAGCACCCATTGCTCACCATCAGATCAACCTTTGATTTTACATCATATGTTATTCACCA CTGGAGCTTCACCTTTGTTAC
WI-1172b	179	C T A		TGAAGAAATG GCTGATACCA	ATGTGCATTTT TCACTGCAG		TGAACGTGTGGTTAAACTAGGCAATTGGTTAAATCAATTTAAAAACAGGCCCTAGAAACAGTG ACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTTCTGCTTC AAAGAAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCTGCTGCAAGTGAATAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1172a	17	C A	---				TGAACGTGTGGTTAAAC/CATAGGCAATTGGTTAAATCAATTTAAAAACAGGCCCTAGAAACA GTGACCACACCTCAAGCAATGATTATCCCTAGCACTCAGATTATGTTCTTGAAATACCATTTTCTGCT TTCAAAAGAAAGACATGAGGGCTTCTTGAAGAAATGGCTGATACCAAGCCTGCAGTGAAATAATGCA CATGATGAGCCTGGAACATGTTGT
WI-1177	35	G C A		GCAGATTGGA AGTGTGAAAA	CACCTACATTT CTGAATATTTA GACTCTTT		AGAGGCAGATTGGAAGTGTGAAAAAATGAAAGAA/GCJAAGAAAAAGAGTCTAAATATTCAG AAATGTAAGTGTGCTGCCCTCAACTGTTCTTTACCCACTTAATCTGCAATTTTGAAACTAGATTGAAT TCCCTTGCAAAACCCCTTGATCATGGATACCCGAGTTAAACCGTTAATTAAAGACATTAAACATGG CCTGGTG
WI-1231b	141	G A	---				TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAACATCCCATATTC CAACTAAGCAGGAGTGTTCACAAATAAACAACTAGGCTCTTTATTCCTCTCTTTCATTAATTTCTT TCAC/GAJTTATTCCTCACCCCTGAACGCCCTTCTCTCGTAGTGACATTTTAAATCCACTTTAG ACATTCGGACC
WI-1231a	126	T C A		GGCTCTTTATT CTCCTTCTTTC	CGTTCAGGGTG AGGGAATAA		TCCATGGTTTGGTTGCTACTGACTTTGTTAGCCTTACTGCCACTATGCATTGGAACATCCCATATTC CAACTAAGCAGGAGTGTTCACAAATAAACAACTAGGCTCTTTATTCCTCTCTTTCATTAATTTT CTTTCACGTTATTCCTCACCCCTGAACGCCCTTCTCTCGTAGTGACATTTTAAATCCACTTTAGA CATTCCGGACC
WI-472	114	G C ACAGAAAAG		ACATACATAT CCATTATACA	GACCTTCTTT TCCAGCCC		GAAGGCAGGACTGTGTTTGGAGGACAAAAGTAAATCTTTTATATCTTTTAAATTTTATT TTTTCAGGCATATAGACATACATATCCATTATACACAGAAAAG/GC/GGGCTGGAAAAGAAAG GTCAAGTGAGATTTCAGATATTTCTTAAATGCAAGGCTGACAAATTTGGGCTTGATT

WI-478	46	C T	GCATGCTCTGTG T TACTCTATTT TGTTT C	AAATGCCACAG GTGGCT	AAACCACTGCAACCTTCAAGCATGTCTGTGTTACTCTATTTTGTTCCTAGCCACCTGTGGCATTTC CAAAATATGATAATCTCTGCCACCATACTGCTTTAAACACAATAAGAACTGGCAGCAAAATATAGC ATAAGCTTACTTCTAATAATCAAAGGCTACCATCAGTACCTTAGCACATTTAAAAAATAAAACCAAC ACTGCCCA
WI-533	29	T C	ATCACAGCAG AGTACCTTTCT AACT	CCTTCCAAOCT CTACACAATCT T	AGCCATCACAGCAGAGTACCTTTCTAACTTTCJATAAGATTGTGTAGAGGTTGGAAGGAGGACAGGA CTGTTCTGTTGGTATAATGACCCCTGTGTCCAGTTAATCCA
WI-601b	112	T A	---	---	TCACCTATCTCTTTTGTGTGAGAACACACTTAAATCTAAGAATGATCAATTTCAAAATAAAGATGG TAGTGAGCGAACACAGAAGAGGTTTTCATTGACTCCTAACTGAGTAC[T/A]CAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-601a	74	C T	---	---	TCACCTATCTCTTTTGTGTGAGAACACACTTAAATCTAAGAATGATCAATTTCAAAATAAAGATGG TAGTGAG[C/T]GAACAGAGAAGGTTTCATTGACTCCTAACTGAGTACTCAAAACGAGCAGGTGCT CACAGTCAGGAAGCAGGTGCTGAGTACAGGAT
WI-863	107	A G	CTCCTTCACAA CCTCACCA	CTTCCCGGTAA GCCAAGT	AACAAAACAGACACCCCTCGGCTTCTTCCACAGTCACATGGGTGCCAAACAATCCCACATTCCT ACATCCTCCCACTGGGCTGCCCTTCCACAACTCACCA[A/G]ACTTGGCTTACCGGAAGCATAAA GCCAAGCATTTAGTCTTTATTGCAACATGGTCTGGCTGCAATAC
WI-919	36	G A	ACTGCTTGCTT GTTGATTTAAT C	TTATTCTAATC CCACATGACAG C	ACTCACTGCTTGCTTGTTGATTTAATCAACCTAGCC[G/A]GCTGTCAATGTGGGATTAGAATAAATA AACACAAAATGAACACACAGATTGCTAACAAAGCAGATTCTTTTTCAGGCACACGTAAGAT AATAACTTCAA
WI-991	37	A T	---	---	TGCATTCAATTATGCACCAATAATACTTCTGTACAT[A/T]CATTATTGTATTTCATTATCACAAAAT TATGAGTGAGGGATGATTGTTATCCCTATTTACAGATGAGAACACTGAGACTTAGAAGAAGTATCT TTCCCAAAGTCACAAAGTTAGTGACAGAGCCGGATTCCGAATCCATCAACTTGAATCCAGAGAAAAT GTTCTGCATCACTGTACACACACTGACTCCTTTTCTCCTTTGAAAACAAGGC
WI-1011	70	G C	CAGTATCTGA AGTTTTGTCT CCA	AGGAACACCTA CAAAATGACTT CT	CTTCTGACCTGTTTGACGTGGATACTGTTTTGAAGGCTCTGTCTCAGTATCTGAAGTTTTGTCTCC A[G/C]AGAAGTCAATTTGTAGGTGTTCTGCGGCTTTTGTCTACGTTTCCATTTCTCTAATACACTGC CGTCTTAAGGGAGGCTTGACAGCATTTATCAGATGGCTGTTTGTGTCATTTCTGTGCACTGAAG
WI-5381	178	A T	---	---	TTCAATGCAAGGTCCTCAGTTTACAGAACTCAAGGAAGAAAGGCCCTAGAGATGACACCAGAA ATGAGAGTGGCTTGCTCATGAAAATTGGACAGCATGTTCCAAAGCAGAGGGAACAGCATGGAGAAGA AAAATCATACTCTATCCACGTGCAGAAACTGGCAATTAGTTTTGT[A/T]TACTAAACACAAAATGT TTAACTGGGGTCCACAAACAGGATATGTTGGCAAATGGTATTCTGTGATG
WI-5791b	76	G A	---	---	CTATGTATTCCATCTAGCAAAAGCAAGACTATTTGGATAAGTTTCACAAAGATGAGAACAGGTCCTA GAACCTCAG[G/A]ATCGAAAGGAAGTTTCATCTAGTCCATAGACCCTATCTCACTGACCCAAAAGGTA AAAAATAAAATAAAGTAAAGAACTTACATCAGATTGTGCAATTTCTTATTTTGCCACCCTGTTTGT TAGGAA

WI-5791a	44 C G ---			CTATGTATTCATCTAGCAAAAGCAAGACTATTGGATAAGTTTC/GJACAAAGATGAGAACAGGTC CTAGAACCTCAGGATCGAAAGGAAGTTTCATCTAGTCCATAGACCCCTATCTCACTGACCCAAAGGTA AAAAAATAAAATAAAGTAAGAACTTACATCAGATTGTGCATTCTTATTTGCCACCCCTGTTTGT TAGGAA
WI-5406c	120 C T ---			CACTCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/J]TATGAGCCAC ACTTCTCAITTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGGAAGAAAGAGAGAGGCAA GG
WI-5406b	118 C A A	CCAGGATGTC AAGGTGAGAA	AATGAGAAGT GTGGGCTCAT	CACTCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAGGCC TTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAAC[C/J]TATGAGCCAC ACTTCTCAITTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGGAAGAAAGAGAGAGGCAA GG
WI-5406a	42 A G ---			CACTCTGCTGTTGTCCATGGGTGCCACAGACTCTTCCAGAAGAGCCACTTCCACAGATGCAACAG GCCTTTTGAAGGAGGCCAGTTCTCAGCATGAGCCAGGATGTCAAGGTGAGAAACCCCTATGAGCCAC ACTTCTCAITTCCTTAGAATTCTTGGACTCTGTGAAGAGGAAGGAAGAAAGAGAGAGGCAA GG
WI-5798	48 G C TG	TTTATTCTCC TTGTTTCTTT	ACTGTTAGAA ACCAGTATTT TCAAT	CCATTCCTTCTCCTCCCTCCCTTTATCTCCCTGTTTCTTTTG[C/J]ATTGAAAAATACTGGTT TTCTAACAGTGTGCTGGTATGGATACCTATGTTATAACATGCATAGTTCTATATGGGTATCA
WI-5415	54 T A TTT	TCTTCATGAAT TCATCTTTTCAG	GGACTAATTCA TGATCCGATCT	CCTGCTAATAATAATTTAAGCACGATTGTGCTTCATGAATTCATCTTTCAGTTTTT/AJTAGATCGGAT CATGAATTAGTCCAGGCTTTTAGTTGTAATCGAAATTGGA
WI-5437	41 C T G	TCCAGAGAA AAATCCAAGA	AGTTTCTAAAC ACAAAATATG GTTTAAG	TGTTTTAACCCAGGCAGACCTCCAGAGAAAAATCCAAGAG[C/T]CTTAACCATATTTTGTGTTTA GAACTCCCTGTGCCAACCACTCTTGATGTGAGTGAC
WI-5481b	131 A G CTGCAGTGG	TGTCATTTATG	TTACTTCCAGG CTCCAAGTATT	AAGCCAAATTCACATTAGTTGATGAATTTTACAGTATCTAATGCATGGGCATCTGTTTCAAC TCTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCG[A/G]A ATACTGGAGCCTGGAAGTAAGACTTGGCTATTTTCACAATTA
WI-5481a	29 G A AATTT	CCAATTTTAC ATTAGTTGATG	CCCATGCATTA GATACTGTAAA ATT	AAGCCAAATTCACATTAGTTGATGAATTTT[G/A]AATTTTACAGTATCTAATGCATGGGCATCTGTTT AACTCTGTTTTTCAAGAGGTAGTATATGCTGAAAAATCTATTTTGTCAATTTATGCTGCAGTCGAA ATACTGGAGCCTGGAAGTAAGACTTGGCTATTTTCACAATTA
WI-5492	38 T C ---			TCATGAGTCTTCTTCAAGATGCTTGTAAAGTCCCA[T/C]CAAGAAAGGATCCCATGGCCTAAT GAAGATGTACCTCCACCTTAGGATATTTTGCAGACCAA



WI-5826	134	T C	---	---	TATTTTTTTTCTCAATTCCTGGAGCACACCATGCTCTTTCTATTTCATGCTTCACATTTATTTTTT TTTCACCTTAGTTAAATGCTTTTCCCTTGATCTAGCAATGGCCAGTTTATACATATCTTTAGT[C] TTTCAAAATTAATGCCACCATAGAAATAATTTTCTAACCAACAGCCAAACAGCCTCACTCTTCCTT CCTGGTGCACTTACTTTACAC
WI-5546	40	C T	A	CCTGTATTTTA	CCTTATAACCCCAATACTTTTTCAGGTGAAAAGGGAAAAC[C]TACCCTATGTTTGCTAAAATACAGG AGTATAACAGCATGACATGTTAAGGGAATTACAAATGCTTGAGTGTAATTTCTGATGTGGGAAATAT TAGAAAATTAAGCGAGAGAGGCA
WI-5552	97	C T	TTT	GGCACCAGCCTT TTT	TGTTTGTCTGCACCTCCCAACAAGTGGTCAATGAGCCTCAAGGGTTTTGATTGAGCGGTATGGGT GGGGCTATCGGCACCAGCCTTTTAGAGT[C]TCCCTGGGCAATTTGTGCACTAGTGTGAGA
WI-5838b	161	C T	---	---	TAAGTTGATTTAAACACTCTGTGCTCAATTTTCTCACCTATAAAATAAGATAATAGTATCTAAAA AAAAAGAGAGAGAAATTAAGAGTGATAGACATGAATAACTCTGATGATAGTGGTTGTATCCCTGAA TCCTGCAATATACACATGATTCAATGAT[C]TCCATTTTGAAAATTAAGCTTTTGAATTGTTTTCCA ATG
WI-5573	58	C T	AGGTGGGA	AGAGTAATGTG TC	TCGGGTATTAGGATGCGTTACCCCTCGATGATGGCGTTTCATAAGGAGGTGGGA[C]TJGACAC ATTACTCTCCAACTGTTTCATCAGAACACTTCAACAGCG
WI-5850b	134	G A	---	---	CAGGACCTTGGAGCCTTTGCTGTTTGCTCTCCACCTCACTCTTTCTGCTGCCCATGGTGGAGC CTCTCTCAGGCTTCTCTATGACGGCTCTATCTTCTATATGGGGCAATATCCAATGTCCCATTC[G/A TTTTGCCATTTCCTGTATATCAAAACAGAGAGCAGAGGGTGG
WI-5850a	92	C T	---	---	CAGGACCTTGGAGCCTTTGCTGTTTGCTCTCCACCTCACTCTTTCTGCTGCCCATGGTGGAGC CTCTCTCAGGCTTCTCTATGCA[C]TJGGGTCTATCTTCTATATGGGCAATATCCAATGTCCCATTCG TTTTGCCATTTCCTGTATATCAAAACAGAGAGCAGAGGGTGG
WI-5612b	125	A T	TTC	ACTG	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATTTCTAACATCACAATATCTTATTCTGCCTG TCACACTAATTTGCAAGCATTCAATTGATTGACTATTAATGAGCATCGTGTCAATTC[A]TJGAGTGTT TTAGGTTTCTCAAGAGAAATTAAGTGTCTTCTGTTTCTGTAACCTCAAGTA
WI-5612a	44	T A	---	---	TGCCTGATTGACACATAGTTATCTGACAGTAAATCATTTCTAACATTAJACACAATATCTTATTCTGC CTGTCACACTAATTTGCAAGCATTCAATTGATTGACTATTAATGAGCATCGTGTCAATTCACAGTGTT TTAGGTTTCTCAAGAGAAATTAAGTGTCTTCTGTTTCTGTAACCTCAAGTA
WI-5636	26	A C	CCGCAATAA	CATCGAGGACT TTGGGA	TGAGAGCCAAATTTATCCGCAATAA[A/C]TTCCTCCAAAGTCTCGATGGAGGCATTTCAGAAATCGGG GCAGGGGAGGCAGAGGTGAGACAGATGTGAAGAAC



WI-5865c	103	C G ---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAAATCTTTTTTTCATTATGCATTCTGACTCACTCACTGCTCTATCAAAAATTAAAC/GJAAATATTAATATTTTATTTACAGAGGAACTCAGAAGCCAGAAAAATGACCAAGACACAGTCAGTCTCCATCTTCAAAAGGTCACAGTCTCTTCA GAGAAGACAGACAACCTAAATAATCCAGG
WI-5865b	99	T A ---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAAATCTTTTTTTCATTATGCATTCTGACTCACTCACTGCTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGGAACTCAGAAGCCAGAAAAATGACCAAGACACAGTCCAGTCTCCATCTTCAAAAGGTCACAGTCTCTTCA GAGAAGACAGACAACCTAAATAATCCAGG
WI-5865	165	T A ---	---	TTAGAAACCTCCATTATTCTGCCATGGTACATCTTTTAAAGAAATCTTTTTTTCATTATGCATTCTGACTCACTCACTGCTCTATCAAAAATTAAACAAATATTAATATTTTATTTACAGAGGAACTC AGAAGCCAGAAAAATGACCAAGACACAGTAA/JCCAGTCTCCATCTTCAAAAGGTCACAGTCTCTC AGAGAAGACAGACAACCTAAATAATCCAGG
WI-5874	76	T G ACAGAAAA	CATAGCATGG ATAATATTAT ATATGT	CTCAGACATTCTTTCATTAGTTGTTAAATTTTGTGTTTTCATAGCATGGATAATATATACAGAA AAAAATTTT/GJTACATATCAAAATGACTGAAACCTACTAGGTAGCAATTTGTTTGTCAATTTGCT CATGGAGCCGACGTTCCAGCTCTCAGTTTTCATC/JTTTTTTCATAATTTACTCTCTTTCTGTG ACAATGTTCTGCTTCTGTTTCAACTCTCTCATTTGCTGATTGGATGGTAGTCATAAAATATGGGTGATT C AGAAAATAAGTAATG
WI-5752	36	A T TTTTCCATC	GACAGAAAAG AGAGTAAATT ATGAAAAA	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAAAGTGTTCCTCGATAAATA/C/GJC CATTAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAAGCCGAGTTTTCGATTACACACA GTTGCTGTTTTAACCTCTCTAAATCCGATAAATAGCCATTAGGTATTAGATAAGC/GAJTCCACGAAA CATTGTTGAAAAACGAAGCCACGTTTTCCGATTACACACAGTTAGTTGCTGTT
WI-5760b	61	C G ---	---	TTAGCAGAAACAACAAAAATGTCACAACACTGCAGTAAAGAAAGTGTTCCTCGATAAATAACCCAT TAGGTATTAGATAAGCATCCCATAAACATTGTTGAAACGAAGCCGAGTTTTCGATTACACACAGTT GTCTGTTTTAACCTCTCTAAATCCGATAAATAGCCATTAGGTATTAGATAAGC/GAJTCCACGAAA ACATTGTTGAAAAACGAAGCCACGTTTTCCGATTACACACAGTTAGTTGCTGTT
WI-5760	187	G A ---	---	AATATCTGGCCTTTTCTCTTAGGAGGAGATTCTCACCATGGGAATCTTG/GJTGCAAGTTAGAT CCCACCTCACTATTGAGAAGCTAAAGTGTAAGACTACTCATTTCTCAGTCTTCTGCTG
WI-5944	52	A G GGAATCTTG	TTCTCACCATG AAGTAACTTG	GAGTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCCTCAACTTCACATTACAGCAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGCATGTAATTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTAC/JTJTGCTCTGTGCGGTATCTGCTCCAATCACCATTCCACTTATTTCTCTAT GCTGAATGAAACGGTTATATTACAG
WI-5967b	148	CT ---	---	

WI-5967	165	CT	---			GAGTTAATGAATCCTGTTCCCTCCTAAACCTCCTGTTCCGCCAACTTCACATTGACAGATATT CTTTCATGGGTTATTTGCCCAAGTCATGAGGAGATGATGTAATTTGTGATCATTTCAAGAGTGTGAG TAATGCTTGGTACTTGTCTGTGCGGTATC/TTGTCTCCAATCACCCATTCCACTTTTATTTCTCTATTAT GCTGAATGAAACGGTTATATTACAG
WI-6093	53	GC	---			GGGTAAGATCCAGAGCCACAGGTGAACCTGCCGGTATTGAAGTCTTTGGGCCA/GC/GTCTGTAATG ATCTGACTTCTCCAGAACCCCTCTCTCTCTGGAAGTTCCAACTGTGCACTGAGCCCATTTGTAGGGA GCATTTGAACCAAAACCCAGCGACACTGTGACATTTGACTTTTTCAGCAAAACCTTGATTGACGGTGAC ACACCATGCTTCGAGAAGGAATGAGG
WI-6141	80	TC	AGGTACTT	CTTCTTAATTA AGCATCTACA	TGAAAACCCCA GAACAGTG	GACTCTGTCTCAAGAAAAAAATTGAAAAATTGAATAATTAAAGCACTTCTTAATTAAAGCAT CTACAAGGTACTTA/T/C/CACTGTCTGGGGTTTTCATCTCTTACCTTTTAGACTTCAGGAAATT CAGAAAAATGCATGAAACAGGATTGTTACATGCAGAGAAAAATAGGGGAGATAAAATTTGTCTTTT CTC
WI-6450	45	T	G	CCAATGACTT ATTCTATATCT TGTCACA	TTGTTTGAAAT GTGTGGTACTT CT	ATAGGACAGTTTTTCTTCCAATGACTTATCTATATCTTGTACAT/GJAGAAGTACCACACATTTCA AACAAAGAGCCAGGCTATGCCAGGGTGGGATTTTTCACGGTCATGGTAATATGTCATGTAAAGACTA TTTTACTGGCCTTCTTTTATGCATAAAACAAGGTATTGGTCTATTCAACAAACATGTGTCAATACAG CAGTTGTCATGTCCCTCTGTGTAAGATAATAGTCTTTATAGAATAATGTGGTTTGAATAAAGCCACA AATTATTCTATAAAACAACA/C/T/AAGGAACGAGGCTCAAAAGTGAACAAACGGCCTTAGTTTC TAAGTGAAGACTAAGACGATATAGGAAAAATATAATCCGTGACCTCTTA
WI-6461	88	CT	---		---	GAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCTATTGAGTGAAGTATGTTATCATAAAGACATGCAAAACCTTTTCACAGTCTTGT CCTGG/G/A/AAATATCTCACAAAATTAATTATAAATTGGCATGCGACTTTCTGATTTAGCCTGACAGG ATTGTTCCCTT
WI-7466c	141	GA	TTGTCTCTGG	TTTTACAGTC TTTGTCTCTGG	AGTCGCATGCC AATTTATAATT	GAACTATCCTTTAGTGGTGCCACATTTTCTATTCTGATTTTGGTCACACAGGGACTTTCTGGGCT ATGAAATAGTCT/T/C/ATTGAGTGAAGTATGTTATCATAAAGACATGCAAAACCTTTTCACAGTCTT TGTCCTGGGAATATCTCACAAAATTAATTATAAATTGGCATGCGACTTTCTGATTTAGCCTGACAGGA TTGTCTCTTT
WI-7466b	80	TC	GTC	GACTTCTGGG CTATGAAATA	ACTGAA	TGCTTTTAAAAATAACAATGACCACCACTGACACCATAGTCTGTCTCCATTTGCCACGTCTTCCTC AGTAGAATAAGACAGGGACTTTGTCTGGCTGCTATCT/C/ATTCTCTCAGAGAGCACTTGGCCCT CATAGGCATTCCATAGATATTGTTGAATGAATGTGCTTTTGTGCATATTGATTCCTACATTGTATACA TTCTCAGGAGGACATTTGGCCTAT
WI-9814	104	CA	---		---	CCTCTAACAAAGAAACTTGACTTCTCACTCAAAATACCTTCTCTATAATTTT/JGJAGTAACCA AAATATTCTTCAAAATAAATTATCTTTTAAATTAGAAGAACGACAGTGTAGAGGTAGTACATTCA CCAAC
WI-9720b	55	AG	---		---	

WI-9720a	47 A G ---			CCTCTAACAGAAACCTTGACTTCCTCAACTCAAAATACCCCTTCTCT[AG]ATAATTTAAGTAACCA AAATATTCCTTCAAAATAAATTAATCTTTTAATTAGAAGAAGCAACAGTGTTAGAGGTAGTACATTCA CCACC
WI-9825	123 A T ---			CACGCTCTAAGCAGGATGTGGCTTATGAGATACTTTGCATTGTCTGTCTGCACACCTTGAATCTGCC TGCTGGCTCCCTTACTTTACCTCTCTGTGATGTGCAGATGAAGGCTCAGGGTCTT[AT]GAGGATTAG TAAGATCTCTTTCTAAGACAGGAGAGATTATTTACAAGAAGAACTCACAGGGTTAGTTTGCATT TAAGAATTGCCAGTCTTTTGTCTGTCATCATCTTGAACATTAATCCACATG
WI-9748	74 C G ---			CCACTTCAGTAAATCAATTTGTAGCAGTATTTCTAAAGATTTCTAATTTTATATGTTTACCCTTT GTCATT[CG]TCAGACCAAGTACATGTTTTCACACAGCCATCTTCTTTCTGGAATCTTTCAGAAT TACAGTTATGATGTCCTTTTATATTCCTCA
WI-9943	91 T C ---			TGAGGCTATGATTGCAGATTGTAGTACTAATACTTATTAGCAATTTCAATGTTGTGGGCAGTGT CGTTGTGTTTTATATCCATCTTC[TC]ATTTTAAATTTCTACTGAGCAGAAAAAATGTATACATT AACCTTTGCTCCCTATTTGTACCTTTAATATTGCATTTACACCTTCTCTTTTGTCAATTAGGGA
WI-9891	39 T C ---			AGGGCCCTTCACAGATCCGTCAGCTCAACACTGCCTCTT[TC]AGTGAGCCTGTGAACCAACCAAGAC GGCTGGTCATCAGTGTCATCCTCTCTTTCGGGACAACTATCTTTAAAGAAAAAAGAGTGT CTTTGAATGTATCCATTTATCCCAATAATCTTGTGTTAATAAATTCCTTATTAGGCCAAATCCAAT GTGCTGAAATATCTGCCAAGCATGTCATTTCTACACAAAGGATTGCAAA
WI-9897b	84 C T ---			CTCAGAAATTATCAGATCTTCCCAAAATGTATGTTCTGTTCTCAACATCCTATTTTCTCAAAC ATTTATCTAGCCTGTA[CT]AAGTCATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTGAGCA ACCCACAGGATTAGAAATTAGCACTTATTTTGTACCCACATTA
WI-9897a	83 A T ---			CTCAGAAATTATCAGATCTTCCCAAAATGTATGTTCTGTTCTCAACATCCTATTTTCTCAAAC ATTTATCTAGCCTGTA[CT]AAGTCATCCAGTGAGGCTGTTTATTCAATCTATGTGAAATTTGAGCA ACCCACAGGATTAGAAATTAGCACTTATTTTGTACCCACATTA
WI-9935b	115 C A ---			AGATAACCCCTGGAAACTAGAAGAAATTAATAACGTGTTGCA[CT]ACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTTCAGACACAGCAAGAAAGCC TGATATTAAGAGGCACCTTGCAATA
WI-9935a	42 C T ---			AGATAACCCCTGGAAACTAGAAGAAATTAATAACGTGTTGCA[CT]ACCTCACCAGAACTGGAAGG AGTCTGACTGTGTTCTTATGGGTGCTTGGACTGGCAGGGGGAGTTTCAGACACAGCAAGAAAGCC TGATATTAAGAGGCACCTTGCAATA
WI-9983	146 C T ---			CCTGTTAGTGCCAGAGTCCATGCTCTTGGCCACAATGTTAGGCTGCCCTCCCATTTTCTTGTCTGA TTCCCCAAACCCAAAGTTCTACCCCAATCTGATCAATGTCTGACTAGGTCATGGCTGTCAGGGTAA AGCATTATGA[CT]AGACACAAAGACAAAGAGGTTAAAGTTGCTGCTCAAGAGAGAGACATAA AAACAAATGGATCTGGAACCTAAGTAAAGGCTTCGAGGAGGAGGTGAGCAAGG



WI-10019	139	A T A T C T	T G A T G T A A T G C T A T G T A G C A A	T T G A T T A C T G T G C T T A G G G A	A T A T C A G T G G T T G A G T A T A C A G C A A T C T A T T T G T T A T T A T G T G T C T A T A A T C A A T G G T T C T A A C A T T C A A T A A G A T C T T T T G C T C T G C T C A G A T G C T T T C A A T G A T G A T A A T G C T A T G T A G C A A T C T A T A T T C C C C T A A G C A C A G T A A T C A A G G C C T T C T A C C C C A
WI-10020b	122	T A T T T	G C G A G A A A A G A A A T C A T G A C	G A C T G T T A A T T T A T T T A A T C A T T A G T C T G G	T T T A C T T C A T T G T C A T C T T G A C T C G T A T T A A T A A T A A T A T T A T G T T A A C T G G C T C T G A A A A G A A T T T A G G C A T G C A T A G A G A A T A G C A G T G T T T T A T T G G C G A G A A A A G A A A T C A T G A C T T T T T A A A A A A T A C C A G A C T A A T G A T T A A T A A T A A T T A A C A G T C C T A G G G T T C C G G A A G T G G C C T A A A G C A C G T A G T A G C C C T C C T T A G A
WI-10020a	39	T C A T A A A T T	T G T C A T C T T G A C T C G T A T T A A	A A A T T C T T T T C A G A G C C A G T T A A C	T T T A C T T C A T T G T C A T C T T G A C T C G T A T T A A T A A T A A T A T T A T T A T T A A C T G G C T C T G A A A G A A T T T A G G C A T G C A T A G A G A A T A G C A G T G T T T T A T T G G C G A G A A A A G A A A T C A T G A C T T T T T A A A A A T A C C A G A C T A A T G A T T A A T A A T A A T T A A C A G T C C T A G G G T T C C G G A A G T G G C C T A A A G C A C G T A G T A G C C C T C C T T A G A
WI-10084b	170	C T T T T A C A T G	C C T T T A G A T A T A T T G T G A T T G T	A C C T T T C T G A A G C C A G A T T T C	T C T G A G T C T T T C T G A G A C A C T T G C C A T G G T C A A G G T A G C A G G A T C A G G A A G G C A T T A T A A T A A T A T A A T T T G C A G A G C A T C T C T C T A T G C A C C A G A T A T T G T G T G A C A C A C T C T G T T T A A T C C A G T A T C C C T A C T C C T T A G A T A T A T T G T G A T T G T T T A C A T G C T G G C T T C A G A A A G G T T A G G T G T T T
WI-10084a	54	C A G G G A A G G	G T A G C A G G A T	C A A A T T A T A T T T A T T A T	T C T G A G T C T T T C T G A G A C A C T T G C C A T G G T C A A G G T A G C A G G A T C A G G A A G G C A T T A T A A T A A A T A T A A T T T G C A G A G C A T C T C T C T A T G C A C C A G A T A T T G T G T G A C A C A C T C T G T T T A A T C C A G T A T C C C T A C T C C T T A G A T A T A T T G T G A T T G T T T A C A T G C G A A A T C T G G C T T C A G A A A G G T T A G G T G T T T
WI-10289	29	T C C A A C T C T T	T C T C C T G T C C C	A T T C T T G T G T A T T G A A T G G A A T T A A	C C A G G A T T C T C T G T C C C C A A C T C T A T T A T C T T A A T T C C A T T C A A C A A G A A T T T A T A G A A T A T G C A C C A C A T G C C A C A A A G A C A C C C T T A T A T A G T
WI-1319	40	A T A T T C T T T	T G G C A C T T A G A A C A T A G T T T	G C C A C A C A C C C C T A T G G T	A A G A A A T C C T T G T G C A C T T A G A A C A T A G T T A T T C T T T A T T A C C A T A G G G T G T G G C T T A T C T T T T A C C T G C A T G C T T T A G G T C T G T T A T A A T T T G G T A T C T T T T G C C A C A A A G A G T C T G T T C T G A C A G T C T T A T G A T C T C T A T T T A A C A T T A A C A C T G G T C A G A T G T T T A A A C T T G T T G A A C C T G C A G C
WI-10316	104	T C C T C T T	C T G T T G A T T T C T A C C T C T A T T	G C T T T G G A A T G T A T C C A A A A G T T T	A G C A A C G T G T A C A A C T T A G T A G G T G T A A T C A G A A G C A T C T A T A T T A T T C A C C A G T C A C C A C C C T G G A C T A T A G T C T G T T G A T T T T C T A C C T C T A T T C T C T A T T C T A A A C T T T T G G A T A C A T T C C A A A G C A T C A T G G T C A C T T C C A G T T A T G A A G G A T G T T T A A A A G C C C A G C C A G T G A G T T G T G C A C A A T T T T G G A G A C A T T C T G T G A C C C C A A C T T A A A C A C T T C T C C C A C A C T A C A A G T T A A C A C T T C A G T T A C C A G G T A T T G A G C A G A
WI-2572	61	C T ---	---	---	



WI-10368	31	C	T	TGAAGCAACC	CAAGATATTAT	GAGGAAGCTGCCTGAAGCAACCAGGTCTTGTTCCTACCCCTCTTAGAGAAATAATAATATCTT
				AGGTCTTGT	ATTTATCTCT	GAGATAGGAGGAGCAGCCTGAGGACAGTCTGGGTTTGTCTACCCACTGGAAGCAGAATATCC
					AAGAGGG	TTCAAAGCTTTTCCAGTGAGTCATGTTGCTGCTAACTATATGACCCCTGATGGATTGCCTTTCAGGG
WI-10391	32	A	G	ATGACTCCCA	GGAGTTAGGA	T
					GTCAAGAAGTT	CCTCCGTTCTCTGTCTCAGGTATGACTCCCAAGTCAACTTCTTGACTCCTAACTCCCATCTCGGTG
WI-10567c	146	A	C	GCAA	GTAGCT	TCTGCTTCCAGGGGACGCACTGACACAGCCTTTTGTCTGTGTGACAAACAGACATTGCAGAAAG
						TGATGCTGCTGACCTCCAGGATA
WI-10567b	82	A	C	...	...	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGTCTCAATAATATTCTTTTTCATATT
						TTCCAAATTATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAGTCTT
WI-10567a	60	T	C	CTTT	TAG	CTAATAGCAA/CJAGCTACTGGAAGCGGCAAGAAATTAACCCCT
						AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGTCTCAATAATATTCTTTTTCATATT
						TTCCAAATTATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAG
						TCTTCTAATAGCAAAGCTACTGGAAGCGGCAAGAAATTAACCCCT
WI-11153b	84	C	G	TACTTTA	C	AGCGATGAAATTTATATGTTATGCTGACTAGCGGGTGTCTCAATAATATTCTTTTTCATATT
						ATTTTCCAAATTATTAATACTAGAAATTTTACCACACAGAAATTTTAAACATTTTAAGTTACCCAGAGT
						CTTCTAATAGCAAAGCTACTGGAAGCGGCAAGAAATTAACCCCT
						CGTTGGGAATATTTCTATCTCACCTAAATATGCGTGATTAATAATATACATTTTAACAACTTCAAA
						TTGCTTTAAGTACTTTA/C/GJGAAGACCTTGACTGTGGATTTTGGATTTTTCCTTTTCTTTAATA
WI-11153a	33	C	A	AATTATG	GTAT	AAACATGCATATTTAAGTTGTGCAAGATGTACTTATATGTTAATATCTGATATCAGCATCCCTT
						TATGTATT
						CGTTGGGAATATTTCTATCTCACCTAAATATG/CJAGTGATTAATAATATACATTTTAACAACTTC
						AAATTGCTTTAAGTACTTTACGAAGACCTTGACTGTGGATTTTGGATTTTTCCTTTTCTTTAATA
						AAACATGCATATTTAAGTTGTGCAAGATGTACTTATATGTTAATATCTGATATCAGCATCCCTT
WI-2616	125	T	C	ATCC	GTCCCAGT	TATGTATT
						GTTGTGAACTCCAGTATCATTTCCCTCAAACCCAGCTTAATCACAATCAGCTTTTCTTTCTGTA
						GAGCTCAAACCTCAGTCTGAATGAATGCTGCAAAATGTAAAGAAATGATCCTA/CJACTGGG
						ACTACAGCCATGGAGAAAGCAATGTAGTCAGCAAAATGTTAACAG
WI-11163	58	C	T	TGAGA	T	TGACTCAAAGGAAACACACACAAAAGTTTACCAGTGAATATGACCAAAATGAGA/CJAAAT
						TTGTTAAAAAAACCTCAAATGAAGAGACAAATATAGTTCAAGATTTCAGGTTCAATATTGT
						ACCTACAAATAGGATAGTCATGTTGTGGCAGACTTTTCTTTTCTTTTCTTTTGT/GJCTCTTA
						GAATCCATTTTGTCTTTTGGCCAGCATTCCTCTCCCATATTTTAAAGGAGAGAAATTCACCTTTTCT
						CTGTTGGATGATCACAGGTTCTGCTCTTCCCAATCCAGAGGAGGAGTACTATTACCCCATGGGTCTAT
WI-10656	59	T	G	---	---	AGAGAGGATTAAACAGGGGTGATGCCTGCAATGGGAATATTGAAACC

WI-11169b	154	T G T T T T	TTAACCAAGA GTTTTTCATTG	CTAACTTAAAA ATCCTCATTCA AAATATAA	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAATTAAGCCTAAGTAGTGCTTTTAAACCAAGAGTTTTCATTCTTTT TTTAAAAAAGAGCAGACATG/GTTTATCATGTGTCTGATAAATTTTATATTTGAATGAGGATT TTTAAGTTAGCAT
WI-11169a	95	A G T T G A A A A	AATAAGTGAA AGTAACTGAC	AAACTCTTGGT TAAAAAGCAC TACTT	CAGCATAGAGGCTGTAGTGACCTTGAGTTAGATTCTCTATCGAGAAAGCAATAAGTGAAAGTAA CTGACTTGAAAAAATAATTAAGCCTAAGTAGTGCTTTTAAACCAAGAGTTTTCATTCTT TTTTTTAAAAAAGAGCAGACATTTATCATGTGTCTGATAAATTTTATATTTGAATGAGGAT TTTTAAGTTAGCAT
WI-10685	25	A G	---	---	CAAGTGCTTGGACCTTGGATAGGTG/GJACCGGCTGAAGTTGGACAGTTGTTGGTTAGTTGGAG ACCAAAATTCAGTCATCCTGTATATAGATCTTGTCTTGGTTTACCACTAGGGTCACTAAAG AGAGATGGGAGACAGTCTCAATCTGTCTAATAATTCCAAATAGCCATGGGTTTGGACAAAATAC AAGGTTAGTGCTCTCTAACTTAATGGGCATA
WI-10686	133	C T A A G G	TGCCCCGTGTC AATGATTCTT TCTGCTCAAAG	CAATCTCTAAA TTCATGTGTAG ACACA	AATAACCTGTGGCACATAAGGCAATACTGAGCCCATACAGAGTGTATTTATGTTAATATTGAAA AAAGTCAAGAGAAACAGATGATATAGTTCTGTCTAGAACTACTTGAATCTGATGCCCTGTCCAAGG C/TTGTGTCTACACATGAATTTAGAGATTGAATGAATAATGGCAAAATTCAGAAAAGGG GGTAGGATGATTCTAGAAATGCCACTTACAGCCACTGAAATATATTGCCCTCCAAATGATTCTTCTG CTCAAAGAGT/AJTTTTTTTAAAGTTATCTACTTATTTATATTCTGCTTTTTCAAAAGAAATGTGAGA ACAGTACAAAATGTGTTCAGTATAGCAAAATTAATTAATAAGTAAGAAAAGAAAGCCAATT TGGGC
WI-10694	144	A G T A T A G T T T T C	TGCAAATGCTT TATGAGTTTTC	GGCATTITGTA AAGGAGGAAA	TAGAGAGTCTTTCAGTTTCAGGGTTGGAGGGGTGGTGAGGTGAGATTCACCTTCTTAGAAGCACTGGC TATGTACAGAAAGATAAAGTCTGAGAAAGAACTAGTTCTAAAGTGTTCAGTCTTTTGCAAATGCTTTA TGAGTTTTC/GJTTTCTCCTTACAAAATGCCATCAATTCCTCAAGGAAAAAAAAGCTTTCT T
WI-2716	23	T C C	TGAATTCATCC AGAAAAACAG	TCTCTTTTCTC TCTTGTGTCA TTC	GTGAATTCATCCAGAAAAACAGCTT/CJGAATGACAACAAGAGAGAAAGAGAAATAAGGTTTTTGT ATACGACAAGTGGCTCAAGCAATTTCTCTGTCCAGTGCATGGAGCAGTG
WI-10719	115	T C G C C A T T C T A G	TGACTCTCAAG GCCATTCTAG	GCACTGCCAGC AGCC	CAGGCCCAACTCTGTCTAATTAAGTGTTTTAGAACAGACACCTCAGTCACACAAAGTTTCTTGTATGT GCCACCATAAACAGTTACTGGAGGATGACTCTCAAGGCCATTCTAGT/CJGGCTGCTGGCAGTGCTT TTCCAGCCTGCTGCCATAACTAA
WI-10721	40	A G C T T G C C A	TGGCTCTGCTA CTTGCCA	GAACTCCAC ATAAATAAAT CTCA	CAACCAATTCAGATTAAATTTTGGCTCTGCTACTTGCCAA/GJATGAGATTATTTATGTGGAGTT TCTGAAGATCCCATGGTAAATAGTATTCCTCTCCCTGCTTAGGTTTGAAGAAGTTGAA

WI-11204b	88	T C ---			GCACACGAAATTGATTATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGGTG AAAGAGAAAACCTTTCACCTTTTCJATTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAATTTTAAATTGGGAGAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATTATTTCAGAAG GCAACATC
WI-11204a	80	T A AACTT	GTAAAAGGG TGAAAAGAAA	TGATCACTTAA AATGTACATAAA TACCTTT	GCACACGAAATTGATTATATTGGCTGACTTTGAGGAGGAGAACAGGGAGTTGAGGTAAAGGGGTG AAAAGAAAACCTTTT/AJCACCTTTTAAAGTAACATAAAGGTATTATGTACATTTTAAAGTGAT CAAAAATTTTAAATTGGGAGAGAGATTAGTGAATCAGAAAAATAAGTCTGAGGAAATTATTTCAGAAG GCAACATC
WI-10732	80	C A ATTGGTTCAC	GCTGTGTCTTC ATTGGTTCAC	AAGACAATG CATAACAGAA CTTTAA	ACATGTATTTCCTTATAGTGTGTCAGCCTTCTACCCCAAGAAATATCCCTGGTTTATTGCTGTGCTTC ATTGGTTCACCTC/AJTTAAAGTTCTGTATGCATTGTCTTGAGTCCACATAGGTGTTAATCATTTCCA CACCACCTCTGTTAACTGTC
WI-11206	127	A T ACTC	GGTTGTGTTTT CTGTATGTACA	GAGTGACAATC CTAATGGTTGG	TAGCTTTTCTTTGTACGAGTGTCTATAAAGAAATTACCACCTCTGTACATTTTGTAAAGATAGCACAG AGAGAAGCATTACAGGGCACAGCAACATGAGGTGTGTTTCTGTATGTACAACTC/AJTCCAA CCATTAGGATTGTCACCTCTCATATATAGACAGAAATTCAGTGGTGTGATTGAAATTCACACATGGA ATAAGTCTA
WI-11215	68	C T ---		---	GAAAAAAAGTTTAAATTGGATTGCTTAGTTGTCTTAAATTTGACCTACTTTCAGATTTATTTTAGT IC/TJATTTTCTATAATAATTTCTTGTAGTGTGATTTTCTATAAATTAAGGAACAGATATTT ACACAGAGAAGACAGGATTGCTTGAATTAGTATAACATTTCTTATTCCAAGCCCCCATTCACCATGT TTT
WI-11219b	89	G A AGAGAAA	GAGAGAAATAT TCCAAAAAGT	GGTCTCTAAT TTTTCTACACT TTCT	ATGAAAAATGCATTAGAAGAAATTGGAGGATAAAATTGAGAGAAATATTCAAAAAGTAGAGAAAA GAGACAAAGAGATGAAAAATAGGA[G/AJAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11219a	18	G A ---		---	ATGAAAAATGCATTAGA[G/AJAAATTGGAGGATAAAATTGAGAGAAATATTCAAAAAGTAGAGAA AAAGAGACAAAGAGATGAAAAATAGGAGAGAAAGTGTAGAAAAATTAGAGGACCATTCTATACAG TCCAATATTTGAATAATAGTTATTCAAAAAAAGAGGCAAGAAATGAAGGGGAGAAAAATCCAC AAACATCTC
WI-11222b	136	G A GGCTGG	CATACCACTGC GGCTGG	CCTGGTAGCCA AGTTGTGA	AGCCACAGTGGAAATCATTTACACTACCGAAATCAGCAATGTCTAAATTTGGGGCTTTGGATTTTGT TTTTGTTTTTCCATAGACCCCGTTGAACTATTGTTAAACATTTACCAGCATACCAGCTGCGGCTG G[G/AJTCACAACCTTGGCTACCGAGGAGAACTGACACAGACTTCGTATTGCTTTCACAGGCTACTGG AAAGCC



WI-11228a	25 C T A	GCCACAGTGG AATCATTTAC	TTTTAGCATTT GCTGATTTGG	AGCCACAGTGGGAATCATTTACACTA/C/TTCGAAATCAGCAAAATGCTAAATTTGGGGCTTTGGATTTT TGTTTTTGTGTTTTCCATAGACCCACCCTGTTGAACCTATTGTTAAACATTTACCAGCATACCAGCTGCGG CTGGGTCAACAACCTTGGCTACCGAGGAACCTGACACAGACTTCGTAATTTGCTTTTCACAGGCTACTGGA AAGCC
WI-10775	39 C T	TTTATGCCATA TTAATTCATTA CACTC	CTAGATGTATT TGCTAAGAAA ATATGATG	TTGCAAGTTTGTGTTTTATGCCATATTAATTCATTACACTC/C/TACATCATATTTCTTAGCAAAATACA TCTAGACACCTGGCACTCAGTAAGGGATATTCCTGGCACGATAATCATTTGTTATCATTAGACATTGCA GGAACCACCATATGGATGGATAAATGTGTTGTTTAAATGAAGGCAAGCAATTA TTGCATGCATTTATACGAAAGGAATTAATAATCTTCCTTATAGTTGAATTTTAAGTAAATAAAA GTTATACATATAATACAAAAGTTGTAAAGTATAGTAACAAATGAATTAGAAAATTGTCAGTGGTTGC TAGTACAGGAATCAAAATTTGGACTATGAACA/C/GACATAGTTGCTAAGGATATTCACAAAATTAT TTCATGA
WI-11226	165 A C	---	---	---
WI-10778	62 A G	GCAAGGGAGG AACATTTACA G	CTGGTGACATC AGAGATGGAC	CAGTGGCTGGCTACTGACAAACGTAACATCGTGGCAGGTGGCAAGGGAGGAACATTTACAG/A/GJG TCCATCTCTGATGTACACGAGGGCCAGGAAGGTTGATCTGGAG
WI-10789	21 C T	GGGACACACT GCTCTAGACC	TTGAGGGACCC TGGA	TGGGACACACTGCTCTAGACC/C/TTCOCAGGGTCCCTCAAGGTGGGTGTAGAGGCCCTACTGCCCT GCCCTGGGACGACAGGCATCAGGGCCTTAGTCTCTGTTGAGGAGAGTGAAGGGCCACCAOC
WI-10810	58 C T	CATCTTCATGG GCAGGAAT	CAACCCCTAAG AACACAGAA ATG	ACAGAAAATGCCTAGGTCTTGTAGCAAGAGAGAAAGCATCTTCATGGGCAGGAATTTCTTCATT CTGTGTTTCTTAGGTTGTGGCTGGCCATCAGTTCACTCAGCCCTGTCCCTGATCCAGCAACATT TCCGTAACCTACCCCTCTAGAAGTCATGCAAGAGAAATGATGA
WI-10828	23 T C	---	---	GGACCAACAGAAATTAATTTGGCA/T/CJAGGGTTTCTTAAACTATTTCTGCAGAACATTAGTAAAGT TTAAATAAGGATCAGGCTACCGAATACAGTTAGGGAACATGTGGATGAATATTTCTTTAGTAGAG GACTTCTAAAGGCTATAATATTTGGATACATTAGGCTCATTATGAATCTCAAAAGGAGCATGTAGT AGGCATATCTAA
WI-10832	91 G C	CATTAACTGCTC AGGCTCTOC	CCTAACTGCAG GTGACTTAGAA A	TATGCCCTCCCAACGAGCCATCCACGCTGCTCTTAGCACAATAAATAAGATATCATCTGAATG GGCACATTAATCTGCAGGCTCTCC/CJ/TTCCTAAGTCACCTGCAGTTAGGTCTGCAGACACTGTGTA TACCATATAATCTGATTTCTGAGCAGGAGGGGAGGAGATGAGAGAGGGCTGCTCCGTGAAATAC TAGTTCGG
WI-10834	96 C T	AGAAATTAACCT GTTCAAAAGT GTGTTAAT	TGGCCCTATAA AATTGGTATTA AG	GATTTGAGTATTATCAAAATTGCCCAAGAGCCATTAAACAAGATTTAATAGTTAAAGCCAAACTATA AAGAAATTAACCTGTTCAAAAGTGTGTTAAT/C/TCTTAATACCAATTTATAGGGCCACCATTAACTT CTGAAGAAAGGTCAGCATATGCAACTAAATTTCTAAAGTCCAGT
WI-2287	24 T C	---	---	GGATGATGTTCTGTGGTCCCTTTAT/CJAAAGCCTCTTGCATCCCAATGTGTAAATTTATTCT TGGTATTTCTCGCTTACCCATAGTCACCTGTCAAGTGTCCACCT



WI-2296	81 A G	TGTTACTTTGA TTCCTTGCTCT	GCAAATCACAC AGCTAACTGG	TGGAGGGTTAGAAATGCAGGTGGCATCCTAGAAAGGTCTCAGGCTTTAGAAATAAGTTGTTACTTTGA TTCCTTGCTCTGACIAGCCAGTTAGCTGTGTGATTTGCAGAAGTTACATTTGTTTGTG
WI-2300	77 G T	GGCACAGAAG CCAGTCATAC	GGTTGGGTCAA TTTTAAAGCA	TTTCATCATGCTGCTCTTCCCTGGAAATTTCCCTTTATTTAGCGGGGAGGTGGTAGGCACAGAAGC CAGTCATACI[GT]TGGCTTTAAATTGACCCCAACCATTTACTAAGAAATAGCATTCA
WI-2371	55 G T	GTCCTGTTCTT CCAGCTTCT	CAAAGATTGAC AGCCACCAC	CAATGATCCCCCAACATTTCCAGGGAAGGTCTGGTCTTGTCTTCCAGCTTCTGTTGGTGGCT GTCAATCTTTGACATTCCTTGTCTTGCAGCTGTATAATTCCAATCCTTGCCTCCAGCTTTACATGATGT TCTCTCGTGTGTCTGTG
WI-2395	122 A C	GAACATATTT GTAGAAAAAT TACTATCCAA	TCACCTTTCTA TTTATTCTGAA TTCA	GGGGGCACAAATTTAGCTACAGTGCATATTAAAAGATAACATAGAAATATCATATAACTTGGTTTAC TGAAATCTGAAAACTTAGGATGAGTGAACATATTGTAGAAAAATTACTATCCAA[VC]CTGAATTC AGAATAATAGAAAGGTGAATCATCTTATATCATTAAGAAAGCTAAATTATTAGTAACAATCTTTA CATTACACAAACCCA
WI-2437c	192 G A ---		---	CACGAGCCACCACTTACAACTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAAATCACAACTTTCTAAATAATAGACACCAAAAAATTCCTCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTG[G/A]GCTGTG GTGCCAAGGACGCATTATG
WI-2437b	179 G A ---		---	CACGAGCCACCACTTACAACTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAAATCACAACTTTCTAAATAATAGACACCAAAAAATTCCTCAATGCTCTAA ATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACI[G/A]AACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2437a	128 G A ---		---	CACGAGCCACCACTTACAACTCTGTGGGAGTCTGGCTTTGATTATTTGGGGACAAAAATAATTT CAGCTTGAAGAGAGATTCCAAATCACAACTTTCTAAATAATAGACACCAAAAAATTCCTCAAT[G/A]CTC TAAATAGATGGACTCAACCCCTTCTCTCTGCAAGAGGCAATCGACGAACATCACAGTGGGCTGTG GTGCCAAGGACGCATTATG
WI-2440	71 G A	GCAACCTACT GACAAATTTAA TTTTAGTT	AACAACTCTGC TATTGGTCTCA C	CAGTAGGAAACGGGTCTTCTTAGACCCCTCCAGAAATAATGTCAACCTACTGACAATTTAATTTTA GTTG[G/A]GTGAGACCAATAGCAGAGTTGTTACCTGCAGAACT
WI-1356	123 T C	TGTTTAGGAA ATAATGACAA GAAAAA	TGGTTACAACT GTACCAAACAT G	CTGTAACCTACACACATCCTCTGTAACTCTAGGTTACTTGTATAACAAACACAATGTAAATGCT ACATAAATAATTGTCTACTATATTGTTTAGGAAATAATGACAAAGAAAAAAGCCCT[C]GTACAT GTTTGGTACAGTTGTAACCAAGCCATTTTCCCCCAATATTTTCAATCCACAGTTGTTTAAATCCACAG AAACCACGAATG
WI-2886	46 C A	CAGAGTCTGG GGGAGAAGA	TTGCCATGCTT TATCTCGTT	ACAGTTAAGAAAAGGCTGCAGCCGTTGCAGAGTCTGGGGGAGAGA[G/A]AACGAGATAAAGCATG GCAAAGACCACGCTGAAAGTATCCAGGGTGTGTATGTGCACATAGGAAGATCACTTACCTCAGCA TAGGAGGAGGGCTAGGCAAGGAAGGTGTGAGAAAGAACAGAGGAGCGTT

WI-2906b	77	T A ---			---	CCTGAACACCTGGAGCACTTCCCTCCCTGGACACCTTCATCTTGTCTGGAACCTTTGCTGGAATGCTCTTTCCCTCT/AJGAGCTTTGCTTGGCTTACTTTTCTTTTCTTTAGGTTTCAGCTTCAAGTGACCTCCTTAGAGTTGGTTTGTGACCAACAAA
WI-2906a	50	A C TCTTGCTGG	GACACCTTCAT		AGAGCATTCCA GGCAAAGT	CCTGAACACCTGGAGCACTTCCCTCCCTGGACACCTTCATCTTGTCTGG/AJCAJACTTTGCTCTGGAATGCTCTTCCCTCTGAGCTTTGCTTGGCTTACTTTTCTTTTCCCTTAGGTTTCAGCTTCAAAAGTGACCTCCTTAGAGTTGGTTTGTGACCAACAAA
WI-1736	175	CT ---			---	TACTCCTCATTCCTCATGTCCCTAGACGTACTCAGATTCCTATGCCCTGAACATTTATTTCCCTAAATAGATTTCCACCCAGCACTATTTACACAGAACAGCATGGAGCAGTTTGGAGTCTGGCTCTTAGAGAACTTAAAGGACAGTGGTTTCCATCTGTCTTCCA/CJTAGAGATCTAGGGTGTCTTTGGAAACCACCTTGG
WI-1851	136	G A GTGTTAAGTA	GCATTGAATT AACTATAGAT		CACTAGCAATG TTAACTGAAG TTG	AATACCCACGTCTAACACCATCACACTGATCATCAATCAGGTTTTAACATATTAATCTGGGAGGACACAAACATTTAGACCATAGCATTGAATTAACATATAGATGTGTTAAGTAATTATATTAACATGGTACA/GAJACAACCTCAGTTTAACATTGCTAGTATCCATGTGGATACCATGTACCTTCTTACATCATGTGA
WI-3000	62	G A AGAGACCCC	CCCAAACAC AGAGACCCC		ATTGACTAAGA CTCA	CTGATGTTTGGGAAGCACTGTCTTACATCTCTAAATGTGACGACCCAAACACAGAGACCCCG/AJTGAGTCTTAGTCAATCCTATAGTGGCAGTACCTGAATCAGTGCCTGGTGCATAGTAGACACT
WI-1754	177	G A TAGTC	TTTTCTCCCTT CTTAAAGAGA		AAAGTCGAATT GCTCTGG	ATGGATCTGCTCAATTATAGTCCAGATAAACAGCCCTTCTCCCGCCACCCCGGATTATTTTACTTAAGGGTTTAGCAAATTCACCTGACAAAGAGTTAGGTTTCAACATTTGACCCCTCATAAAGTGATTTTCTCTCTTCTGTTTGTCTTCTCCCTTCTTAAAGAGATAGTC/GAJCCAGAGGCAATTCGACTTTCTGTAGCCACAAGATT
WI-3167	37	T A TAGATTC	AAATTC AAC ACAGATCTAT		TGTGATAGTTT TGAGATGGGTG	ACAACACAGCAAATTC AACACAGATCTATTAGATTC/AJACCCCATCTCAA AAATCATCATCAAAGAAGCAAGGAGACATATTACTGGTGAGGAAGCCAAATTCAA
WI-3208	140	G A AGATAAAGA	GTGGAGTGGGC		TCACTCAAAC AGGGCTTGG	CAAGCACACATTCAGGCAGTGGGCAGGTAGGGAAGGTGGGCAACTTGCAGCAGAGAGGAGGAAGAAGTTTCAGACCCGTTGGTAGGATAAGTGGATCCAAACCCCTTTGTAGGGCAGGTGGTGAGTGGGCAGATAAAGA/GAJCCAAAGCCCTAGTTTGAGTGACACTGTGGGATTCAAG
WI-1775	47	CT TTTTCTCTG	CCTGCATGGTC		AGTTGAGATTT ATGACAAATGAT GTAAA	ACTCCACCAACAGTTTGTGAGCCAAACCCCTGCATGGTCTTTTCTCTG/CJTTTACATCATTTGTCATAAATCTCAACTGACACATCAGTGTCTCTGCCACCCCA
WI-3402	55	G A ACAT	AGCATATTCA TTGATTTTCTCT		GAGGACTTAAA AAGGAGCAATT G	CTGCCCTTTACATCCAAAGCCAGTTACTCGAGCATATTCAATTGATTTCTTACAT/GAJCAAATGCTCTCTTTTAAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCCCTTAGGACCTTTTAAAGTCTCAACTTTTAAAGCGGAAGTTGAGACATGCACAAAATAGATTTCCCTTAGGA

WI-3416	33	C T	CCAAGTTGTA GCATTCAGAA	ACGAGCACAA CTACCTCTAAG AG	TCTGGTTCCTCCAAGTTGTAGCATTCAGAAAGTC/C/TCTCTTAGAGGTAGTTGTGCTCGTCGTTAAAA TATGTTTTCAAGATAGTATCTCCCTGTTGTCACTTCTCCTCCAAACAAGTGTAACCAACAGCATTTGTTAAG GAAATGTGCAATGCTTGCTACCTCTGACGCACACATAATTAATCCCATTCCTAAAAAGACCAGG
WI-3453	70	C T	TTCTTAGGCC ATCAGAGAA	TCAATTTTCCC CATGACTTC	TCCTATTCTACAACAACAGAAATTTAACAAATTGAATAATCAGCTACTCTTCTTAGGCCCATCAGAG AATC/TGAAGTCATGGGAAAAATTGATGCCATGTGAATTGGAGAAACAGACAGGCATATATGGAG AATTACAGTTTACCAGGGACACAAATCCCACTTCCAGAGCCATCATCTGTAAAGAC
WI-3474b	109	G A	---	---	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTAGCACAGTATTTTAATGAGGTGGTGTGGAGAAAAATTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3474a	90	A G	AC	CAACCATCAAT TTTCTCCCA	CATGCTAGGTAGATCTGATCATGAAGTTTGAACAACTTAATCATCAAGTGTGTCAACTGGTTTGA GTCAGTTTCCCTAATTTAGCACI/AGTATTTTAATGAGGTGGTGTGGAGAAAAATTGATGGTTGCG TAGTTGAGTTTCTGTCCACC
WI-3502	79	C T	CCTGGGTTTCT GGATGICT	GGGTGAOCTG TCCTCA	TTTGACCCCATACATGAGAAATAAACCATAAAGAAATGGTGGAAAAATAAACGGGAGAGACCTGGG TTTCTGGATGTC/T/GAGGACAGGGTCACCCAC
WI-3600b	146	G C	GGTTTCTAACC TGGATATAAA CATCT	CCAGTGCAGCC TTCCAT	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCCTGCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTG/GAGGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGTTTCTAACCTGGATA TAAACATCT/G/CATGGAAGGCTGCACCTGGATGAGGTCACAAA
WI-3600a	78	T G	CCATGCCOCTG ATAGTTCTG	GGAAACGAGTT TAGGTGGCTC	TCACGGCAAGTTCTGCAGCAGTGTCTTGACTCCTGCTGTTTCCAGAGTCTGATTATCCATGCCCTG ATAGTTCTG/T/GAGGCCACCTAAACTCGTTTCTGCTTAAGTTATCCAGAGGTGTTTCTAACCTGG ATATAACATCTGATGGAAGGCTGCACCTGGATGAGGTCACAAA
WI-3678	125	G T	---	---	TAAATCATGCTTATTTTACAAAGGTAATCCACTCACAAATAGGCAATTGATGTGATCTCTTTCTGTAA GAAAAGCTCATGCTCTTCTGAACCTTCTACTGTGCTGTTATGATGCACCTG/TCCCTTTGG ATAGATGGTTGATAGGAGATGGTTGTTAAGACACAAATTTACCTTGTGTGTTTCAGGCAGAAATAG ACTCTCTGTGTATCACTGAATGAGTTCCAAAAGCCTTTATGTCTTAC
WI-3687	67	A C	---	---	AAAGCGATGTTGAGATACCACATTCCTCATGAAAAGTAAAAACACACACAAAAATATGACATAAAA T/A/CJAAAACTACTATAGTTTATGAAAATGACTTCGAAAATTCAGAGAAAGTCACTTAAACAGG ATTCTCAATTCATCCAGAATACTCCTCTGTCATTCITTAACCTTTGACTGCACAG
WI-3735	72	T C	CCTCAGTTATG TATCAAATGA CAAAAC	GGCTCACCAAT CATGTTTTT	TCTAAAATGTGAAACC AAAGAAATCCTGACACGACCTAACTGCCAGTCTCAGTTATGTATCAAAATGA AAAAC/T/CJACACCGGTTCAATGAAAAACAATGATTGGTGAGCCATGTCCCTTATTTAATGAAAAA GATCTTGGGCAATTAACTC



WI-1819	51	C T ---				GAAAAGCAGGAAGCCAGGCAGGACAAACTTTTGAAAAGTCTTTTCAGCAC[C/T]TTCGTGGATCCG AATTTTAGTGTGATTTGGCAGGCAATGCGGGTAACATGTTCCAGTGTTTTAACTTGACAGAAATTGC CAGATTAGCGATTGTTGACTTGTCCAAATTAATGAAATGTGGAAAAAAGGGTGTAACTGTT AAGCTGCTGCAATGTTTAGACACGAGGGTGGGGAGGTGGAATACC
WI-3746	116	G A ---				GGCCTATTACATGACACTGGGCCAAGATCTTGCTTCCCTTCTTCTCAATAGATACTAACTAGAAA ACTGCCCTGGCCAGGAAGATGGTTGTCTTCATCATCTGTCTGTG[C/G/A]GCCCCAGGATAAAGCA GGCA
WI-3867	49	T C CAA	ACAGTCATTT AGTCTTCCTGA	TAAGATAACC ATACTAGGTAC	ATCCG	AGCAATGAGTTAACTCCTTACATGAACAGTCATTTAGTCTTCTGACAA[T/C]CGGATGTACCTAGT ATGGTTATCTTATCTGACAGACAAAGGACACTGTGACACAGAGATTGTTACTTGAACAAAGACACAGT CATTAAGTGGAGAACCCAGCATTTCTAATCAGGCTCAGTGATCTGCCAAACCAACCTTCTGCTATAG CATC
WI-3898	25	A C G	TGACCAATGTC TTTAGAAGCA	TGTOGGTGTG CTCTCC		CAATGACCAATGTCTTTAGAAAGCAG[A/C]GGAGAGGACACCCGACGAGACACAGGAAGGAGTGAG GTGAAGATGAAGCAGTGTGACGACGCCACAAGGTGAGGAAGCAAGGTTGCTGGCCACT
WI-3901	114	A G ---				GGACCATTGTCCCTCAGAAAGTACATTCAAGCCCTGGAOGGTGCTGCTCCTAACACTGTGACCTCAGGCA AGTCATGTCTGCTTCTGAACCTCGGCTTCTCACCTGACAAGTG[G/A]TATCATGTGTGCTACACTGC AGTGTTTATAATGCTGCAT
WI-3914	99	C T GC				CTGAGGAGATTGATGCTACTTTACCTGAGGAACTTTTATTACCTCCCCTGAGTTTGTGCTTGCAA GACATTGCTGATTCTTCTCAAGACTCACAGC[C/T]ACCATCCTTCTTCTAGACCTATAACTAG ACTCAAGTCCCAGCAGGCCCTTAAAGGTAAGGTACAAAGTGTGACCCATGGGAGGTATGTTACGCTA CAAAGAG
WI-4019	33	G A A	CCAAGAGCGT CCTATGAATC	AACAGCAATA ACAGGAACAA	ATG	CCACTCCCAGGCCAAGAGCGTCTATGAATCAT[G/A]CATTTGTTCCTGTTATTGCTGTTACAGAGT GGCAACTCTTGCAAGGGAGGGGTACAAAGTGAATTTTAGATGCTGCAGGAGACGAAGGTC
WI-4091	84	A T	TTGAGGTCTTA GTCATTGCATG	TGAGTTCCTAT TAAGTGACAAT	ATTGTT	TAATTACATTGCTCTTGTGTTGTGCATTTATTGCTTCTTATGTAACACAATCACCAACATTGAGG TCTTAGTCATTGCATG[A/T]TGATAACAATAATTGTCACCTTAATAGGAACCTCAAGCATAGTTATGTGT ACATTTATTGCTAACAGCAG
WI-4160	117	A G	CCTATAATTTA GCAACAATAT	TGCAGGTAGAA TTTTCTAATAT	AGCC	TCCTCTTCTGTAATAGGAAGTCTGATTAGATGCCCTTTTGAGGTTAGGTTGGCTTCTAAGATGGTAATT ATCTGTCCAAAGTTTTTGTTTCTCTATAATTTAGCAACAATATCAACAGAA[A/G]GGCTATATTAGAAA ATTCTACCTGCATCCCCCTGGATCTGAACGTTCTTCATGATACT
WI-4168	32	A G	GGTGAGAGTC AAATTGATAC	ATTGCCAAACA GATTTTCAGA		CGTTGCTGTGAGAGTCAAAATTGATACAAACA[A/G]TCTGAAAAATCTGTTTGGCAATCTATTAAGG CAAATATATACCAGCAGTGTGGTCTAGCAATTTCACTGCTGGCATTACCTAACATAAATGAT



WI-4177	68	T C	TGAATAAGCA CGTATTAAATT TACCTA	AAGCAGCAA ATCATGATG	ATGCCGCGATATACTTTCCAAATGACTAGTATGAATAAGCACGTTAAATTTACCTATTATATTT ATT/C]CATCATGATTTGCTGCCCTCTTTCCAAATTTACTACAAATTGTATTGTCCACATGAGGCACATG ATCCCATTAAACCCAAATAG
WI-4199	51	A C	CTCCCCAAGTT AGTCAATATA AAAA	ATATGTTGATT AGGTATAACA ATATGTGTG	GGCATGAGCACAGAGGCTGAAACCACTCCCCAAGTTAGTCAATATAAAAAA]A/C]CACACATATTG TTATACCTAATCAACATATAAATGTTATAGATTAAACAGTCCACAGCAAACAA
WI-5163	24	C T	CTGTCACCTGGT CTGCTGT	AAAGGAACAC AGGAACAGAC C	TTCTGCTGTCACTGGTCTGCCCTG]C/]GGTCTGTTCCTGTCTTCAATGTTCAACTGCTTGTTAT CTGTGCCCACTAAGGTATCAGGTTTATATGGCACAGGATGAGGGCTTTGTAGACCAGAGTTTTCTT GGAAATTGCAACATTGGGCAT
WI-4250b	117	A G	---	---	TAAAGTGCAATTAAGTGTACAAAGTCCACAAATACCTCTTCCACCAAGTGTCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTGTGAAACAGGGTGGGAGGATCCTGTAAAGG]A/G]TAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4250a	94	G T	TCAATATGAG TCTTGTGAAAC AGG	CTTTTACAGGA TCTTCCCAC	TAAGTGCAATTAAGTGTACAAAGTCCACAAATACCTCTTCCACCAAGTGTCTAAAGCAGTTTTTAATAACA GGTTCAATATGAGTCTTGTGAAACAGGG]G/]GTGGGAAGGATCCTGTAAAGGATAAATATTGTTTT CCATAATATTGAAGATGTG
WI-4255	68	G C	TGCTCCCCAT CACCT	G	TAAATGTCTCTGGGAGATAATAGGAAAGTCCCATCCCTCTGATACCTTGGTTGCTCCCCCATCACCT ]G/C]CCTTACACAACTTGAAGTAGGCCCATCCAAACACTGGTGCAGAAAGATAACTGTGCGAC
WI-4256	57	C T	---	---	ACAGCCTCTTCAAATGGCACAATCAAAGCACCAAGTAAAGCAGAGGCAAAATCTGG]C/]CTCAC CATTGGAAAGTCTTCTGAAGGATAAGGGAGTGAATGACTGCTAGAAGAGAAATGATGGCCTT
WI-4325b	71	C T	---	---	AGTTCACCTGCCTAGATGAGTAGACCATGTTGTCTTTGTTAAATGTACATGGGCAGGACCGGAATGG GATG]C/]TACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCGCCAC CCAGGACACTGCCATATCT
WI-4325a	58	C T	---	---	AGTTCACCTGCCTAGATGAGTAGACCATGTTGTCTTTGTTAAATGTACATGGGCAGGAC]C/]GGAAA TGGGATGCTACTATAGATAATCTTTTTTAAATGACTCTTCTTGGTCTCTTCAAGATATCACCGCCAC CCAGGACACTGCCATATCT
WI-4347	158	A G	---	---	TGGGCAGAAAGTCGGGTATGGCAAGTCAGGGTGGTTAACTTGGATGCCACTTCTGCTGTCACTTCT CTAGACTCTTGACCTGCAGGAGGATCCCTGGCTCCTGAGTTTTATCATCTCCACCTCCAGCCCCAG GGCCCTGTATCTGTTCAAGGCC]A/]G]GAATCGTCACGGCTCACAACTGTGGGAGGTAGGAATGACGA G
WI-1936	117	T C	---	---	CCAGTCTAGGCTGCAAGGACTTCAATTCTGGGGCAAGTCTGGTGTGTAGGGTCAGAGGCAGCG ACCTGAGGGACACAAACAGTGGGACACCGGGGTACTTGTATCACCT]C/]CTCCCGCAACCCCA AGCAGCACAGCTTGACGCTCCAGGAAGACTCCTTACTTCCACTTGAGAAAGGAGAGGGGAAGAGA AAAGAGGACTTTGACACACAACCTTGA

WI-5204	54 C T	---	---	TAGATTTGATTGATGACAATAGGGAAGCCTTTGTTAAATTGGGTTTGAAGAA(C)TGAAGAAAA TGGAAAGGGAAGAAATTGACAGAAACCAAGAGAGTGTGAGGGCAGCAATCCAGTTTGACTGGA ATATAGAGTGATGTCAGGGTTG
WI-5215	70 A G	CTCAAAA	GGACCTTAAT ATTTAACAGA TTCCG	TTTTCCCTTATTATTAGGAAGCAAAATGTTTCATACAGGACCTTAATATTAAACAGACTCAAAAA TAT(A/G)GCGAAACTATCTTTACAAAATTATCTCCATAGCAAGTAGACATTTTAGCACATTTTCCT GTAGTCAAGGTTTTAAAGGCCAAATGAAGTTGACTAAAGACAAAT
WI-4448	112 T G	ATATAA	TTGTATCAAA GAGATGGGGT GTCTTT	CCCTGAAATGTGCTTTGCTTCTCTCTCCAACTCTCTAGGGAACCTTTTCCATGTCAGGTGAAGGTTTGA AGAGTACTTTAAATTAACCTGTATCAAGAGATGGGTATATAAT(G)AAAGAACCATGTAAAGATT CTTTAATTAGTGAATTCATCAGGGCTCTTCCACTGTCTATCAGTAA
WI-4456	49 C T	TATAGTTCC	AGTTGAATTA TTCAGAAAAT GCATGAACCTG	ACACATTTTCTTTGCTTTAAGTTGAATTATTCAGAAAAATTATAGTTCC(C)TCAAGTTTCATGCATAA CAGGAACACCAGGTTGGGCAATTGATTGATTGT
WI-4461	49 A G	CCCTCC	TCACTGTTATT TTAAAATTAT ACCAATTTC	CTGAACTAATGAGGTGCTAAATCACTGTTATTTTAAATATCCTTCC(A/G)TGAAATTGGTGAAA GGTCAAGAAATGAATCCCACTTTTAGATTTCTGGAAATTTTATTGCGATGATAATGCAATGGGC CTACTGGATTTTACTTTGCTCAAGCCAGACACACGAAAGTATATAAGAAACAGTTAGTAATCTT TCACCTTTT(G/A)TATTCTCTTCTACCTCAGGGAATC
WI-4465a	41 A G	ACACGAAAGT	AAGCCAGACA GAGTGAATAA ATGAATGCCA	CTACTGGATTTTACTTTGCTCAAGCCAGACACGAAAGT(A/G)TATAAGAAACAGTTAGTAAT CTTTCACCTTTGTTATTTCTCTTCTACCTCAGGGAATC
WI-1949b	160 T C	TAATC	GAGTGAATAA ATGAATGCCA GACAAAA	GGGGTTAGGACCTCGAGATCTTTTCAGAAAGCACAAATTCAAACCATAATGGCAGTGCACAGGTAAACA GTGGTGAGATGCTCTGAGTTT(G)CAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAAT GGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-1949a	86 T G	ATGCTCTGAGT	CAGTGGTGAG CCATGTCAGCA GCCTTG	GGGGTTAGGACCTCGAGATCTTTTCAGAAAGCACAAATTCAAACCATAATGGCAGTGCACAGGTAAACA GTGGTGAGATGCTCTGAGTTT(G)CAAGGCTGCTGACATGGTCAATGCTGAATATATGTTGAAGAAAT AAAGGAGTGAATAAATGAATGCCATAATCTCTGTGTTTTTGTCCCACTCTCACACCTTTCCCTGG CACA
WI-4529	64 T C	AAGATG	CCAAGTAAGT CTATCATCTG AAAA	TGAGAGAGTTTTTGGATTATTATCCTCTGCAACACTCCAAGTAAGTCTATCATCTGAAGATG(T/C) GAGTTCTCTTTATATCCTATGATTATTTTTCAGGAAGTGTATTTTGAATATATAACTCCTGGGT CCATCCAGGTCTAGGGTCAATGGCATCCATGGTGGTGGACAAAGATGGGCCCTAGGATCATTT

WI-4540	110 A G	GCACATGTGG CATCC	GACAATGCAGC CATGCA	AGCTTTCCCTTTCTTAAAAATTGGTGCCATAGTACTGGCTTCTGTGTGCATCAGGAAGCAAGCCTAT TGCTCGGTAAACAGTACTTTGCAATAAGCACCATGTGGCATCC/A/GTGCATGGCTGCATTGTCCAGTC AAATGAGACAACCTCCTAT
WI-4582	226 T C		---	AGCAAGCATCTGGCAAGCCTCGGTGACCAGAACATTAATTAACCAACACACCTGCTCCAAATGT CCATGTTAATGCAATTATAGAAGACTCCAGTAGCATTCAAGGCCAGTTTAACTTATTCCTGTACACA ATAAATTTATGGGAGACAGCATTGTAAATTCAAATCAATAATGACTCGGTTGGCTGTACAAGCAT AACAGAACGCTTGCAAAATATGGTT/CJCTCCTTGCTAGAAACCATTTGAT
WI-1965	105 G C	GCCATTGAGG AAGTGTTTAA	GAATGGATGGG TCATCTCCT	CAAAGGTTAGTTTAACTTGGGGGCAAGACAAAGTTATGAGTACTCAATAACCTATGTTCAAGGG TAACCAACACCTTTTGGCCATTGAGGAAGTGTAAAG/CJAGAGAGATGACCCATCCATTCTCTGG GCTTCTTATATGACACCATACTATTCCACACAGATGTGGAGTCATTTATTTGGTTGGTGTATGACAGT CATGG
WI-5248b	99 C T	CACTGTTTTCT ATTGACCGGTAC	AGAAAAAGAG AAGAAAGGAA AAA	TGTTTAAACCATACAGTTTGTGCTGCTACGTTGTAGAGCAACCCAGAAATTAACACGCCTAC CATTTTCACTGTTTCTATTGACCGTACTTG/CJCTTTTGTCTTTTCCCTTCTCTCTTTTCTG CCCTCTTTAACTATT
WI-5248a	38 G C	AGTTTGTGCTG CTACGTTGTT	TTTTAATTTTC TGGGGTTGCT	TGTTTAAACCATACAGTTTGTGCTGCTACGTTGTAAAG/CJAGCAACCCAGAAATTAACACGCC TACCATTTTCACTGTTTCTATTGACCGTACTTGCTCTTTTCCCTTCTCTCTTTTCTG CCCTCTTTAACTATT
WI-4596	69 T A	TGAAGCAGAA AGCACTGTGA	CAGGAGATGGG CCTAATAATG	CATTGGTGGTCCAACTTCTCGGTGACATTACTCTGTTGACTTGTCTGAAGCAGAAAGCACTGTGA C/T/AJCATTTATTAGGCCCATCTCTGCTGAGCCTGCTACAGCAATTTGTAAACATATGGCATTGGG ACATATCTCTGAGCCCATCAACTATTGACAAAGATTCTCTTTTAAACAA
WI-5252	119 A C		---	GAAATAGGGCAAAATTAAGACTTCAATAATTAAGAGTCTTGGGAAAGGATTGTGATGATCATTTG AATCTGTTTAAATACAGAAATTAATACTGAATACCTGTGTGAATCATTTGCTTT/A/CJTACCATGTACA TATTATATGAATTAACAATGTAAATAGTATGACTAAGAAATATTGGGCCCT
WI-4606	61 A G	GCAATGCTAG AAAATTATGC	TTAGGTGCTTA AGTTGTCTACT TGG	TGCAAAAAGGAAATGATAACCAGGACTGTTGTTCAAGCAATGCTAGAAAATTATGCCTA/JVGJC CAAGTAGACAACCTTAAGCACCTAAGGCAGAAATGAAGTTTCTCTCTTGTCAATTAAGTCTCTATTCA ATTACCATTTATCGGGTAATTAACACACTGGAAAGTAATGCCAGGCTAATTGTTAGATTATGATAAT TACACGTCCTTGTATGCT
WI-5257	77 C A	GAGGCATGAA GCAAGAGG	OCAGGGGCAGA TGAAAG	CAATGAGAAAGTTACCAGATGGGGCAAAATTAAGCATATGAAAATACCAAGTGTGGCAGAGGCATG AAGCAAAGAGG/CJCTTTTCATCTGCCCTGGTGGTTTTCAGTAACCTGCAACATGTCTTTGCCCTCC CGGATGAAAAGATACCCCTTCTATGACTCAGCAATCCACTCTAGGTATGCACCCCTAAACATGGGTG GCAAAAT
WI-4649	50 C T	GAGACCATCT TTCCGAATG	TGCTAGGTG TACTTACAAGA AATCATC	TCACCTGTTAGAAATTTCTTCTCTCAGTGAGACCATTTCTCCGAATG/CJTGATGATTTCTTGTA AGTACACCTAGTACATCTATGAGCACACAATTAACAAGTACTTGCTACCTGAATTTGATTTTTTAA AAAATCCTCCCAATATTG



WI-4650	148	A	G	GCACAAAGAA AGTATAAGTT	CTGAAGTGTTA AACTGGATTTG G	AACTGTGTGATGATGTTTGTGTAATTTCTGGAGAGTCAGTTACTCTCACTAGATCATAAAGGG GACTTGGGAACCAAAAGTATCTCAAGACATTTAATCCTAGAGACACAAGAAAGTATAAGTTGTCTC TTATAATTGCTTTT[A/G]CCAAATCCAGTTTAAACACTTCAGTAACGTT
WI-4677	82	T	C	TCCAAAAGTG ATTAGGTGAA AAA	TTTCAACAGTG TCATTATTCAA CTT	AATTCAGATTTTGAACATACGTCGACATTTTGGAAAAAATTTGTCCAAAAGTGATTAGGTGAAAAAAT GAGTTGAAATAAATGTT[C]AAGTTGAATAATGACACTGTTGAAAAATGATGAATCTGCTTTCAATTCA CATGGAAAGGAGACTAGAACACACAGCAGGTTTATAGGGGAATACTCAT
WI-4698	135	C	G	---	---	ATGATGTCTATCATGAGGAATCTGTAGAAAAATTTTACCTGGCAATTGATTCAAATAAAGTTTGTCC TCACCTGGGAAACTGCTTATCTTGATGTGACATTTCTTTTGTGACGGAAAGAAACTTCAA C/GTTTCGAGAAGGCTTAGATTATATCGCTGAAGCCCATTTCTG
WI-4722	88	G	A	TGCACTATGG AACACCACAC	AATATGGAATC TGCATTCAGTT G	CTTCCATTCTGCCAGTTAGATGACTGCCCTCTCCACAGCCTAGAAAAAGATGGGAGATTATTTTC TGCACATATGGAACACCACAC[G/A]CAACTGAATGCAGATTCCATATTGAATACTGGGAAATCAGTGA AAG
WI-2020	145	C	A	---	---	GCCACAGTAAAGAGGAAATGGAGCCATGTAAACAGAGGAGAGCTTTCTGAAGATCAGTGTATTGTCA TAAAGTCAAGTAAATCAGTTTGTGATGGTTGAGATTTTCAAGAAACGTGAAATTTATTGAGTAACCATGGG TCAACTATGAT[C/A]CCAAAACACAGCAGTGTGTCTAAAAATATGATAGTTTCTTCTCCTGTCCACC GCAATGAAAAGGAGTT
WI-2028	176	T	C	TGTTACGTTT CCCTGTCATC	GGTTGGAAACT CAAATTACCTA GAA	GACTACAGCGCACAGACAGGCAATTTGTGTGGCTTGACAGGTGTTGTTTGTGTTTAAAGTTAGATT TGAATCCTTTAAAGAAAGAAAGTGGCTCTTCAAGTTTACTACAGACCTCATCTCCTGTTCTCTTG CACCCAGTCCACTTCACTGTTTACGTTCCCTGCTCATCT[C]TTCTAGGTAATTTGAGTTTCCAACC TGTGG
WI-2033	183	T	C	GGGTGCTAGA ACTAATCCCTC A	CAGTGGTTCCA CGTTCTCC	ATGTGTATGAGTCCACATTCGCAGATTCAACCAACTATGGATAGAAAAATATAGTATTTCCAGATGG GCAGCCCAAGGATCAGAGGGCTAATTTTAAATTTTCCAGGTTATACAGGACCAGTGTGGAATTTT AGCATTTCTGGGTTTGGCATCCATCAGGGTGCTAGAACTAATCCCTCA[T/C]GGAGAAACGTGGAACC ACTGATATACCAAT
WI-4745	131	T	C	---	---	TTATGGATACATGTTTCTGGTGAAGGACAAAGAGTTGAAGCAAAAGGACAAAGGAGATCAACTGGG TAGAATAACTCATCGATCCACAGGCTCTTCCACCATCTCCATCTTCTACTCTGAT[C] AGGCAGACTTATATGGAAAAAAGGGA
WI-2034	150	T	C	CCACAGTGCA CCAAGGAC	GGGTAAAGAT AGAGTGCAGGT CC	CCACGACTATGTCTTCAGAGTCCCTGGTACTGACAGAGAGGCTTTGAGGAACCATGTGGCCCAAGA CCTCCTTCTGCGGTTTCAGTGAAAGACGATGAACCTCTTCTATCTTCTACAGCAGCTGGACTTCACCA CAGTGCACCAAGGACT[C]GGACCTGCACCTCTATCTTTACCCCTTCCGACACACAGATGCTGAGATGCC ACACTCTGAGTG



WI-2038	155	C T	TGTGCTTTAA GTGTGTAAGT ATTAATTAG	ATTCCTCTTG AAAGAAACAT CA	TCAGGTGACAAGAAAGTCACATTTCTTCAATCACTCACCATTGTCTGTATTGTCTCTTGCAAGTGT ATCCAAGGATGTCACCTTTTGGAACTCTGTAGATCAGAAAACTGTGCTTTAAAGTGTGTAAGTATTA ATTAGATTCTATTGATA[C/T]TGATGTTCTTCAAGAGGAAATTTGTGTAAGAGGATTCCCAAT TGCAATTCATTGGC
WI-4782	113	C T	GATGCAGAAG ATAACTAGAA AATGC	GAACTCTCTG GTTATTTTCT GTTG	TCATTGACTTTTAGAGTTCCCTTCAGTCTTTATGTCTTATTTCTTTAGGAAAACTAGGCTAGGAGAA CACAATTCAGGTTCTCTCCAGATGCAGAAGATACTAGAAAATGC[C/T]GAACAGAGAAATAACCA GAAGAGTTCAATATGTTTTCAGAACGATTAC
WI-4788	65	A G	GCATAGAATC ATCTTGCTAAG TTCC	GGATAAAAT AAAATTTTGGC ATAA	AGGAGAGTTTGGCTCTTTCCGGACTCTTGGAATTCAGTGCATAGAAATCATCTTGCTAAGTTCC[AG TTGAAAAAAATATGCCAAATTTTAAATTTATCCAACTTTAAGTCGAGATTATAATTGATATT AAAACTATATTGAGTCTTTCTAAAGATGGCGTATCACTCTA
WI-5300	38	T C	TCCAGAGAC CACTTCATTC	CTACTCTTCT ATTCATAATC CAAAA	CTTACTTCCAAAGTGTTCAGAGACCCTTCATTC[C/T]TTTGGATTATGAAATAGAAAGAGT AGGTGTTATTATTCCTCTTTTACCAGGTGAAATTTGAGGCTCAGAGACAAGGTAGATGATGAGCCCA AGTCAAGTACAGAGCCA
WI-4818b	121	G T	TGATAATGGG GOCCTGTT	CCTTCCCTTTA TATGTATGCCA GA	TATAATGTTTTGTTCATAGTTGCCATAGACTAGGTTATGTCCACACATGAATAACAATCTTATATA ATAATTTATTCAGAGGAAATATACATATGGGTGATAATGGGCCCTGT[G/T]CTCTGGCATA CATATAAAGGAAGGCTAA
WI-4818a	43	A G C	TTGCCATAGAC TAGGTTATGTC G	CATATGTATAT TTTCTTCTTG AATAAAT	TATAATGTTTTGTTCATAGTTGCCATAGACTAGGTTATGTCC[AG]CACATGAATAACAATCTTAT ATAATAATTTATTCAGAGGAAATATACATATGGGTGATAATGGGCCCTGTGCTCTGGCATA CATATAAAGGAAGGCTAA
WI-5317	139	T C	TTCCATTCTG GTAGCAGGT	GATGCAAGA AGAAATGAGTC C	TTTTCCATTTGTTGATTCCTTTTGTCTGAGCCCTTAGATCTCCTTTAAATTAATAGCAAGGTTAAT AATATAATAATGATGTTATATATTACAAATTTCACTCAACAGGAATTCCTTTCTGGTAGCAGGT ATA[T/C]GGACTCATTCTCTTTCATCTATTTCTAGGTTATTTGCAGCCCGAGATCTACCCAGG
WI-4888	56	G A	GCAAGATATA AAGATTAGA AAGATAACA	CAATCCACTA CCTCATTTAT CA	AAATGAGTAACCAAGTTACTCGGCAAGATATAAAGATTAAAGAAAGATAACAAGA[G/A]ATGAAT AAATGAGGTAGTGGAAATGCTTGATAACTGGAGTAGTCCTT
WI-5328	44	A G	---	---	AACATTTTAAACCATGCTACATTTTACAAACACTGAAAGACAG[AG]AAAAAAGAAATATTTTG CCTCAAAAGCTCTTAAGAGATTATGTAATAAAGAAAAAATATGAATCAGAAAAAGGAAAGAAAT AGAAACACGTGATACTGGAAGGAG
WI-4897	93	A G	---	---	GCCTTTTGAGTTAAGTCTTTTGTAGTGTGCTTTTTTCCCCCACTAGGTACTCTCGGCCCAAT CCCCAAAAGAAATAAGCGCTTGG[AG]GATAAACACATCTTC
WI-5345	29	G A	---	---	CCCTGCTATAGGTCAGTTTAAATCTG[AG]CCTGCTATGGTTGTTGTTGAAGCCACATCCACT GAGGTATATTCTGTCTGCATTTCTATATCACTCAGCTTTCAGATCCACTCCATCAACTTGACG

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WI-5370	143 T	C	AATAAGATGG TACCTTAAC	CAAAGTTGGTA CAGAGAAATTC	AAA	TGCACTGTTACTTCTTGAAATCATAAAGGATCTGAGAGCCTACAGTATATGGCAACATTAACCAAT CTTTTGAAATTTACCTGTATCCCATCATGTTTCATTTGCAAAATAAGATGGTACCTTAACCTA ATAAACAAATTCCTTGAAATCTCTGTACCAACTTGTCTTTC
WI-9711b	423 T	A	---	---	---	GATCTCCTTCATCCCTCTCCAGAAGAGGAGAAAGGAAACACAAAGAAACGCTGGTGCAGAGCC CCAATTCCTACTTCACTGATGTGAATGCCAGGTGAGGAGACGGCTTGTGTAGTGGGAAAGCAC TGACCTCAACAGTTGGAAATGTTAGTGTAGCTGTCTGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9711a	390 C	A	---	---	---	GATCTCCTTCATCCCTCTCCAGAAGAGGAGAAAGGAAACACAAAGAAACGCTGGTGCAGAGCC CCAATTCCTACTTCACTGATGTGAATGCCAGGTGAGGAGACGGCTTGTGTAGTGGGAAAGCAC TGACCTCAACAGTTGGAAATGTTAGTGTAGCTGTCTGTATCCTTGAAGCTGTGCAGCAGCTT CAGTTCTTCGCTGTGGAAATATTTCCCTGATACCTCTTAAATTTGAATG
WI-9702c	345 G	A	---	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCTATTCAGCAATTCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTTGCAACTTCTCAGTTTATTTAATCTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATTCAGGTGCTACAGCATCTGATAG
WI-9702b	344 C	T	---	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCTATTCAGCAATTCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTTGCAACTTCTCAGTTTATTTAATCTAATGATCTCTGTGACTT TTATACTAGCTTTAAGAGGTTTTCATTCAGGTGCTACAGCATCTGATAG
WI-9702a	179 C	T	---	---	---	GGAGGAATTCAGGGTGAATGGACTGCTCCGCTCCTGAGTTCACTGCTACTCAGCCTGAGGTTGCAG ACTGGTCTGAAGGTGTACAGGTGCCCTCTGTGCTATTCAGCAATTCCTACTGGTATGTATCAGGAT AGAGGTGAATCAAGCTGATATTTTGCAACTTCTCAGTTTATTTAATCTAATGATCTCTGTGACTT CTTTTATACTAGCTTTAAGAGGTTTTCATTCAGGTGCTACAGCATCTG
TGR- A003N21	49 C	A	---	---	---	TATAGTATTTAAGCAAGCTAGAACGACGGCTGTGGTGGTGAATTTGGTTC/AJAGCATATCTTAGGT ATATAATAACTTTGAAGCCATAACTTTTAAGTGGAGTGGTTGATTTCTTTTAAATTTATTTGGGA GGGTTTGGATTTTAACCTTTTAAATGTTGTTAAATTAAGTTTTTGTAAAGGAAACCATCTCTG TGATTACCTCTCAATCTATTGT
TGR- A004V30	203 C	T	---	---	---	AGAATGGCTACTTCATAGGGCAGAGCAGCCACTTTTGGCTAATTTTAAACATCCAAAGCTAATAAT AATCAAGAAGAAATAGAGAACATTAAACAAATAAATTAATGTTCTATTTGGGAATACCTAATATCAG ATACTAACAAGTACAGTGATAAGAATAAAGATAAATATCACACATACCTTCTAGGTTAGTAGA AAAGTC/G,TTCTTCTAGGTTAGTAGAAAGTT

[illegible]



WI-7593	46	G A ---	---	TTTTGTTGCTCTGGACACCCACTGCTCCAGGATGAAGGAGAG[G/A]AATGAGATCAGTTTGGG CACTTCCTCTTGAAATATAAGAATCAACAAGTTACAGTCATGTTGGGACTTCTTCTCTCTCCAA
WI-6962	78	A G ---	---	AGTGCACTTTGGGGAAAGGGCTCCAGTGTTATCTGGACCAGTTCTTCATTTTCAGGTGGGACTCTT GATCCAGAGA[G/G]GACAAAGCTCCTCAGTGAGCTGGTGATATATCCAAGACAGAACCCCAAGTCTCC TGACTCCTGGCCTTCTATGCCCCTCTATCCTATCATAGATAACATTCTCCACAGCCTCACTTCACTCCAC CTATTCTCTGAAATATTCCTGAGAGAACAGAGAGATTAGATAAGA
WI-7059	43	C G GGCATC	AAGGCAACCA GGTCA	GCAGAGAAGAGAACCATGCCAGGGGAGAGGCAACCCAGCCATC[G/G]TGACCCAGCGAGGAGCCAA CTATCCCAATATACCTGGTGAAATATACCAAAATCTGCAATCTCCAGAGGAAATTAAGAAATAAA GATGAATTGTTGCAACTCTTAAAAAA
WI-9063	53	A C TT	CACTTCACTGA AAGACACCAT CCTTGGGT	AGCAGCCATCACATGATCTGTTTTCACCACTTCACTGAAGACACCATTTATAC]TACCCAAAGGG CAGAAAGTAGAACTTACTATTCAATTAATGTTTGACACAAATTGGAATTGTC
WI-7079	293	T G ---	---	AAGGGCATTGAGACTATAAAGCAGTAGACAAATCCCACATACCATCTGTAGAGTTGGAAGTGCATT CTTTAAAGTTTATATGCATATATTTAGGGCTGCTAGACTTACTTCTCTATTTTCTTTCCATTGCT TATTCTTGAGCACAAATGATAATCAATTATTACATTTATACATCAOCTTTTGACTTTTCCAAAGCCC TTTACAGCTCTTGGCATTTTCTGCTAGGCTGTGAGTAACTGGGAT
WI-9074	38	A G AAAAG	GGTAAAGTT CTTTTGTCTCT TT	TGGATGCCGAGGTAAAGTTCTTTTGTCTCTAAAGAA[G/A]AAGGAAC TAGTCAAAAATCTGTCC GTGACCTATCAGTTATTAATTTTAAGGATGTTGCCACTGGCAAAATGTAAGTGT
WI-7104b	249	C T ---	---	GGAGTTGCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGGTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGCCAGCAAGAGGGCTTGGTTCTGAGGAAGCAGATGTTTCATGCT GTGAGGCTTGACCAAGGTGGGGGCCACAGCACAGCAGCATCTTTC]T]
WI-7104	157	C A ---	---	GGAGTTGCCCTTCTAAGGGAAGGAGATCTTTATCTTCTGGTTGGCTTGACCAGTCACGTTGGGA GAAGAGAGAGAGTGCCAGGAGACCTGAGGGCAGCCGGTCTACTTTGGACTGAGAGAAGGGAGCC CCAGGCTGGAGCAGCATGAGGC[G/A]CAGCAAGAAGGGCTTGGTTCTGAGGAAGCAGATGTTTCAT GCTGTAGGCTTGCAACCAAGGTGGGGGCCACAGCACAGCAGCATCTTTCCT
WI-8974	34	C T AAGAACTCA	CCTGAGCCCTC GCTGGC	CATACAAATGAGAGCCCTGAGCCCTCAAGAACTCA[G/T]GCCAGCTCAGCCCTACACCAGTTTCCACC TGGAGTTCATGCAAGGGCAAAAGGCAGTGCCATGCAAGCTGTTAA
WI-9161	61	C T CCTGGC	GCTTACAGGAG AGACTAGACA GGAA	CTGTGAGGGTGACGTTAGCATTACCCCAOCTCATTTTAGTTGCCAAGCATTGCCCTGGC[G/T]TTC CTGTCTAGTCTCTCTGTAGGCCAAAGAAATGAACATTCCA
WI-9014c	93	T C ---	---	CCCTGTTCCCATGCTGACCTGTGTTTCTCTCCAGTCATCTTCTGTTCCAGAGAGGTGGGGCTGGAT GTCTCCATCTCTGCTCAACTTAT]T]GTCGACTGAGCTGCAACTCT

WI-9014b	44 C T ---	---	CCCTGTTCCATGCTGACCTGTGTTTCCCTCCAGTCATCTTTTC/TJTGTTCCAGAGAGGTGGGGCTG GATGTCCTCATCTCTGTCTCAACTTTATGTGCACTGAGCTGCAACTTCT
WI-7023b	206 C A ---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAGACCTGCGTGTCT CAGTGCCCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGTCCCC TCTTTTGGCCCGCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTAACAC A/C/AJACACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7023a	56 A C ---	---	TCTGAGAGAAATGACTTGTGGGAGACACCCCTGCAGATCCTCATGGTTTGTGACAG/A/CJCCCTGCGT GCTCAGTGCCCTTTAAGTGCATCCCGCTGTGCTGACTTTGAGTGGGATCAACATCTGTCTACGGGTC CCCTCTTTTGGCCCGCAGTATTCATGGCAGGGTTTGTGGACACCTACTAGCTTCCCTTCCCATTAAC CACACACACATTCTTGCTCTACCCAAAGCTCTGGCTGGCAGCACTAA
WI-7093	54 C T ---	---	CTGAAATCCCCCTCTCTGCTGCTGGATCCGGGACCCCTTTGCCCTTCCCTCTGGCTCCAGCC CTACAGACTTGTGTGACCTCAGGCCAGTGTGCCGACCTCTCTGGCCCTCAGTTTCCAGCTATG AAACAGCTATCTCACAAAGTTGTGTGAAGCAGAGAGAAAGCTGGAGGAAGCCGTGGGCCAAT GGGAGAGCTCTTGTTATTATTAATATTGTTGCCGCTGTGTGTGTGTTGTTA
WI-9171	62 G A ---	---	ACATATCTGAAAAATGTTGAAAGCCTAAGCCAGGAATAAAAGAAAGTAGAGATAATAATCA[G/A] TTCTTTACAACCGATGGTAATTAAAGCTTGATTACAAAGACTTCATGC
WI-9174	47 T C T	TCTAGGGTA TATAGACAGG ACTG	GTGTGAGACCATCATGTGCCAGTCTAGGACCCCATTCCTCTATTAT/CJAGTCTCTGTCTATATA CCCTCTAGAAACAGAAAGCAATTTTATAGGCAGCTATGTCAAAATTGAG
WI-7753	52 A G	CAGAGTCTTG AAATACAGGG A	AAGCCAGATGCACATCCCTGGAAGGACATCCATGTTCCGAGAAGAACAGATTA/GIATCCCTGTATT TCAAGACCTCTGTGCACTTATTATGAACCTGCCCTGCTCCACAGAACACAGCAATTCCTCAGGCTA AGCTGCCGGTTCTTAATCCATCTGCTAAGTTAATGTTGGTAGAA
WI-9186	76 G A CCGA	AAAGGAAAG TCTGACCTAGG T	AAAGAACTACAGAGGACGATGTCCAAACAAATAATGGCATCACCTGTCAAAAATGGAGTTCCACT TCTCCCGCA[G/A]ACCTAGGTCAGACTTCCCTTTCATCTT
WI-9193	94 G A CA	GGTGTGTGTGG TAGGGG	TTGGACAAACCTAGAAATTTCTCCCTTTATGTATCTCTATCGATTGTGTAGCAATTGACAGAGATAA CTCAGAATAATTGCTGCTGCTTAAAGCA[G/A]TACCCCTTACCACACACACCCCTGTCTC
WI-9015	48 C T ---	---	TTTGGATTGATATCGTGAAATCCTCAGCCGAGAAATTTGGGCTGGATTG/CJTGCTTTGGTTAATACAT CTTTCCCTAAAGAAAGATAAACACAAATCCATTCCAGGTAGCTCGGCACTAAGAA
WI-7254	37 A G	GGTCTGAGAG CATTAGGA	GGAGCCAGGAGACAGGGTCTGAGAGGAGGCCAC[G]GTCCCTAATGACACCCACTCTAGCC CTGAGGCTCGTCCCTCAGACTGGGGAAGAGTCCAAAGGAAGGAGGAGGAGCCACTCTCAATGC TCAATGGCTCCCTGAATCAAGACAGG

[illegible]



WI-9281	68 G A	---	GCTAACACTTT TTAAAACCGT	CATTATTTTG AAAGCTATTCA GACA	ACTGGTGGGAGACTGTGAGGATCCAGGATTCTGCTGGCCAGAGGGCCTTGCTGGCTACTGG [G]A]TGTAGTTGCAGTCCTGTGTGCTTCCCTCTCTTATGACTGIGICCC
WI-7848	142 A G	CTC	GTATATTACA ATGATCACCG	CCCCACAGAAC TATTGTAAAAC AA	TTCTGAAAATATAACAGCCATTGAGCTATTTAAACTTGTAAATTTTAACTTACAAAATATAA AATATGAAGACATAAACCAGTTGCCATCTGCGTGACAATAAAACATAATGCTAACACACTTTTAA ACCGTCTC[A]G]TGTCTGAATAGCTTTCAAAATAAAATGTGAAATGTT
WI-9304	70 G A	ACTGA			TCACGTTTGGTGCTTCTCAGATTTCTGAGGAAATGCTTTGTATTGTATATTACAATGATCACCGACT GA[G]A]AATATTGTTTACAATAGTTCTGTGGGCTGTTTTTTTGT
WI-7933b	314 C A	---		---	TTACAGAAACTTGCCTGTGCCTGTGTGCCCTCCCATGCTAGGGCGGAGGGGTCTTTTCTTCTTCTTCC TACCTACCCCTTTTCTCTTGGCCAGGG[G]C]CCTCGTATCCTACCTTTCTTGTCCCTGGGCTGGCTGCAC AGAGGATTGCCCTTCTCTTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGCACAA AGTCTAAGGGACCATGGCTGCCTGCCTTGGGAGGAACCATAGCTCCCT
WI-7933	96 G C	---		---	TTACAGAAACTTGCCTGTGCCTGTGTGCCCTCCCATGCTAGGGCGGAGGGGTCTTTTCTTCTTCTTCC TACCTACCCCTTTTCTCTTGGCCAGGG[G]C]CCTCGTATCCTACCTTTCTTGTCCCTGGGCTGGCTG CACAGAGGATTGCCCTTCTCTTTTTCAGAGCTGGCCCTCGATGCCAAATTAGCATTTAGTATTTTGC CAAAGTCTAAGGGACCATGGCTGCCTGCCTTGGGAGGAACCATAGCT
WI-7374	182 T A	---		---	CCAGATGTGCCCATCACGTTTTTCTGAGGCTTTTGTACTTTAGTAAATGCTTCCACTAAACTGAAA CCATGGTGAGAAAGTTTGACTTTTGTAAATATTTTGAATGTAAATGAAAGAAAGTACTGTATATTA AAAGTTGGTTTGAACCAACTTTCTAGCTGCTGTTGAAGAATATATTGTT[A]CAGAAACACAAAGGCTT GAT
WI-9343	78 C T	CCTCTGCCA	CAAACAACAT CCTCTGCCA	AAATGAAACTT ACGTTTGTG TG	GGTCTGCTCCTGCTACCTTGACCCCTTCCCTTCTGCTTCTCTCTCATCATCATCCCAACAACAT CCTCTGCCA[C]T]ACACAACAACGTAAGTTTCATTGGGCAAA
WI-7386b	104 T A	---		---	CTATATGTGAGAGGGCGTGATATCTGGATGGAAGTTGGGCTGGATGATCTCCAAAGTCGTTTCAACTCT TAAAGACATCTTAATCCTGAATGTAAACAATTTGTTA[T]A]GTGTTTGAATCAGAAATTTGATTTTGA ACTTGAGTAATTCATCCTT
WI-9357	75 A G	---		---	AAGAAGGAGCTCAGTTACGGGGTTTTTAAACCTTCATGAAAACCTGAAGAGTTCACTTTGTATTAT GCTCTTA[A]G]TGATTACAGACTGATGCCAGACAACCTTGGGAAGA
WI-9360	79 T C	TTGG	CCTTAGAAAA TCTGCTTTAAC	CCTAGGGAACA CAATTAGAGGA A	TGAAGGGGTGTGGCATCTGTGTTTCTGATGCTTACTACAATATGTGAACCCTACTTTAGAAAATCTG CTTTAACTTGG[T]C]ATTCCCTCTAATTGTGTTCCCTAGGAAATGACTGICCCAAG
WI-7423	107 T C	GTTC	TGCTGGGCTGT	GGTCCAGAAGA GCGG GCGG	TGCTCCCTGTCCCATCTGCAGTGGACCCAGGCCACCCCTTTGAGGAGGTGGGTGAAGTCTCTCT GGCAGGGATTGTGACACTGCATTGCTGGGCTGTGTTCC[T]C]CGGGCTCTTCTGGACCTTGCACCGTG GATACCAGGCCATGTGCCATGGTATTTGGGTCTGGGAGGGTGGTGAATAAAGGCATAGTGTCT

WI-7424	131	T A	CAAGAGAGAG AGAGGAAAGA	TGCAAAAGAAA GAATGAAAGTT G	CCAGGAGCACTAGAGAGGGGGAAGAGCAGAAGTTAGAGAAAAAGCCACCGGAGGAAAGG AAAAACATCGGCCAACCTAGAAACGTTTTTCATTCGTCATTCCAAGAGAGAGAGGAAAGAAAAA TT/AJACAACCTTTCATTCCTTTCGACGTTTCATAAACATTCACATA
X86400	118	A C	---	---	TCCTGCAAGAAGTCTCAAGCCTTTTGTGATTTTGTGCAATAAGTACAGCTTTCGATAAGAGTGAAA TTGGGCTAGCTTAAATGGATCCATAAACTTTCTTCTAATTTTAAAGTGAGA/VCTCTTTTAAACACCT GTTAAATTTAATGTAGCAGTCTGAGAATCTAAATTTATGTACCACCTCGTTTATTTGTTTCATTCATCCA TCCCTTTTCCCATGAATATTCA
WI-8053	242	T A	---	---	GTGGCCACTACATGTTATAGAAACCATCATCTTGTGCACACAGCAGCTCTATGAATAAAGGCTGAG TTATCACTAAGCAGGAGAGAAAGCATTAATAAGGTGCCATTAAAGGGACTTTTAAATCAACCTAA TAAACTCTAATCTGCTGACTTTTAAAGATCTAAGGTCAATTTAATACATGCTGAAAAGGGTCACA ATTAATCTTTGATCTTTTACTCACTGTAACTTATATAAT/AITTCAGAAC
WI-6190	165	G A	---	---	TACAAATGAATTGCTTTTATTCGGTATGCATCCACATTTTCAGCATTTAGTGGTCTCTGAACAGCAAG TGGAAAGAGCGCAGCAATTTGCCAGGAGGTCAAGCCACCAATTTCCGGGATCTGCTGTGCACACOGG GTTCCCTTCTTAATCCCTGCTGAGGATCTTGIG/AJGAAGCAGCAGCAGCAACCAAAAGGCATGCA CCGGATTCAAGGTTCTTTTGTCCAGTTGTCAATTCCTAACTAGACCCCA
WI-6275	148	G C	---	---	AACAGTCACCACCAACCATGACAACCTGCCAGGCAAGGCTTGTCTCCCTCCCTCTTGGCTCCC ATGTGCTAGTCAGCAAGGTGCGGAGGACCGATGTTAGCTTCCGCCAAAGGGAGTATTACAGAGA GAGGCTTGGGAAAG/CJGGAAAGGAAACCTGGACAGGCTTTTCAGCACTGAGAAATCACTTAAACTG ATTTGCTTTCAGTAACCTGGTATGTCTGAA
WI-6421	41	G T	---	---	ACCAAGAGATCAGCTGTCTAAACAGCAGCTTTTGTGATTTGTGTTGGCTTCTGAAAGAACCTTGC TGACAGCTTCTCACTGACCTGACGAGGACGGAACCGTAOCCTGAGAGGGGATGGGGCTCTCTCAGAAA GAATATTTGGGGCAGAACCTGGAACCTGGCACTGCCAGGACATCCCAATATCCCTCTCTCTCAGGG CTCACCCGACATCTCAGCCCAATGAAGGCTCTGAA
WI-6905	215	T A	---	---	GGGTGAGACGGGTTTATTGTGCACATTTACACAGCTCAGCGTCTGGGCTGGCAGCGGCATGCTC CTGTGTCGGGCTGCTCTACAAGGGCGTTCACTTTTCTTCAACCACACTATGTACAGTCAGTCTCCAA GGTGATGGGCTACAGTGTGCTGATCAGTGAGTGTGTACACACATTTTACATAAATTACACAGGACTC ATACATGAAAAAT/AJAGAGCCTAAGGGCCTGTATTTAATGAGAAAAAA
WI-9420	202	G A	---	---	AACCTGTTTACAAAAATAGGCTTTGCAAACTTCACTACTGAATTGTAAAGTCAATGACTGTGTTT TAAATATGTACCAAGGAAATACAAATTGGATAATGATCATTTTTCATGCTCAGGAGAGAACAGCAC AGAAATAAGGATACTGCACAAGGTGCAAGGAAACCGGAAACCCATTGTGTACACTGTCTTCACACAG IG/AJGCACTTCTTCTCACCTTAACCTGCAGCTGTGCAAGATGCCTCAGTGTG

WI-9448	184	G A ---	---	TGGGGCTGCTTTTAGACTTCATTCTAGAGCAGACACCTAGTGAGAGGAATACCTGGGAGAGAGAC TGCCCTTGCCCATGGTGTAAACCTACATGAGGGGACTGAAATCTCTTTGGATGCCAGTCCAGATCCC TTTTAAGAAAAATGGGCTTGTTCCAAAGGCTGAGAGCTGGCACCAAC[G/A]CACTGGTTTCTAAA TCTCTGGCTTGGATTTATCCAAGCGCATGTTCTTAACGTGCCCGTGAGCAG
WI-9470	204	G A ---	---	ATGTCAGAAGAGACACAGACAAGGAGTTTTCCCTTTTAAATGCTAAACAAGTGCCACTAATCCACA GATCTGAAAAAGTACAGCTCTCCAGTTGATAAATCAGATTCAGGCTTTTCTTGTCAGTCCGCTTA TGAGATCAGGAATATGATCTCCCTAAAGCCCAAGATTCCTACTAGAGCCGCTGGGACACTGATGAC AA[G/A]GCAATCAACTCATCTCCTCAAGCTCACCAAGGCTCACCTTCCCAAG
WI-1245b	201	G T ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGTGCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGTGGT TTATTAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCCTCTTCTGAGGC[G/ T]CTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1245a	85	T C ---	---	GATGATTTCTGAAGTCTCAGCAGCCCTGATTCTAAGCCTCATAAGGAAGAGTAGGTGTTAATGGCA TCCTAGGGCAATGGTAGGT[C]GCCCTGATGCAGATCTGCTGTGAGCCATGTGCTGGCATCACAGGGGT GGTTTATTAATTTCAATTTATCATCTGGACAGCCCTTCTTATAACGTACATCCTTGCCCTCTTCTGAGGC GCTAAGATCCCCAAGGTGGCTCCTGTATCCAGAAA
WI-1031	149	G A ---	---	TTCAGTGATAAGGACAGGTCTAGAACAAGCGTTCCCAACCCTGGCACCAATGACAGTTTGACCAAA TAACTCTTTGTTTCAGGGGACTGTCTACACATTGTGGGATGTTAGCAGCCTCGTGGCTTCTACCCA CTAGATGCCAGCA[G/A]CACAAACCCCTCCCAACAATCATGACAATGAAAATGTCTTTAGACATT GCCAAATATACCTTGTGGGACAAATGGCCCTGATTGAGAACCACCTGGT
WI-5385	110	G A ---	---	AATGAGTCATTGTGGAGTTAGAGGAGTTACTGAAAATGGTGACTCCCAATGGTGGGATTGGAAGAGG GAAGTCTCGATAATTTTAACATATGTTTCTTGCCAGGAATCG[G/A]CAATGCTAATCTATTGCTTAA TTCTTTATCAACAGACTCTTTGAATCAATTTAGAGATACTCAGTGACCCCATGGCTAGAGTTCCCTGAC CCCTGCTACGGGAACATTGAATGCA
WI-5403	199	T G ---	---	ACCAACCGTTGGCAAGGCTCCCCAAGACTCAACCCCAACTTTGGTGCTTACCCTATGCCGGGTG GGATTGAAGAAATAACCATATAATAATTGCTACAATTTTCCAGTAGTTACCAGGCACCAAGCCTAT TGGAAGAAATCATAAATGTAACCTACAAATGTATTGCTCTGCTGCTGGCTGGTCCAGGCATAGAGTT/G JGGCCTACAACCCATTTTATCATTTGAACCCCTCAGAAGCATCCAGTTGGGCT
WI-5801b	157	G A ---	---	TGGTATTTTCCCTTTTCTAAAATGTTATGATTAAATTAGTGCTTTGTAGAATTTGAAAAAATGTAAA TCAGAGAACAGAAAGAAAATAAGTATAGTTGAACCTCTAACAAATTTTAGATTTTAAAGGCCTAG GGAAAGAAAGAGAGCCTGGGA[G/A]AGGGAATGAGAAAAGCACCAACCAAGAAAAAAGTGTGT GGCTTAAGGGAAGCCCAAGGAAGTTAAGT



WI-5801a	48 A G ---	---	TGGTATTTTCTCTTAAATGTTATGATTAATAGTGTCTTTGTA/GJGAATTTGAAAAATGT AATCAGAGAAAGAGAAATAAGTATAGTTGAACCTCTAACAATTTAGATTTTAAAGGCC TAGGGAAGAAAGAGAGCCTGGGAAGAGGGAATGAGAAAGCACAAACCAGAAAAAAGTGTGT GGCTTAAGGGAAGCCAAAGGAAAGTTAAGT
WI-5896	61 C A ---	---	TTCTATTTAATCCTGTGCCCATTTGCAAGACTGCATTGAGTCTGCATGAGCCTTAGTTTC/JAATAA AAGCCGCTCAGACCGAGGACAATGTTCAAGAACTAAATGACTGCAGGTGAGCAATTTCTGTATTA TACAAACTGGGACCAAGATGACTTTATAATAGTGCAAGAGACAATCAGGCAGACTGGGAGGAGCC TTATAATAGATTATAAGGCTGTGTGAGTTTATTTAAGTT
WI-7461	153 C T ---	---	TATTACTAGGTTTCATAGAGCCCGTTGTAATGATAATAGCCAAATAGTTAAAGAGGCTGCAGGCC AATTCTAAGCCTCCTCACTTCCCTTCGAACCCAGCCTCAGAGATGACACTTAGGCTGCACATTCCTG TGGCAGGAGCTGTGTCT/JGTTCCTGTGTTGGTCCCGGAACCCAGTGTGTGTGCTGCTGCACAGAG GAGGCCCTGAGTAGCATGTGCTGCA
WI-9716	221 G A ---	---	AGAAGACAGGAGCACTGGGATCAAGGACTGATAAACTCTGAGGCTTTAATGGTCCCTGTCTTAAC GCTTTTGGTATACTTTCTTCTGAAGACCAAGCCTTTCAAACTCTCAGAACACAGGCAAGATGCAT ATTCTGTAGTTTTCAGATGTGTACTTCTACATTTCTGGAAACTAGATGAGTTAGGCTCTCTTCATCT CAATTGAAATTTCTAGAA/G/AJAAACACCTAATTGGCTCATCTTGGATCA
WI-9760	49 C T ---	---	TTTTCGTTAAGTCTTGTGAAGCCACACAGAGTGTATCTACTCTCTTTAC/JAAGTGTACTTTGCA TATATTTATGGGATGATTTCTATCCCTACTTAAGATTTTCTCTCTCAGGTTAAATATCCATTTCT TTGTTCAAGGAGTTTCTTATTTGGCCTTCTTTCTAAACCCCTTAACCATCTGCTTATTTCTGCTTGACA CATGCTATTTAATCAAGGTGACATT
WI-9855	31 A C ---	---	GAAAACTCGTTGGCTCAAAGGAAACTGTAG/JCAAATTTCTTTTTTTTATTTTGTTTTAACTC AAAGAGTGGAGTTTGCAATTGACCTTGTGATGGCAGCTGCTCTTTTGTGTTGGTGAATCTCTAGT GGCAGCTTTGCAAAAGCAATTTAGAGCAAAAGGTGGTGGCATGGAGTTGTGTGAGGTGCTGAAAAG TAGCAATGGAAGAAAGGTTAATGGA
WI-10312	41 A G ---	---	AAGGCCAGTGGGAAAGCAGAGACAAACACTCQAAGAAATAC/JAGATATAAACATCATCATCA GTAGAGATGGGATGACCTAGGAGGTCTGCTGATGAGGCTGTGAGACCAAAAGACATTTGGGTCT TGAGGGTTGAATAGGAGTTTGTCTGGTGAAGTCTTGGCCAGTCCCATAGTAGGTGTTCCATAATAAC AGTGACTAAACTGAGGTAGAGTACAGACAGAAAGAAATTTCA
WI-11152	179 C T ---	---	GATTCCTTTGGACATGCAGAGCAGATACGGCAAGGCATCTTGGCATTTGGAAGGAACGAGCCCTA ATTCATAGAAACAGACTCTACAAAGGAGCCAGTTAAAGGTCTCGCACCCAGGGAGCTGGTGGCCAAAG TCAGTCAAGGCATAAAGGGGAGCAAGTGGGACAAAGGCTTGTCA/C/TCTGTGCAGAAACATTGAA AACAGCCAGTACATGCCACTGATAGA

WI-1968	167	A G ---	---	TGGTGAGGAGCTGAAGGCTGAAAGAAATAGTCTCTGCTCTGCTCTTTTCGTTGGAAATGGATGAGTCCTTTACAAAATTTTCCCTCTTGCCATGGGTGTTATGTTAGAAATCATGGAGTTGGAAGACTTAGATTCAATTTGGGGCTGTACAGTTTACTGGAAGTTGTTAGTTGAACCTTGAGCAAGTGCTCTCTTAATGTCTCTCA
WI-4701	198	G A ---	---	GGCTCAATGCCCTTCCCTGTAA GGGTTCATTTAACAGCCTTCCCACTGGGTCTCAGATTGCACGGAGATGTAAATAAGGAAGAGATAGAAAATGGTGCCCACTATTGACTTGATAACACCTACAAAACACACATTAACCTCCTCCCCACTCTACCCGCCAAAGTCTACCTTTTGGTCTTTTATTCTGCTAATGACCATACTATTTCCCAATTAGA[G/A]CCATGTCAATTTTTCAGAAAAGCAGTATA
WI-4823	164	C A ---	---	TTTATCTTTCCAAACCATGTGTGTTTCTTCCACATACCTTACGTAAATTTAATCATGTCAATTTAATTAATTTGCACTTACTTGGTGGCTACAGACATTGCTTCCAAATTTGTAATTCCTAACACAGCAAGCATAACTGATGTGTCATCTTTGTATTCCTAAAC[A/A]AAGAAAAGTGCTTTTGTGCATCTGCCCTCTCTGTCTTCTCTGTTTCACTCTGTATTTCCCTATTTCAGCAATCAATGATTA
WI-4860	72	A G ---	---	AAAAAACAACCTTCATTGACATTCTAAGAAGATAAAGAAAACAACGATCCACTGTGTGTTGCTTGATTTA/GJGGAGATAAAACCTGATCTCTAAGAAAATTAACCAAAGCAGTACACTAAATAGCCTTTGTGTGTGTTTTCAGGAAAGAAAGCCAACTCAACTAAGTTGCTAAGAAAATAATGTTTCATATCACTCTAACTTCCACATAGAGCAATTAATATAGCA
WI-9705	111	C A ---	---	TGAAAGGACCAGTTGCAATGCCCTACCAAGGTAAAGTAAATCGGAGGGGCAGGAAGTAGGAGTTGCTTCCGGATGTTGCATAAATTCAGGTTCTTTAAGGAGTTGGGCTGCC[C/A]AAAAATTTGTTAACACTGATGCCGTCTACAAACGCACATAGAAAATCGGTGGTAGATTGCGGTTCTCTAGTAAGTAGCTAATGTTTAGATA
TIGR-A004Z48	177	A G ---	---	TGATTGTTGAATTAATGTTGCTGTGTTCTTGGTG CAAATAATCTCTGCTTAGAAGTTGCTCTAGGGCCATGGATTCATGTAAGGTGGGCAGGGTGGACTGAAGATCTGTTGGCAGGGCTCACAGAGACGGGGTGAGGGGAGAGATCGTGGTTTCATGAGATCCCATCTTGGGCAATACGGTTATCCCGTGTCTTCATACGCCACAG[A/G]TCTCCAAATTCAGGGGCTCCC
U17579	34	T G ---	---	GTGGGATGGTGGAGCCCAATGAAGACCAGGTAGATGATGCCACCTAGAGATG GGGATTCATGTGTCTGTCTCATCCAATAAGCACTT/GJCATGACCTCAGCCCCATACTCTTTCTTCCC TATGTTCCCAGAGACAGAATAGACCTGGCCCCCTTCCCTTCTAGGGGATCACAATATTGGAAGGATGAGGACTCCAACAGCCAGCTCCCATGCCAAATAGAACGATGAGTGCTGGGATCAATTTCTATGGGAGCC
WI-7747b	88	T G ---	---	TGGGAGAGGGATCCTTCTAGTTGA GTGAGAGCGAGGCTGAGCCTACAGATGAACCTCTTCTGGCCTGCTTTCGTTAACTGTGTATGTACATATATATATTTTAAATTTGATT/GJAAAGCTGATTACTGTCAATAAACAGCTTCATGCCCTTTGTAAAGTTATTTCTGTTTGGTGGTATCCTGCCAGTGTTGTTGTAAATAAGAGATTGGAGCACTCTGAGTTTACCAATTTGTATAAAGTATATAATTTTATGTTTGTGTTCTGA

WI-7747a	44	T C ---	---	GTGAGCGAGGCTGAGCTACAGATGAACCTCTTCTGGCCTGCTCJTTCGTTAACTGTGTATGTAC ATATATATATTTTAAATTGATTAAAGCTGATTACTGTCAATAAACAGCTTCATGCCTTTGTAAAGTT ATTTCTTGTTTGTTGGGTATCCTGCCAGTGTGTTGTAATAAGAGATTTGGAGCACTCTGA GTTACCATTTGTAATAAAGTATATAATTTTATGTTTGTCTCTGA
WI-7189	197	T C ---	---	TCCAGAAATTTCTCTTCAGCTCATTTGTCTCTCTCACAAATTAAGGGAGTAGGTTAAGTGAAGGT CACATACCATTTTCCCTTCAACAATAATATTTTACAGAAAGCAGGAGCAAAATATGGCCTTT CTTCTAAGAGATATAATGTTCACTAATGTGGTTATTTTATATTAAGCCTACAACATTTTTCJAG TTTGCAAATAGAACTAATACTGGTGAAATTTACCTAAACCTTGGTTATT
WI-7850	57	G A ---	---	AGCCCCAGCTGGACTCATGGATGTGCACCCCTTGTCCCTGCTCTTCTGCCCTGG[G/A]CTCATGTA TCTGGCAGCTCTGGTACCCCTCTGTGGTGCCATCTCTACCTCTGACACAGACTGCTGCTTGAAGCT GAGAAGGCACAGGGCAAGGAGCCAGGACACAGAGCCTCAGCCAGCCAGGATCCGCTCCTCATTTT ATTGGTGATGATGAATGGGAATGAATCAGGGGCTGTCTACTAGAGCC
WI-7907	69	G C ---	---	CTCTTCTCTTCATCCCATCAACCCCTAAATAGGTCAGGTGAGGAGGCTGGGAAGAGGTGGGAGGAGG G[G/C]JAGAAAGTGAAGGAAGATAGGAAGGATATTACCTCTTCTGTTATTTTAAAGAAACATTTGTTT GGTGGCAGCAATCTCCCTGTCCCTATCACTGTTAGAGGCCATAATTTATATCTATAAATATATAAA AGCAAGTCAAACTTGGATGTATCAAGGTAAATATTGTCAAAGTTTAAAT
WI-7919	242	T C ---	---	GAAGGCAGCTGGATCACTTCCCGCAGTCTTGGGCAGCGCTTGTGTGGAACACGAGAGCTCCTCCT CAGGGGCCCTGGCAGCTCAGCTTCTATTCTGTATGATGATATTGGTTAAACACTGTCAATAATAGAGAT GTGCCAGATTTAGATTTTCTTACCTAATCTGTTTAAATTTGTAACTTTATCCATTTGAAAGTGTC AGCCCATTCAGATAAGCTATAATCTGGTCTTTAAGGAA[T/C]JACAACTT
WI-7928	101	T G ---	---	CTCCCTTCTATGTCTCTCAGCAGCAGTGGGGCACACTTGTTCATCTTCTGACCGTTTGTGGGCTA TTCCCTGTCAGTGCAGACATCGTCAAAATTCA[T/G]JACAAGAGGAAATTTTCATGCAGAAAGCTGTA TGCAGGATGCTCACTGATGTTTGGCAGCTTTAAACTGAAATTCACCTCTTATATAGGATTTTCTTTT CTATCTCCATCTCCTCATTAAAAATACGTACATTTTCGAGGTAATGGTA
WI-7936	131	T A ---	---	TTTTAGTCAAGACTTAAAGGGGCCAATGAATTAATATATACATACTGCTGTTGTTATTTCTGAA GGTAGCATTTCTTGGAGTTAAATGCACATATAGACACATACACCCAAACACTTACACCAAC[T/A] ACTGAATGAAGAAATTTTGGTAACCGAGGCCATTTTGGTGGGAATCCAAGATTGCTCTCCCATATG CAGAAATAGACAAAAGTATATTAAACAAAGTTTCAGAGTATATTGTTGAA
WI-7944	99	T C ---	---	TACACGTTCCAGCCGTTGCCCACTCATCTGGGCTTGTCTTTGTTGGGGGCGAGATTGGGTTGG AATGCTTTCCATCTCCAGGAGACTTTCATG[T/C]JAGCCCCAAAGTACAGCCTGGACCACCCCTGGTGTG TGAGCTAGTAAGATTACCTGAGCTGCAGCTGAGCCTGAGCCCAATGGGACAGTTACACTTGACAGA CAAAGATGGTGAGATTGGCATGCCATTGAACTAAGAGCTCTCAAGTCA



WI-7805	101 A G ---			TTTCTAGGCTGTACAGTCTGATGCATGATTTTTTATAAATAATTTTCTACTCTTGTAATTTGGATCTT TTTACTTTGAGCATATATTTAGAATATATGTGTAGTGTAAAGGATCTCCACAATGTCTGCAGTGTG AAGGCAGGTTTCATTGTGGAATAGTTTAAACAGTCAAGGAGGCTAACTGGTCAGTATTAAATGTGTAGC CCTACCAAAATAGCCAGTAGTATCTGAAATGAAATAAATAATGAAGTAT
WI-7416	137 G T ---			GGCCAGGAGATTAGCAACAAGGATTCTCTGTTACTTGGCCCTTTTATCTTCCCTCTTGCC CAGTCCCTTCTCTCCAGCTTCATGTGAAGCTCTGCACAGACAAGACTCAGTGTCTTGGCAGTGCT [G/T]CTACTCCTCAGGTGCAGCATACATAACCAGTAAGAGACTAAATCTGCAATATATAAAGAGCTC CTACAAATCAGTAACATGAAGAACAACACTCAAAAATTGGCAAAATGTCATCAG
WI-140	252 C T ---			ATTTGAAGATTTGGAGGGCTTTGCAGAGGAAATAGATTTCAATTGGATCCCAAACTATAATGACA AGTTTTTAATTAGGTGTGATCAAGGCTTCTAAAGTGAAATGCAAGTTGTTACCAGTAAAGTTTATA TCTTCCATTACGCCAGCTCATTTGCCAGAAATTCAGGTGAGTGGATTGGCCAGACTATCTGGCAAG GATGAAATTTAGTTTAAATGTGTCTATTGCTGTATTGGCATTCTC/T
WI-198	218 C T ---			GAGGTCTTTCAGCAACATGGAAGCCCTACTGCTTCAACCCGAGTTCGCCGATCAAGTGTGGCAAC CATGATGAAACTCTTGCCATGTTTGTAGTACCCTGGACCAAGTAGTCAATCCATCCTGACTTTTAA TTCTAACACAGCCTTTGATGGGACAATCTCTGCTAAAGACTAACCACTTCTTATCTTATCTTCAGCTA CCTGCTTCCCTTTC/TGTTTAAACAAGCATAGATATTTCTGAACAAC
WI-205c	146 T C ---			TTATGGTCCCAAGACAGATTTAAAGAAAGAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTG/TCCAAAGGCTTGATGGGAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTTGTTTAAAAACTGCATATGCCCTTATTTTGTGTTTAGTTCCC
WI-205b	146 T C ---			TTATGGTCCCAAGACAGATTTAAAGAAAGAAATAAGCCTCATCTCCTAACTATGACTTGGTCGG AAGCCAAGAACCTACTTCAACATTTGACCCATAACCTTCTCTTGAGATGATGGCTGACTTTTCAAT GCATGAGTTTG/TCCAAAGGCTTGATGGGAAATCTCAACATTTGTTACCTAAGAAAGAGGATGT ATCTTACTTTTGTTTAAAAACTGCATATGCCCTTATTTTGTGTTTAGTTCCC
WI-234	165 G C ---			GAAGACTGAGTTTCCAGGAGGTTCAGCCGTTCCTCGGGCCCATATGGCTAATAAGGAGCTTGAGCA GGGATTCAACCTGTTTGCAACCCCAAGTCTTCCAGAGGTCTCAGACTACCTCCTCATCTCCCT CTCCCCCACAACACAAATACAGAGATTG/CJAATTCAGGAGCCAGTTTCTAGGTGGCTTTGAGC AATCATACACAGTAATCTCTTGGTGTCTTAGTTTCTCAAAATGGGAAATGG
WI-276b	25 A G ---			AGCTTTTGAAATCCAAAACACATTA/GJCTTGACTCTCTTATCCTCTCTTGTGTAACATCTATCC CTGAGGCAGAAATACAGAACACCCCTGTGGCTGCTGAACGGAGGATGGGGGGGAGACAT CGGTCAATGTATCAAGCATCTCTCTGCTGCTGAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTTATCCTCCTTGCTATCCCTGATGACTGGGCAAA

WI-276	25	A G ---	---	AGCTTTTGAATCCAAACACACATAGJCTTGACTCTCTTATCCTCCTCTTGTGTAACATCTATCC CTGAGGCAGAAATACAGAACACCTGTGGCTGCTGAACGAGGAGGATGGGGGGGAGACAT CGGTCAATGTATCAAGCATCTCTGCTGCTGAAAGACCTCTCCTGAAAGACATGAGCTATTAGGAGC TCTGGCAAGGGCTTGTCTTATCCTCTGCTATCCCTGATGACTGGGCAAA
WI-427	59	G A ---	---	TTTCCCAATCCACAGGTAAACATAATAATGGATGTATAGAAATTTAGAACTACTTCCIG/AJGTTT TTCCCTGGGAAATATTACAAACATTTGTGGTCTGCAATCAGGTTAAAGACATAGTGTGCCA TTGTGTCATCAGACAGGTAGAGGCTGACTCTGGCAGGATTAGCTACCACTAGCTGTGAGACTTTATGT ATTCAATTTATTAGAGCCAGGGTCTGCTGTGTCACCCAGCTTTCAGTGCAGT
WI-562c	106	T C ---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGTTACAGATTAGCCCGAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTCTTTTATTAATAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562b	106	T C ---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGTTACAGATTAGCCCGAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTCTTTTATTAATAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-562	103	T C ---	---	CTCTTCACTCCAACACTATATTGCTTACTTAATGTTACAGATTAGCCCGAGAAAGGAGCCTGTCTC AATACACTAGATATAGTTACTGTGATTATATATTTAAIT/CJAAATGGTCTCTTTTATTAATAAAAA AAAGNTATCTAAAGAGAAACCATATAATCTCTCAGGTAATATGGCCACAGCCAAACCCAGTCT TTCTAAACCTAAAGACTCTCATAAAGGCCCTATCACATAACTTCTCCACTTCC
WI-597c	141	A G ---	---	GTGTAATTTGGTGGCTTTGCCAAGCTTTCCACAGTAACCTTTAGAAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATG/A/GJTAATGACCCCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAAATTATAAC TTGATCTAATATTTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597b	141	A G ---	---	GTGTAATTTGGTGGCTTTGCCAAGCTTTCCACAGTAACCTTTAGAAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGTATCCTTAGGATATTCT GATACATG/A/GJTAATGACCCCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAAATTATAAC TTGATCTAATATTTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTTAAT
WI-597	136	A G ---	---	GTGTAATTTGGTGGCTTTGCCAAGCTTTCCACAGTAACCTTTAGAAATNTNAAAGGTGGAAGGTAAGG ATGAGGAAGAAAGAGGGNGTAAGAAACAAAGATGTCTATGTTGAAGAGTATCCTTAGGATATTCT GAT/A/GJCATGATAATGACCCCTCCATGACTCTGGTACCTCATCATTTACCAATGTGAGAAATTATAAC TTGATCTAATATTTTCACAACTAATAATACCTGAGAGAAATAAGTCTATTTAAT

WI-611	66 G C ---			TTCAAAATTTAACACCAATTGGGTATATTATAATTTNGCTCTATCCATAGTTCTAACCCCTCTTCTCTG/ CJACAGTGAGACACCTGCCCTTCTATTGTCCTTGACGTATTACGTATTTCGATCAGTCACCCCATCTGGA ACCAAGGTTTTCATTTCTGCTGACCCCTCCCTCCCTACCCCTACTTGGGCTCTGACTTCCCTTCCCTGGGCT GAACCTTCTCTGTGGCTGTCCGCTTCCCTCTGCTTGGGCTCCAATAC
WI-681b	156 A G ---			TGAAGCCCTCTCTATACCCAAGTGCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATTCATAAGTTTCATACAGGGGAAGCACTTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJVGJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCTATGTTT
WI-681	156 A G ---			TGAAGCCCTCTCTATACCCAAGTGCTTTATCTTAAATGCTGTGGTGCAAGTATCTACCCCTTA GGGATATTGTGAGAAATTCATAAGTTTCATACAGGGGAAGCACTTTGTNCCTGGTATGTCATAAGCAA TCCATAATTGTTATAGCTATTJVGJTTATACTATGGCACCATTGGGACACAGATTATATATGTCAGA CACCACGNATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCTATGTTT
WI-867b	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGAGGCCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCGJAJTTTGTTGTTTGGC CAAATAATATCTCCCGAGGACGTCTCTTTCTAATCCCTGAAACCTGAGAAATGTTATCTTATGTC AGTGCTATGGTTTGAATGTGTCGCCCAACAAAGCACACATTAGAAACTTA
WI-867	113 A G ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGAGGCCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCGJAJTTTGTTGTTTGGC CAAATAATATCTCCCGAGGACGTCTCTTTCTAATCCCTGAAACCTGAGAAATGTTATCTTATGTC AGTGCTATGGTTTGAATGTGTCGCCCAACAAAGCACACATTAGAAACTTA
WI-867	119 G A ---			AATCTTAACAGCCTTTTGATGCCAAAGCCACTTTCAGTCTTAATCTTTTGAGGCCCTAAGATCAGTG CAACCCCTCCAAGGCTCCCGAGTATCTGGCACATCTTCCCTTTTCATCTCCGJAJTTTGTTGTTTGGC CAAATAATATCTCCCGAGGACGTCTCTTTCTAATCCCTGAAACCTGAGAAATGTTATCTTATGTC AGTGCTATGGTTTGAATGTGTCGCCCAACAAAGCACACATTAGAAACTTA
WI-871b	123 C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAAGGTACCACAAATGTAACTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAAATGAGACATTGTAAAGTTTGTAAATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTATTGTACATAA
WI-871	123 C G ---			TCATCAGACCTGAGATTCAGCATGAAATCTACCAAAGGTACCACAAATGTAACTTGTCCAAACGA ATCTCAGTTTCTGCATATGTAAATGGGAATGATAAGAGCACCCACCTACCTCATG[C/G]AACTGTT GAGAGAAATAAATGAGACATTGTAAAGTTTGTAAATGCACCTGTTATGGCCTGAATTGTGTACCC TAAATTCATATGTTGAAGCCCTAACACCCAATATGNCTGTATTGTACATAA



WI-884	198	T C ---	---	AGGTTCTGGACTTGATGCTGGGAACAATTGGTNGCTGGAGAAATTCCTATTTGAGTNTTCACAGAT CAGTAGAGCCAAATGGGAAGGTATCCTAGTCCATCCCTTTATTAGGAACCTTCTGATCTATTGGGA ACTTCCCTCCTAATAGATCAGGAAATCCACCTCATTTAATCATGGACAACNNAAAGGAATA[T/C]G ATCCCGCATGCAACATTTATTAGTGAAACATGATGAATGAACATAAT
WI-921b	205	G A ---	---	CAGTTCCCAAGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCCTCTCAGCCTCGCCGCCCAAGAAAGTCTTNGCCAGGAAAGCAGGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTTCTCCGAG
WI-921	205	G A ---	---	CAGTTCCCAAGGCTCTGGGGGANGAGCGGTGGGACGCTGCCGGAAGCAGTTCGACACTGACTGA TGCTTTGCTGCAGGGGCTCTGCTCTGAAGCCGGACACTGCCAGGTGCACACAGGGACAGTTATACTGG CAGTGATGCCTCTCAGCCTCGCCGCCCAAGAAAGTCTTNGCCAGGAAAGCAGGATCCATCTAC TCT[G/A]GGGAGAGATCTGACAATTTAATCAGGAGGAAGAAATTTCTCCGAG
WI-945c	90	G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCTGAGTAATAAGAAA AATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAACANTAGGTGCAGCACANNNGGGTT TTCTCTGGTCATAGAACTCTTAAAGGGAATCATGACAGATTTTCTTGCTTTA
WI-945b	90	G C ---	---	GGCTGGGATGAGAGGTCTACTTGTGTACTGGAGGTTTCACTGGCTTGTGCTAGAACTAGNAAAGNA GAAAGAGACAGNGATTGGCTAAC[G/C]CATGGCAGTAGTGGGCCCAAGGCTGAGTAATAAGAAA AATCATTAGATAAATGTCTCATGACCAAAACAAGTTCAACANTAGGTGCAGCACANNNGGGTT TTCTCTGGTCATAGAACTCTTAAAGGGAATCATGACAGATTTTCTTGCTTTA
WI-960b	167	C T ---	---	TTGCTTCAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAATGTTTTTGAGTACAT ATCAAGCACAGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGATGTTAAGTTATCTCTTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGTGGTATGGCATAAGAGTACATA
WI-960a	155	G A ---	---	TTGCTTCAAGAAGTTCTTGCTCAGGAAGTTATTCATTCAGCAACCTAAATGTTTTTGAGTACAT ATCAAGCACAGGTTCTGAGCAATGTCTTAGGAAGACCATAAAGGTGAATAATGAGTGTCTTCTACC CTGAGGAATTTATCAAGAT[G/A]TTAAGTTATCTCTTCTTAGAGGTATAAGTCATATAGGCATATTCT ATGTATACTAAAGTGGTATGGCATAAGAGTACATA
WI-1121	181	T C ---	---	TCCCACTGAGTATGGCTTCAGTAGTTTATTATGATGTGCTAGGTACATTGTTTTTATTGTTCTG CGAATTGTTGTATTACTTTGGGAGAAATGCTCAACTATAAATATTGCTTCTGACCCCTTCTGTGTTT CTTCTTAAAGATACAAATAAATGTAACATTAGACCTCTCACTA[T/C]GCTGTTTTTACTCTCCTCTG ATTTTTTTCATTATTTTATTGCTCTGGCTTCATTTTGTAATNG

WI-1147b	204 G A	---	---	TTTGCCATTATTTGAAGATAACCCACACCTTGGTGTCAGGGTTTCACAGGTATTAGTGGTCAGTCA CATAGGCATATAGTACCTGTATGACTTCTATTCAGCCACCGCAACTTCTCCTCTCCCTGGCTC CTGAGCCAAAACAGGCAATTTACCATAAATCACTTTGTTAGGATGAACCTTATCTGGCCAACTGATA C/GA/GCATGACCCACAGCCTCAGGTATATAAAACACTCTCATCAGGCAGA
WI-1158b	147 C T	---	---	GCATTCAGAGGGTTCGTTAATGACATTCACCTGAGGCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAAATGTGATGGTCTCCTGAGTGTCTGAATG[C/G]GCCAGGT TAAGTGTGGG[C/T]CTGGGGTCAGGCTGCCTGGGTCACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1158a	124 C G	---	---	GCATTCAGAGGGTTCGTTAATGACATTCACCTGAGGCCCTGTCTATGTCAGGCCCTTGGTGTGAAGA CGCAATCATGAACAAAATGAAAATACAAATGTGATGGTCTCCTGAGTGTCTGAATG[C/G]GCCAGGT GGCTAAGTGTGGGCTCTGGGGTCAGGCTGCCTGGGTCACATCCTGGCTCCAAACTGCTTTGCTATG GCT
WI-1304	124 T C	---	---	AAGTTTACAGAAAAAATACCAGAAAGTGACTTCAAGANTCAGCTGAGATAGAAACATATGCCCA TCATCTTCAANGTNCCACAGACACTTATCCCTAGACAGCCATTTCTTTTGAATGN[T/C]GNCANT AAAAATGATTTGAAATTGGGAATAAAGCCCTCCCTCTAATGATTTGACAGTGTAGACCTTGCCTAG GGC
WI-1305d	202 C T	---	---	TTCTCAATTCCTCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAATNACACTGTTTTAANTGNNTATA /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305c	46 C T	---	---	TTCTCAATTCCTCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAGATG ATGATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA ACATCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAATNACACTGTTTTAANTGNNTATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305b	153 T C	---	---	TTCTCAATTCCTCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAATNACACTGTTTTAANTGNNTATA TGCAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA
WI-1305	202 C T	---	---	TTCTCAATTCCTCAATCTGTGTGTTACTTTTATTTCTTTCTTCCATTCTATGTTGGTAAATATAAGATG ATTGTGCAAAAGTATTTAAATATCGTCTGATTATACCATTTTNCAGAAAGATAAGGTTTTCCTCACA TCCACTGCTTTCANTAAATNACTCCACTNATGCTNACAAATNACACTGTTTTAANTGNNTATG[C /TJAGGGCGANGTAATANGTATACAGNGANTCATAACAGCCCTGCCTACCA

WI-1306b	248	A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAAATGGACAATCTTGTNGNNNTNG GGCTGGTGACTGTGCTGGTCAATTTAGAAGCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTATCTTCCCTTAVGJGC
WI-1306	240	A G ---	---	TTTCTGCATTGGAATAGTTGACTTCTATGAGNNGCAATAAATGGACAATCTTGTNGNNNTNG GGCTGGTGACTGTGCTGGTCAATTTAGAAGCCATAGAGATGAAAGTAGCCTGCAATAAAAGAGGA AAGTGAAGCTAATCTGAAGCTGTGACCTAAGGNGAGAGTGCCCTNNTTTCTGATGGCTTTTCAGT CTGTGAGTACACTCCTTTGTGAAGGCCAGTTGAAATTTAVGJCTTCCCTAGC
WI-1307b	118	T C ---	---	GACAAGGCTGTACTAGTTTCCAAATCCAAATCTATGTACACTTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTATACTGCTGGGTTGGGGAGCAGTGGTGTAGGCAATTCJGTGAGATTGTCTTT CCTACCCCTTAATGTATCTTNTAATTATNATGCTAAACCGGTAAGTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1307	118	T C ---	---	GACAAGGCTGTACTAGTTTCCAAATCCAAATCTATGTACACTTTCCTCTCACTTCTCAAGTGGACA GATTTCTGCATTATACTGCTGGGTTGGGGAGCAGTGGTGTAGGCAATTCJGTGAGATTGTCTTT CCTACCCCTTAATGTATCTTNTAATTATNATGCTAAACCGGTAAGTGTGATCTATCACTGGTT TCTTTTGGTGTGTTGTTGCTGTTGTTTCTCCTGTAAAGNTGTTT
WI-1325b	169	T C ---	---	GAGAGATGCCAAGACAAGCAGAGAGGAGAGCAACCNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCTTGTCTCTCTTTCJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATTCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGT
WI-1325	165	C T ---	---	GAGAGATGCCAAGACAAGCAGAGGAGAGCAACCNCTGTGGTTTATCGCAGCAAGCN ATGCTGTCTCCATACCCAGAAATGAGCATGTGCTCTCTATGTATAGATCAGATGACATGGAGAC ATTCATTAGGCAACTACAATGTGCTTGTCTCTCTTTCJACCCCTCAGAACTTCTTGAGGGGCAGGC ATTATGATTCCACTTTACATCAGTGGGAATTTGGACTTGGTGAAGTTAGGT
WI-1327b	162	T C ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAAGAGTCTGTATTGTAAA ACACCAAGTCCGGTTAATGGAATGCGTATGTGTAGTNCATATTACAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTTCJBAAGTTGGGTAGCTACCAGGCCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCATCTCTAAG
WI-1327	175	C G ---	---	CTACGATAATTAGGTTGGCAGTGAGGGTATTAAAGCTGTGTAGTGCAAGAGTCTGTATTGTAAA ACACCAAGTCCGGTTAATGGAATGCGTATGTGTAGTNCATATTACAGGACAGGCTGGGGANGACTC CAGCGACACTATGGAGCTGAGAGTCTGTGAAGTTGGGTAGTCJGTACCAGGCCTCCCCAAATGTAGT TCTTNGCTGAAAGTCTCTCCTTACTGAAGAGGCAATGGTTCATCTCTAAG



WI-1341b	136	G A ---	---	TATCAGCATGATTGTGGCTGTGGACACAAAGTCAATTGTGACTTTTGNNTGCNNNTCCTTTTCTNTTT ACCTGATCCACTATCTTCTCTCAAGATCANGTTCAAATTTGGCTTNCCTTTGTNAATTATACCCAAAGC [G/A]GGATTGTGATGATCTGTTTATTTCTGCTTGGACACAGCAGAGTCGTCTCTGNGAGTNTG GTTTCAGGATTGTCTGTTTCCCGAGCCCACTTGCACTTAGCAAGTGT
WI-1349e	192	G C ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTCTGGCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTTCAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTCAGAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAATA
WI-1349d	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTCTGGCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTTCAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTCAGAA ATTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAATAATGAT
WI-1349c	192	G C ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTCTGGCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTTCAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTCAGAA ATAATTTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAATA
WI-1349b	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTCTGGCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTTCAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTCAGAA ATTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAATAATGAT
WI-1349	264	C A ---	---	CTGACAAATGTCATATCTCACTCCTAAACCCACAGGTCATAGATCAGTTAGCTACCCCTCAATCCA GCAACCCAGCTTTGAAATGGATGCAGGGCAGGTGGTAGGTCTGGCTGTGAGTTTGATATATATG GCAGGTGCTCAACAAATGTAGATTTCAGTGAAGGATAGTGTGAATTTCCATCTCTGAGTTCAGAA ATTGAGAAATATGATAGAAATTTGTGAAGTACTAGATTTCAGAAATAATGAT
WI-1403b	57	C T ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGAAT GCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGACGTAGAGTAAGCCATAAAATATACGT AAAGTTTACATCAACATAATTCTTGGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTCA TAATCCCAAAGTGCCAAAGGGTTGTATCTGATTGT
WI-1403	58	T C ---	---	TGGTATTTGGAATGGGTTTCAGACTCCGGGTTCTGGCTTCTGACCTTTGGTAAGTTG[C/T]TCCGA TGCCACTTTATAAGTTAGAGGTATTACCTTGGAGGGGGACGTAGAGTAAGCCATAAAATATACG TAAAGTTTACATCAACATAATTCTTGGCCCTGCATCATGCAATTTGGCAATATGTCACATAGCTGTCTC ATAATCCCAAAGTGCCAAAGGGTTGTATCTGATTGT

WI-1417c	31 C T ---	---	CAGGCCGGAAGAGATTACAGTGGAGAGATGTC/TJTTGGCCAGGGCGGCAGATGTGAGCCCAAGGG GGTGACAGCATGCCCTGCTGGCATTGGAGGGCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCCCTCGACTTCGGAAGTTTAAGGGCTCGGCTTCAAAAAGCTGGTCCGTTTGGAGCGGTTGC AGCGAGGCCCTTAGGTCGTAATTAATGTTTGTAGAAAAGTCGC
WI-1417b	31 C T ---	---	CAGGCCGGAAGAGATTACAGTGGAGAGATGTC/TJTTGGCCAGGGCGGCAGATGTGAGCCCAAGGG GGTGACAGCATGCCCTGCTGGCATTGGAGGGCCAGAGGAATCCAGTGGCCCTCTCAATGACTTG GGTCCCTCGACTTCGGAAGTTTAAGGGCTCGGCTTCAAAAAGCTGGTCCGTTTGGAGCGGTTGC AGCGAGGCCCTTAGGTCGTAATTAATGTTTGTAGAAAAGTCGC
WI-1729	172 A ---	---	CCATGAGCAACAGCATGTTTCTACTCTGTGTATGTTAGGGGGCATGTATATCTGTATTTCTT TTTTATTCTCTCCAAAAGAAATTTCAATTATGCAAAACATTATCAGGCAATGCAGCTCGTAATAAGA TGTGGAGAACTGAAAAGAGAGCTTACATGCACCCCAATAGCAAAACTCTCCACACATTTCCAGCA GATGTATGTGCTCTCCGTGGTNACTTCTCTCCACCATCACCTGTGTTTT
WI-1732b	122 T C ---	---	TGCCTTACTTCTTTGTTTCATCCACCATTACATTTTGTAATTGGAACCTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAGGAGTNTCCCTGGGTCAACCCCTTTCJATTCACTCT CTGCCACATGTCTAGTAAGTGTGAGTATGGGTGCATCAGTATAATCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCAATCATATTTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1732	114 C T ---	---	TGCCTTACTTCTTTGTTTCATCCACCATTACATTTTGTAATTGGAACCTCTAGGAGGTAGAAGGA TATGCTGATCAAAAAGGGGACATATTCAGGAGTNTCCCTGGGTCAACCCCTTTCJATTCACTCT CTGCCACATGTCTAGTAAGTGTGAGTATGGGTGCATCAGTATAATCTGAGCCTCCCAAGGTACAGC CTTCACTACTATTCAATCATATTTGGCTAAGGTATTCATCATATTGGCTAAG
WI-1750	97 A G ---	---	GCGAATTTAATGACTCCAAAGGTAGTAATTCCTTCCCCCAAAAAGGTTTTAAATCTGTGTGGA CATAATGTTTGAATTTGCAGTTCACTTGGTGGTAAAGGTGTGCTGTTTCTGGCAAGAGTCAG TGGGAGTGTCCGGGAAAAGGGCTAAAGTCTTTGTAGTCAGACAAACCGGCTTGCAGTCTGACTGAG CTACATTCACCTTATGATCTCCAGCAGGTTCTTCCA
WI-1780	31 A G ---	---	GGTACACAAAGAAATGCTTCTGGAAATCTACJAGTAGGGCCTTAACATTTTGGCTGAGTATAATC TGTACATGTGTAAATGTGAACCAACCATGAAGCTGGGCAAGAAACAAATTCCTAGGAAAGTACAAATTAC TGGGAAACTGTAGAACAAATAATCTCATAGTTTACACATAGCTGGGAATCACTCATGTTCCTCATCA ACTGGAGAGACCTTGTGAGTACAGAGGACATTCAGAATAATCATAAAAAT
WI-1803c	77 A G ---	---	CCACTCAGTAATAATAGTGTGGAGATAAGTATATGGTAGGCACATAATAATTTTCAGGCAGAA CCATTATGATJAGTAGGTAGGTAGAGCATCACACTTGGGAGGACATATCTGGAGTNAGATATCCTG GGTGCTAATTTCAATATATCTACTAAAGCATGACTTCTAGAAAATTACTTATTACTTGTCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAATAACTGGAATCA

WI-1803b	77 A G	---	---	CCACTCAGTAATAAGTGTGGAGATAAGTATATGTAGGCACATAATAATTTTCAGGCAGAA CCATTATGATAGAGTAGGAGGATCAGACTGGGAGGACATATCTGGAGTACATATCTGGAGTACATATCTG GGTCTAATTTCAAATATATCTACTAAGCATGACTTCTAGAAATTAATCTTACTCTTGTCTCTCAA GGAAATGGGAATACCTATAATACAGTCTTATTGAGGAAATAACTGGAATCA
WI-1837b	112 C T	---	---	TTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCGTTTATAC[CT]CTGTCCCGAGTTTATTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAGACCTTGAAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGAACGTTTAGCTTTCTGTGTGGCT
WI-1837	112 C T	---	---	TTACTTGGGATTTTCATAGCTGATCATAATTTACCAATTTGATAATTCACCTCTTTTCCAGGCTCA AGGCTGATAAGCAGTTATCCAGATAGAATAGACCGTTTATAC[CT]CTGTCCCGAGTTTATTTT AAGGTTTTTTTTCATTGCACCTGATGCCAAACAAACCTCAAGACCTTGAAGTGAATTTTGAGCT CGTGAACAACTGGGAAGTCTGGGAACGTTTAGCTTTCTGTGTGGCT
WI-1840b	79 G T	---	---	TCACCTAGGGAGGTCGCTAAATGTAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT[GT]GAGAATCTGAATATTCAGCACATACAAAGTGTGACACCTTGTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAGTTCCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1840	79 G T	---	---	TCACCTAGGGAGGTCGCTAAATGTAGCTTCATTAAGACACCTCAGACCTATTGGATCAGGATCTT TCAGGTAGCAGT[GT]GAGAATCTGAATATTCAGCACATACAAAGTGTGACACCTTGTAGTAT ATTTATCTCCAGAGTGTTTTGAATTTACTAAAGTTCCTAAAGAGCCATGAAGAAATTATAAGACT ATCGCA
WI-1879b	110 C T	---	---	GGGCTCACTTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTTGAAGTNAAGGACCTGCCNTTTT[CT]GTCTGCNAAATAAACTCCGAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCTGTGCCTTCT CAAGAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1879	110 C T	---	---	GGGCTCACTTTTCATCAGAGCACATATCAGTGATAGTCTGTTTCTCTTTTCATAACTTACTCCCCCG CACTGTAGGNTTCTTTTGAAGTNAAGGACCTGCCNTTTT[CT]GTCTGCNAAATAAACTCCGAAA AAGTGGTTAGTCCACAGGGTTTAAATAGTCTTGTGTAATGAATTTCTGTGCGACCTGTGCCTTCT CAAGAAAAAAACATTGAAAAATCTCCACAGAGCCCTTTACCCACT
WI-1900b	119 C T	---	---	TGTTCTCTGGTCCAGGCACCGGCTAAGTCTTGTCTGCATAATGGAATAATCAACTGGACAACCCNG CTNAGGTAGGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[CT]GCTCTGAGAGGT AAAGTGCCCTGCCCAACGGCGCACAACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTCTTAACTGCCATGAGAAACCACTTTCTTGTCTCC



WI-1900	119 C T ---	---	TGTTCTGTGTCAGGCACCGGGCTAAGTCTTGTCTGCATAATGAATAATCAACTGGACAACCCGNG CTNAGGTAGNTACCTNGGCAATTAGCCCCATCTTACAGCTGCAAAAGAGG[C/T]GCTCTGAGAGGT AAAGTGCCCTGCCCAACGCGCACAACTAGAGAGCAGCCAAACAGGTGTTTGAACCCAGCTCTGCCT GACTTCAGATCTGTGTCTTAACTGCGCATGAGAAACCACTTTTCTTGTCTCC
WI-1943c	165 C T ---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGAACACAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943b	165 C T ---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGAACACAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1943	164 C T ---	---	ATTCCAGTTTCACAGTGGGCACAGGAGTCAGATTAGGGCTAAGTTGGGGGACAGGATGCACAGCGT GTTGGCTCAGGATCTCTGGGAGGTGGCACCTGTGACCTGGCTAANCATGCTACTTTTCAGAGTCAAGC AGCAAGCCAAATGGGTAGGGAAGAACACAGCC[C/T]CTCTGAANCTGGTCCCACGTTGGAGATAGTGAA TACAGGGCACCGNTGAGCATTCAGATGACTCCAAAGCCCCGGCTGGAGTAT
WI-1960c	270 A T ---	---	CCAGGTGAGGCTGAAAGAAGGAAGGCAATTGCTGTTGGAGTGAGGATTTCTGGAGAAGCACCOCT GCAGAGCTTCATTCTGTTTTCAAAAGTGTGCCATGCGANGTCNTCTGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAATAGGTACTTCCCAGCTCTGACTAGACCTTTGGCA GTTGCAATTAATCCGTGTTGCTGAAACTTAAATGCACCTCCCAACTT
WI-1960b	270 A T ---	---	CCAGGTGAGGCTGAAAGAAGGAAGGCAATTGCTGTTGGAGTGAGGATTTCTGGAGAAGCACCOCT GCAGAGCTTCATTCTGTTTTCAAAAGTGTGCCATGCGANGTCNTCTGGTTGTGAGCTCATNGCTGAG TTATCACAGCTCCTGATGACAGATCATGAAATAGGTACTTCCCAGCTCTGACTAGACCTTTGGCA GTTGCAATTAATCCGTGTTGCTGAAACTTAAATGCACCTCCCAACTT
WI-1977	203 T C ---	---	CTGATGCCAAGTGCAGCTTAGAGTNAGGAATCCAGAGAAAGTNTTGGATCTGGTAAGTAGGAGTCA TTCTGGGCATTTCTTCATAGAGTNTTGTCTTGTAGTCTCGTAATAACTGTGCTGAGGAGTTGTT TTTCTACTGCGTCTGTGAAAGCCTTTCCCATCGAGTGATACAGTACTTTCCAGTTATGGAGATT[ /C]TAACAATCAACACTGGCTGAGGCTGTTGG
WI-2012	102 T C ---	---	AAATTCTAGAAGCCAGAGTCAGCTCACGATTTATAAGTTGAAGTAAATGCAATTGATTGTTTCATGT TTTCTCTTAATTCTGCACAAACTAGCTAAAATC[C/T]TTTAAATCAGTTACCAGAGGCAATACCT GGGTTAATGTAGCACTCAAAAGTTATGTAGAGTAGCTGTCTCTGAGTCACCTTTTCTACTCTCATT GGCTTCACCAATGCTTCCACTGGATC

WI-2013	127 C T ---			CTTTAGAGGTGGTCAATTCGGTTCCTCTCGGAAGTGATTCGTGTTAAGAAAAATAGATGCAACG TTGCTAAGTACACCTAACATTTAAACAGTCTCCAGCAGATAAATGCTGATCTGACACTTCCTCTCA CCAGAAAAAGAGAAATACCCATCATGAGGAAGAGAAATGACTTTTGTTCAGTTATGCTCCCGGGTCC CCTTCACTGGAGGATATCTCAGCTTCTGAGCCCTGGTTACTGCAATCC
WI-2032c	166 G A ---			ACCAGACATCCCATCAGGAGTTAGTCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCAAAAAC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACG/AJTGTGGGACCTCTGTCTCAACCTCCGACTTTTCAC AGATCATTTGGTTAGGCTCACTTCTGTAATTGCTTCTGTTTTCAAAAGGG
WI-2032b	219 C G ---			ACCAGACATCCCATCAGGAGTTAGTCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCAAAAAC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GTCTTCTGTAATTGCTTCTGTTTTCAAAAGGG
WI-2032	219 C G ---			ACCAGACATCCCATCAGGAGTTAGTCCTTCTGGCAAGCCAGCCCTGCCCTTCTGATTTCCAAAAAC TCAATTTTCTTNACTTACTCATAATATTGCTAGGATATCCACATAACCAAAAGCCAAACCTAACCC ACATCACCCAACTGGTTTCTAGATGTACACGTGTGGGACCTCTGTCTCAACCTCCGACTTTTCACAGA TCATTGGTTAGGCTCA/C/GTCTTCTGTAATTGCTTCTGTTTTCAAAAGGG
WI-2054b	188 C T ---			CGTTTTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCATGTGTGGTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTTC/C/JTCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGCTGTCTTT
WI-2054	183 T C ---			CGTTTTCTACATCTTGGGNACATAAAGANGAAGAGNAGCTGTCTTTTGTGGTAGTTTGTCT CAGAGCTGCCCTAGAGCNAGGACAAGACAGGTGACCTTTCAAAATACCTTACAGACTTAGGATTTGGA TTTTCATGTGTGGTGGCACAGCCAGGCTCAACAGAACTAATACCTGCTGTTC/C/JTCTGCCTCCAC CAGCCCTATCTCTTAGGCTCAAGGAGAAATTTTACTGGATGGCTGTCTTT
WI-2573d	129 T C ---			TGGGATTAAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCTTAATGTTGTGTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTGCCGTTTCCAGAGGTGTTTCCGTGCTT/C/JGA TATCATCTGATCTTCCCAACCAGGGCTTATTTATGCTAGGTAGGGGTAAAGCAACAGAGGCTGTGT GAAGTGAAATGATTTGCTTGCACAAGGTATATGGCTGGCTTGGACGAG
WI-2573c	165 A C ---			TGGGATTAAACCCCTGTTTCTTCTCCAGTTCAGTGTGCCTTAATGTTGTGTAGAAATTAACA TTAACAGCAGTAAATAGCTCTTAAATGCACCTTGCCGTTTCCAGAGGTGTTTCCGTGCTTTCGATAT CATCTGATCTTCCCAACCAGGGCTTATTT/C/JTGCCTAGGTAGGGGTAAAGCAACAGAGGCTGTG TGAAGTGAAATGATTTGCTTGCACAAGGTATATGGCTGGCTTGGACGAG

WI-2573d	129	T C	---	TGGGATTAAACCCCTGTTTCTCCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACTTGCCGTTCAAGGTGTTCCGTGCTTT/CJTGA TATCATCTGATCTCCCAACCAGGGCTTATTATGCCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGCTTGGACGAG
WI-2573c	165	A C	---	TGGGATTAAACCCCTGTTTCTCCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACTTGCCGTTCAAGGTGTTCCGTGCTTTTGATAT CATCTGATCTCCCAACCAGGGCTTATT/CJTGCCTAGGTAAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGCTTGGACGAG
WI-2573b	165	A C	---	TGGGATTAAACCCCTGTTTCTCCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACTTGCCGTTCAAGGTGTTCCGTGCTTT/CJTGA CATCTGATCTCCCAACCAGGGCTTATT/CJTGCCTAGGTAAAGGGTAAGCAACAGAGGCTGTG TGAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGCTTGGACGAG
WI-2573a	129	T C	---	TGGGATTAAACCCCTGTTTCTCCTCCAGTTCAGTGTGCCTTAATGTTTGTGCTAGAAATTAACA TTAACAGCAGTAAATAAGCTCTTAAATGCACTTGCCGTTCAAGGTGTTCCGTGCTTT/CJTGA TATCATCTGATCTCCCAACCAGGGCTTATTATGCCTAGGTAAAGGGTAAGCAACAGAGGCTGTGT GAAGTGAATGATTGCTTGACAAAGGTCATATGGCTGGCTTGGACGAG
WI-2868b	60	A G	---	GACTTCATGCTCATGAACAAGCATTGTCTTAATTTACAGACATTAAAGCAAGCTTTCC/A/GJCTC CCACTTCCCTCCACTATCACTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTTAGGTCTCTGCAT ATCATGGAAGCCAACTACTCTATTAACGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTATGGAACAGCTGAAATGAATATCGATATAC
WI-2868	60	A G	---	GACTTCATGCTCATGAACAAGCATTGTCTTAATTTACAGACATTAAAGCAAGCTTTCC/A/GJCTC CCACTTCCCTCCACTATCACTCAACCTCTTCATCCACTTTAAAGAGGTTTCTTTAGGTCTCTGCAT ATCATGGAAGCCAACTACTCTATTAACGCTTTCCCAATGATGCAGCCAGTTCTGCATACAGTTTGTA CAGAAATGCTATATTATGGAACAGCTGAAATGAATATCGATATAC
WI-2870b	131	T C	---	CATGCTGTGTAACTCTGTGCTGTGCTGCGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCATTTTAAATTATATCAGAGCTTATGTCCACTTCTGTTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTT
WI-2870	131	T C	---	CATGCTGTGTAACTCTGTGCTGTGCTGCGGGAAATTAGAGCAAGGAATTGTATAATCCTAGGC TTCAAGGAGCTTCTCATCTCATTGAGGAGACAAGATGAACATCAGGAAATGACTGGATAATGA[T/C] AGAAATGAATAGAGCCCATTTTAAATTATATCAGAGCTTATGTCCACTTCTGTTCTGCTGCCATCAC TGGGCTTTTACAAAGGAGGGCTT



WI-2954c	49 T A ---	---	TTAGCACATATCTGTGTGGGACTTAAGTACAGACAAAGGCATAAAAATTAJACGACACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954b	41 A G ---	---	TTAGCACACATATCTGTGTGGGACTTAAGTACAGACAAAGGC[AG]TAAATAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2954a	38 G T ---	---	TTAGCACACATATCTGTGTGGGACTTAAGTACAGACAAAG[GT]GCATAAAAATCAGCACCTGGGGCA CAGAGGAGCTCTATGCATTNAATTCCTCATACCTACCCCTCCTCTCATTCATGAGTCCTTTGAGT CCTTGGAAAGACTCTATTCCCTGGGCAACCCCTTGGTCTCTGGCCATCCATTCGACAAATAAGTCCA GAG
WI-2971b	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCGCATTTCTAAGA[T/C]G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGTAACTCCTCCTCTTCTTAATAAACCTAAC ATTTCCCTTTGTTCCCTGACATTTCTGAAGGCCACGCTGGTCTAGATGTATGTCAGATTGCAATCCT AGTCTTTAATGTTATTCTGAAGAAACCTTTTACTTAGGGATTGTCT
WI-2971	62 T C ---	---	ATTACAAATCCTACCTAGCAACTGCTGACACTTCCAGTTAGACTCACCGCATTTCTAAGA[T/C]G CTGCCAGCACCAATAAGCTTTCTTCAAAACAATTTGTGTAACTCCTCCTCTTCTTAATAAACCTAAC ATTTCCCTTTGTTCCCTGACATTTCTGAAGGCCACGCTGGTCTAGATGTATGTCAGATTGCAATCCT AGTCTTTAATGTTATTCTGAAGAAACCTTTTACTTAGGGATTGTCT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTAA /TJAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151 G C ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTAA AATCTTTCTTCTGGTGT[C]TTAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133 A T ---	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGGC TCCAGTTTNNATCAAGATAAAGACCTGGAAGACCCGAGCCAAAGGAAGGAGCTGGANTTTTTTAA /TJAAATCTTTCTTCTGGTGTAAAGGAAGTTATCTGAAACCCACTGGTACTCTCCAATGGGTAAAG GAATGAGACAGAACTAGCAGAAAGTGTT

WI-2995c	151	GC	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAGACCTGGAAAGACCCGAGCCAAAGGAGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGTG/CJTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995d	133	AT	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAGACCTGGAAAGACCCGAGCCAAAGGAGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGTG/CJTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995c	151	GC	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAGACCTGGAAAGACCCGAGCCAAAGGAGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGTG/CJTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995b	151	GC	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAGACCTGGAAAGACCCGAGCCAAAGGAGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGTG/CJTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-2995a	133	AT	---	TTCTGGGAAAGAAAGATGGGGTTTTNTTGTCTCTGACTACAATCCAGAGATAACATCTTTGCC TCCAGTTTTNATCAAGATAAGACCTGGAAAGACCCGAGCCAAAGGAGAGCTGGANTTTTTTTNA AATCTTTCTTTCTGGTG/CJTAAAGGAAGTTATCTGAAAACCCACTGGTACTCTCCAATGGGTAAAG AATGAGACAGAACTAGCAGAAAGTGTT
WI-3147	85	CT	---	ATTCTGTAATGTTTTCACTGCTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA T/CJGACAAGCAAGAACACACAGAAAGCCCTGTGTTTGCAATCTGGCCTCTTATAAATACCTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAAAGGACAATGGAATGTACTTATTTTINATATCTTAT
WI-3234b	68	TC	---	ATTCTGTAATGTTTTCACTGCTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA T/CJGACAAGCAAGAACACACAGAAAGCCCTGTGTTTGCAATCTGGCCTCTTATAAATACCTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAAAGGACAATGGAATGTACTTATTTTINATATCTTAT
WI-3234	68	TC	---	ATTCTGTAATGTTTTCACTGCTCCAGTAAATCTTTATTGAGGTCCATGTCCATTACCTCTACTTA T/CJGACAAGCAAGAACACACAGAAAGCCCTGTGTTTGCAATCTGGCCTCTTATAAATACCTTTCTG TATATTTTAAACAAGTACTGTAGAGTNATGAATCATTACATCCTTAATAAGCATATCAAAATTTTAC TCAGTAATTCAGAAAGGACAATGGAATGTACTTATTTTINATATCTTAT

WI-3292b	106	G A ---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTTG/AJTGATTTGGATTGGGATGATTACTT GCCATGAATATTTTCCATTGTTTCTCAATTAATGTAATTAATTAAGTAAATATTTATTTNCCATGA GACACAATGGAAATAATGGAAACATTTCATGGAAAAAACCCTTTCAATC
WI-3292	106	G A ---	---	GTTTGTAGACTAGGAGTTTCAGCTTCATCCAAATCCCTTTAAGGATANTTAGCTCTGCACATCC TCCCTGTCCCGTCCCAAGCCTATGTTACTGGTATGCTTG/AJTGATTTGGATTGGGATGATTACTT GCCATGAATATTTTCCATTGTTTCTCAATTAATGTAATTAATTAAGTAAATATTTATTTNCCATGA GACACAATGGAAATAATGGAAACATTTCATGGAAAAAACCCTTTCAATC
WI-3355	19	G C ---	---	CCATGAACCATGGGCTACA[G/C]ATATTCCTAACTTCAGAGTCCCTCCTTACTGGAGGGATCCA CTTTTAAATATGATTTCTTGAAGTGGCTGCATACCTATTCCTTCCAGCACCTTAAACATCATCAGAA AAAAAATCATCAAAAAGTCGAAGTTAGTTTNAATTACCTTCACCTTTTCAATGGAAACCTTTATAA ACTGTGGATCAATTTATATTAATTTTGGATCAGTTTAGATGACTTTNAGTTG
WI-3408	194	G A ---	---	CCATGAAGATGAGTTCCCTCCCTCCCTGGGTACGTCTAAGAATAGCACACCTTGAGAAATTTNACT TAGCACGTGGCATTGTAATGGCTGGATTTCCTCCGCTCTAAGACACACCTTTATGCTTTTCNAAGCTTT CTGGAAATTGGGATGAATCTNACATTCATGTGCAACCTTCGTGTGGATCAGTCTTCC[G/A]JTGCCOC ATCTCTGNAGAGCCACTGGGAAGTCGAAGGAGTGACTTCAAAATCAGG
WI-3505b	131	G A ---	---	TAACTTATGCCCTCATCTGGCTTACTGCTTAGTTCCCATTTGTGCATCAGTGCACCTTAAAAAATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCTTAACACATTACCTATTTTNAACCAAC[G/A] AGGTGATTCCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATTGGGAAATATGTTGCATAT
WI-3505	131	G A ---	---	TAACTTATGCCCTCATCTGGCTTACTGCTTAGTTCCCATTTGTGCATCAGTGCACCTTAAAAAATTTT GAAAAATTGCCATTTTAAATATCTTTGGAACTTCTTAACACATTACCTATTTTNAACCAAC[G/A] AGGTGATTCCTTATGGGAAATATATACAGCAAGAAAAAANANGGAAAAAATGTTGATGATACCT GTTTAAATTGGGAAATATGTTGCATAT
WI-3584b	177	C T ---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAAGT GAAATCAATGTGTCTTCCAGTGTATTCACATGGCACAGTGTCAAGAGGGCTTGAGCGTCTGAGCG TGGACTTCACTGGTTGACTAACGTTAACATGCTGTCTGTTC/TJACAAAGTGTGTGTGTGTGCATC AGTGTACACATGCTACCTTCTTCACAAAAACAA
WI-3564	177	C T ---	---	GCTAGTAAGGTTCCACCTAAATGGTTCCAAGTCAGGAGAGTCACTAAATGTTTGGAGAAATAAAAGT GAAATCAATGTGTCTTCCAGTGTATTCACATGGCACAGTGTCAAGAGGGCTTGAGCGTCTGAGCG TGGACTTCACTGGTTGACTAACGTTAACATGCTGTCTGTTC/TJACAAAGTGTGTGTGTGTGCATC AGTGTACACATGCTACCTTCTTCACAAAAACAA



WI-3649	64	A	---	---	AATGTCCATGCTGTGACTGAOCTGTCTAACACCTTTCTAGTATTCCTTTAGTGAAGATTACACAG[AG] AGACCAGTTTGCTTCACTTAGTAGGGCCAATGATAGACTTTTAGGTGCTACCACAAAGGGTACCTGC ACAGCCACATCATATGTCACAGTATGGTTGCAAGGACCTGTCTAGACTCTTTCTGCCTGCCTTGCTC TTCCTGTTTTACCATAATTAATGATGACATGCAAAACCTCAGAGCCTTTTA
WI-3674b	133	G	---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCTCTCTAA ATTTAACTACCGAGCGAGTGCTTTTATAGTAATTAATAATATGTTTATTTAGAAAATAACAAAATIG /CJAAGAAAATAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACCTTGGTCAAATGATTGTT AATTCCTTAATTAATTGTGTTTTATGTTTTNATTACTGCCAATCAGAGCCAAG
WI-3674	133	G	---	---	ACAGTACACATGGCCCCATTATGGAACAATCATCTGACTTATGTTACCTGAGAAGTTCCTCTCTAA ATTTAACTACCGAGCGAGTGCTTTTATAGTAATTAATAATATGTTTATTTAGAAAATAACAAAATIG /CJAAGAAAATAATGATAGTCAAGTTGTAGACACTATTTAAAATTGTAACCTTGGTCAAATGATTGTT AATTCCTTAATTAATTGTGTTTTATGTTTTNATTACTGCCAATCAGAGCCAAG
WI-3682	137	G	---	---	CAATATAGACCAATGACTGCCACAAGAGAAATTAGTGGATCTACATTTAGAAACCACATGTTTTT ATTGGCTCTTCTCTCTCTCTCTTTTAAATGCTCTCTCCACACCAATTCACCTTATCTTTTCA TIG/AJAGCAATTTGTCCAAATTTAAAGTCAATGAATAATGTACATTTTCAACAAGTATACATTAA GCCCTGCAAAAGTGCTTATATGCTAT
WI-3854b	194	G	---	---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGA CAAAGACCAAGGACAACTGTAGGACTTCTGTCATGGTCTACCTCCTCCTTCTTGATTAATAACTC TGGTTCAGGAAGGCAAGGCGAGTTATGACCACCTTTACAACCTGAGGAAATCAAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGTTTATAACAGAGTCAGAGCCA
WI-3854	194	G	---	---	GGTATGTTGAGGTCAGCTAATGGTCACTGTGGTTGGAGTGAATCTAAATGGATTTTTGCCCTTGA CAAAGACCAAGGACAACTGTAGGACTTCTGTCATGGTCTACCTCCTCCTTCTTGATTAATAACTC TGGTTCAGGAAGGCAAGGCGAGTTATGACCACCTTTACAACCTGAGGAAATCAAAGCAAC[G/A]AGAA GTTAAATGGCCTGTCCCACTCCACAGAAATGTTTATAACAGAGTCAGAGCCA
WI-4039	210	G	---	---	AGCCAGCCACATCATGTTGAGTCTGCTCATCTTCATCTCTTATTTCTCTACTGCCCTTCACTT CCATTAAACAAGAACTCTTGTTGATTACATTGTATGTTGTGGTTACACTACAGAAATCCAGATGACCTC CCCATCTCAAGGTCAACTAATTAACACCTTAATTCTATTTGCAATCTTTGTCTATTACCATTAACATATT CATGG[G/A]TTCTGGGATAAGGGGTAGACATTTTTATGGGAGGCATTA
WI-4110b	130	T	---	---	GAAAAATGATGTTTTGATTTCCCTCTCTATCTTCAGATTATTGGAGTGTCAATTAGAAAACCTGATAGT AACCTTTTATTGATGAACCTGTCTATAATTAACCTTCCCTCTCTCTCTTATTTTGGCTT/CJACA GTTTAGGTAATAAAAGATGCCCAAGAAATTCAGTATTCAGATACAGTAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAGGGAGGAGGTNGGGGTTTCTCTGGGAAGA

WI-4110	130	T C ---			GAAAATGATGTTTGGATTTCCTTCCTATCTTCAGATTATTGGAGTGTGATTAAGAAACTGATAGT AACCTTTTATTGATGAAGTCTGTCTATAATTAAACCTTCCTCTCTCTTATTTTGCC[T/C]ACA GTTTAGGTAATAAAGATGCCCAAGAAATTCAGTATTCAAGTACAGTAAAGTAGCAACCATGGG GTAGGGACAAGTNCAGAAAAGGGAGGAGGTTGGGGTTTCTGGGAAGA
WI-4119b	168	G A ---			ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGCTTGGGTTGGGAAAGTAATAATAG AATGGAAGGATAATAAAGTAACTACGGGGAAGAACAGGACAAAGAACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTTGTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4119	168	G A ---			ACCTCTATGCCTGAAAGCCCTCATGAGTGTCCAGCAAGGCTTGGGTTGGGAAAGTAATAATAG AATGGAAGGATAATAAAGTAACTACGGGGAAGAACAGGACAAAGAACAGACAGAAAGGGGTT AGAGGAAGGAATCAGTTGTGTGCCATTCAAAGTTAA[G/A]CAAGGTACCAAATTTGTTTTCTTTCA TGAGACCGTCTGCATTCTTTTGTTTTAAAGGGCTCTGTTGATCATCATCTTCA
WI-4123b	51	T G ---			CAAAGTCAGATTTTGATTATTCAGGATAACAAATTTTGAAAATAGAAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAACATGATGAATTTCTCGTTACATAATTGTATAGAATTTAGTGGG TTCTTCCATGACATTTGGCTTGTCTTCTCAACAGTGGTGGTTGGATGTTTCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTAGCAACATTTCTGCTGAATGTGTG
WI-4123	51	T G ---			CAAAGTCAGATTTTGATTATTCAGGATAACAAATTTTGAAAATAGAAAAGTG[T/G]TTAAACTATTT CAAATAACAATAAAGAAAACATGATGAATTTCTCGTTACATAATTGTATAGAATTTAGTGGG TTCTTCCATGACATTTGGCTTGTCTTCTCAACAGTGGTGGTTGGATGTTTCTATGCTTTCTC AGGCACAAACAACAGTGAAGAAACCTTAGCAACATTTCTGCTGAATGTGTG
WI-4149b	145	G C ---			TTGTACATGTTTCATTCATCCCTCCCATCTTTCTGTCTTATAAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAGCTTTCTCAGCATCTTCTATATACT GTGCTGT[G/C]CCTTGTGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAGT AGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4149a	137	T C ---			TTGTACATGTTTCATTCATCCCTCCCATCTTTCTGTCTTATAAAGAACCTCGCTTCTTCTCCAAGT CTTACTTCTCCACCTGAGCCACAGATCTCTTTATTTCCATCAAGCTTTCTCAGCATCTTCTATATACT T/C]GTGCTGTGCCCTTGTGAAGAGCCAGAGCCGAGCATACCAACATGATCTTTTGTGAACTGTAG TAGGAGAGACAAGACAGATGTGCGGGTCCCATGATATAAGGTAATTG
WI-4182	188	G A ---			TACACACTTTTCATTTGGTTTCCATTACTGCAGTTAAAGGACCATCCATTATATTACAATCCCTC AGTTCTATGCTTTAGAGTNCATTATAGGACTACTGTAAATTTAGAGGGAATTACTCCTGGAGTA GGGGAATGAGTTAAATAATCTACCATGCCAAATTCAGGAGGACTGTGGTTAA[G/A]ATGTCCTCTCT TGCCCCCTCCCAAGTTCTTAAATCCTAG

WI-4230	93	T	---			AGAGACGTTGAATGGGACATCTTTCTATTTCGATTTTAGTTAAACAATTTGATAAGAATTGATGAAA GTTTGTACATTCAGATTATCTTTATAGCAGCAGAAGTCTGGCAATAATAACAGCACACTGACT TTTCCATGGTAAAAGAAGTTAGAGAAAACAGCCTATTTTCTTAATGTTAAATGTAATTTCTGAAT ACATTTAAATGGAGGAGAAATGAATAGTGACCTTTGAAAATTTTGAAATTTATGG
WI-4241	118	C	T	---		GAAAATTCATTGAAGTTTTGACCTTGAACTGATCTCATTAATACTTTTNCCTTGTAGTGGTTGATTT CATTTTGCACAACAGAACAGACGAGAAAATTTCCACTTAAATTAATCTCCTAAGTATCTATGAT TTAGCACTGTTAGCACCCAGAAACTGTGAAATTAATCTCCTAGATATCTTCAGAAATCTAGGATGGAAG AA
WI-4271b	151	A	---			CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTNTCTACAGGGAGCCCCCAACCTCCCTTTGTCTCAGG CTCTTAGAAGTCCAGTCAGGGGC
WI-4271	151	A	---			CAGGGCTTTTGGGAAGATCAGTTAAAGCAGANCTGGACCTAAAAGACTAAGCACATTTTCAGCAT CAACAAAAGGTGACATGTTACCCATGAAGGTCCCTGGAGGATTAAAGATCAATAAGAGCCTCAGG GGACTGAATCCAAACGGGGAATATTAGAGTNTCTACAGGGAGCCCCCAACCTCCCTTTGTCTCAGG CTCTTAGAAGTCCAGTCAGGGGC
WI-4389b	156	G	A	---		AATCGAAACATTGATTTTTTTGTAAAGGAACACACATTATTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATTCATAACCTTTTGA AGGTAAGATGTGAACCTATACA[G/A]JTNCGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGTATTGTAGGAACTGGAAGCGGTAA
WI-4389	156	G	A	---		AATCGAAACATTGATTTTTTTGTAAAGGAACACACATTATTATGATATTTGTGCCAGTTTAGCATAT GAAATTTGAAAGGGATGAACCTGGAGGAAGAGAGAAATAGAAAGGATATTATTCATAACCTTTTGA AGGTAAGATGTGAACCTATACA[G/A]JTNCGCAAGGAAGTAGAAATGGAACAGACATGATTGACTTA AGAGTATTGTAGGAACTGGAAGCGGTAA
WI-4488	31	A	G	---		GATGACAATTATTGTGATTGGCATTTTAA[A/G]GTACCATTCATTTCTTCTGGCTTTCGTGTGT TGTTGTTGAGAAAGTCAGGGTTAGTCGTATTGCTCCTTTTCTAGTTCTTCTCAGTAGGAAGACTGATC CTAAACAACCTAATTACCCATGCCAAAGTACGTCCAAACTGATCTTTAAAGAACAATAAATCAAATTG TATTATCCTATGCTTAAATGCTCAG
WI-4491	145	G	C	---		ACCATCAATGTATCACCTTCTAAAATTTATTAGATGATTAACCTGGCTCTGTTAAAAATAAAACCT GTCTTGGACATTGAAAATAAACATTACTATTGGTCATTTTCTGCTACTTACAAAGGTACTGCACCTA AACAGTTAAG[G/C]GTTTTTTGGAGGGGAAAATCATAAAATGCATAAAAATTTCTACCACTGTCA TTTCTTGCCCATAAATAAAATTTTACATGCCT



WI-4584	144	A G ---	---	TTGGTTGGCATTAGCCTCATAACAACCTATTTACAATCATAATGTTACTCTTATTTACAACAAG AAAAATGAGGCTTAACATCACACTTCTGCTTAGTCGAGAGCCCAAGATTTGAACCCAGGAATCCATT CACCGGTACAGJTGCTACCTGGGTAAATAATGTTTAAATTAATCTATGGCATTAGATTTCAAGA GTCCTAATGTGGTTTGAATAATAGGTGCTTTAATTTGTTTATCAGTATGC
WI-4639	185	C T ---	---	TTCTGCATTTGAATGTATGGTCAGACTTCAGAGGAACCCAGGAATCTCATTTATTCAGTACAATA TGGTGGCCAGGTGCTCAGGCCCTATTATCAGAGAGATCTCAGTTTAACTTCCAAATCCACCATTAC TGACCATATGACTTGGGGAACATTATCTCACCTATCTGAGTCTGTATCC[C]TCATCTTTAAATTGTA AATTTAAGGACACCTATCATAGTAATATTGTGAGGATAAATGAAATAA
WI-5327	63	A ---	---	AAATGAATCCGCTTAGAGCAATACCAGTAAGGGCTGGTGCAAGATGGTGGCTGAGAGAA/- JGATTACTCATAAAGCATATTAATTTTATAAATATGGAAATTTAACTAGATAATTAATGTGAAT TGAGTTTGAAGTTGCATGAGAGTAGGGAGGAGGTAGTTTCTACTTATAGGTTTATATAAGTNTGCT TCAATAGAAATGGCTCTTTCGGATGACAATGATGAATGTTCTAAGCAGACAG
WI-5390	87	C T ---	---	GCTTTGAGAAATGAAAGGGAGCCTGGACCATTGCAGGGCTTCTTCATCTCTGATTATTTGTGTAT TTATTGTTCACTTATTTATTC]TGCTGTCTCCCTTCTGGTATGCTTGTGTCATGAACAATGAATTG CCCAGTGCCTGCCGATTCTGGCTCCTAGAGGTGTCCAGAAATAAGTTTCGGTGAATAGAAATTG ACGAATGGGTTCAGAAATTGAACCTGTGATCTATGGAAGACAAACGAAT
WI-5404b	87	G A ---	---	CCTTGCCTGCTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTAATTAAGCAGT GCAACATTAATTTAATTTG/A]AAAGAAACTTGTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTTCCTTCTCAGCAGTTTCCATGTGTCGTGAATCCACCCCATCTCTTTTCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTCAACAA
WI-5404	87	G A ---	---	CCTTGCCTGCTTATGCATAATGAGAATAGAGTTGACTCTCCTGTCAAGAAATCAATTAATTAAGCAGT GCAACATTAATTTAATTTG/A]AAAGAAACTTGTCTGAAACTTTGTACTCTTGTAGTNAATTTG AATCTTTCCTTCTCAGCAGTTTCCATGTGTCGTGAATCCACCCCATCTCTTTTCACCAGTAGCAAGATT GCTACTTATATGGAAGGGTTTAGAGTTTCAACAA
WI-5545b	77	A C ---	---	TAGGAAAGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTCTTCACCAGTCACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTCTGACAGCCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAGANTC GAGATACACCATGAATTTATTTTCATTTC
WI-5545	77	A C ---	---	TAGGAAAGGGATGGTGATGGCCTCTGAGACATTTAAATCTATTCTTCACCAGTCACTGCCGCCA TATCTCCTC[A/C]CCAACACCTCTGTTTCTGACAGCCCAAGTTTCCATCAGTTGATATGGGACTATTT GTTGCAAAACAATTGTTAAAGATTGGCTGACTTTGGCTGAATTTGCTACAACCTCCAAAAGANTC GAGATACACCATGAATTTATTTTCATTTC

WI-5860b	134	A G ---	---	ACTCAAGTTGGGGATAAATCAGAAGTTTCTATGTACAACCTAAATTTTGCTAAGATTTTATTGTTCTTTTTATATAAATTATGGATTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACCTAC[AVGJTTATACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCAATTTCCAAATCATCAACTTCTGTAT
WI-5860	134	A G ---	---	ACTCAAGTTGGGGATAAATCAGAAGTTTCTATGTACAACCTAAATTTTGCTAAGATTTTATTGTTCTTTTTATATAAATTATGGATTGTTTTTACTTCCCTAACCAACCTTCTAACTGAGGAACCTAC[AVGJTTATACTGGAATCATGTGAAGACATTCTAAAGGGTACCCAGGTGCACATAGTTTTAAGGGAATCAATTTCCAAATCATCAACTTCTGTAT
WI-6106	208	C G ---	---	GCAACAACCTATTATACCTGATTCCAACCCAGGTCTACTAACATTATCAACCCCTAACCAACATACATATATTGTCCTGTTCTGAATTAATTTTCAATTAGAACTCTGATGAGATTTAGCATGGGATAAGTGCAGTGCAGAGATAGTAACACTGCTCTTTTGTCTCCAGGAGTCTCAATGTGAAGTATAATTTCTTACAGAGTAATTTCGJATAGTAGTCCACCAAAAGTCTATATTGTATGTGAAGGAAAG
WI-6109d	129	T C ---	---	AAGATAGACAAAGATATGCCAGACCAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTACATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAACCTT[C]AAACCTATATTNCTGT[C]CTTGTGCATACCTTAAATGTATAATGTGGGAGAGAGGAATTTTGATGTGNAAATTATCCCCTGAAAATTTTATACCA
WI-6109c	147	T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTACATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAACCTTAAACCTATATTNCTGT[C]CTTGTGCATACCTTAAATGTATAATGTGGGAGAGAGGAATTTTGATGTGNAAATTATCCCCTGAAAATTTTATACCA
WI-6109b	147	T C ---	---	AAGATAGACAAACATATGCCAGACCAACAAACACAGACCTGTCTATATTTCTGAGAGAAATGTACATTGAGTCTTCTCTCTGGGACTATAAGGAGATCAGGTGGAATAAACGGAAGGAAACCTT[C]AAACCTATATTNCTGT[C]CTTGTGCATACCTTAAATGTATAATGTGGGAGAGAGGAATTTTGATGTGNAAATTATCCCCTGAAAATTTTATACCA
WI-6109a	129	T C ---	---	AATGCCTATCACCTTCCATCATCTGCTGCATAACTGATTGATTCAATGCTTATTGTTAGCACCTGCTTCCAAACACATGCTGTTTTGTTCAATGAT[C]GCATATCCCAAGTGCCTTAGACAATGCCTCCCATACAGTGAACAGTATTTGACTAAACACATACCTTGTTAAATCAATAAAATTAATCAACTTGGCATATGCAGGGAAC
WI-6112	96	T C ---	---	GAAC

WI-6244	103	T C	---	TAATTGCACAACTTACATATCAGGGTTTCTGATTGAAAGGAAGAGAATATTCCTTTCTTTAGTGATT GCTTAATAATTAAATCATAATAAGTGCACCATCTCTTC/CJGCTCCTTATAAATGTGTTTAGAAGAAGG AAATTGAGTGTGGGAATTAAAGCAACAGGAGACATTTTATATACTCCTACAGTGGGGGAAGACTT CCTATTTCTTTCCCAAGGATGATACATTCTAC
WI-6268	124	C T	---	CTGGCCTTATAATCCAAGTTTAGGATTAACTTACCCCAACTTAATAGACTTCCAGACAGTTGCAGTT GTCTACAAGATTTCTCCTAGTAGGGCTTTGGGTGTGGCACCCTTTGGCTCATTCTCTACTCTCCCT GGGTCTTATTGACTTTACGGAGCCTAGAGAGCTGGACAAACCTGCTTCTTTGCAGAAAGAGTCG GGTTCCAAAGATTTCGTTACGATTTTAA
WI-6336b	234	C T	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCCC ATATATTCCCCCTTTACATGTTTCTTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCAGTGCAATTATGTCTTGGTAGAGCC/CJTJGAGGACACTGACAGT
WI-6336	234	C T	---	AGGTGCCATTTAATCCATTCAAATTTGGAAGCTACATCTTCAAGGGTCTGAGAGAGCTCACTCCCCCC ATATATTCCCCCTTTACATGTTTCTTTATAAGACATACAGTTTAAATCAATTAAACAACTAAACAGCTT ATATACTGGCAATATATTACAGATGGTTTATGTCAGAGTAATAGATCACATGAAATGGACCATGTG GTACCCAGTGCAATTATGTCTTGGTAGAGCC/CJTJGAGGACACTGACAGT
WI-6381	92	C A	---	TTGGATACAAAATTTCAGTTACACAATCAGTAGCATTCAAATTAGTTATGAGTATTTATACAATTA CAAAAATGNTTCATGTTTTAACAA/C/AJGTATTTTAAAGCTCAACATTTTAAACAGGCACAAT ATTCTAANGGCATATGCATTCACCATGGCTTTGAATGTCCTCACTCCCAACTTCACAATCAAAATC TACAGANGCGGCAAAAGATCAGAGTTTCAG
WI-6436	198	C G	---	GGTTGAGGCATTGGGAAAGGCAGAAATTGAGGCAGTAGAAATGGACATTTTAGGAAAGAGAAGT TCAGAGGCAAAAGTCATGACAGACAGGAAATACAGGCTTAGGAAGACAGTAGTCTGTGTTGAA ATTTGGTGTCAATAAAGAAGTTTAGACTTTGGTGGTTGTAGTAGTGTAGTAGGAGTAGCGTT/C/ GJATTGGGTGATTCCACAGACAAGGTGATGTTCTAAGATTTGATATTTATTGT
WI-6449	186	C T	---	GAGGCTCTTTGCTTTCCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTTGTTCTGATGGTTGGTGTCTCAGACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTTCTATTCACTGCAATCTCTGATCTTATGTCTGGCTCTATTCTATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCCTCTAAATTTTCTGTTGGTATTATA
WI-6449	186	C T	---	GAGGCTCTTTGCTTTCCCTCAGTCAAGGCTGTATCCAGGGTTGATATCTAGCCTATATGCCATATGT GTATGGCTAGTGTTGTTCTGATGGTTGGTGTCTCAGACTGCCAGATTGTTAAATATTTGAAAATC GTATCTGGTTCTATTCACTGCAATCTCTGATCTTATGTCTGGCTCTATTCTATCCCTATTCTCTGA TCTTATGTCAGACCTGAAGTTCCCTCTAAATTTTCTGTTGGTATTATA



WI-6463	72	T C	---	GCTGGAGAAAGACCTCCAAAGAACTAAATCAGAGTCTCTTGAGCAAGAGGAATTGAAAGAAACA[T/C]TGAAATAAATTAAAGTAGAACTCAAGAGCCAAAGTCCCAATTGTGTCCATTATAAGAAATATTTGAATGGAATCTTAAGAAATGATTTTATTGATCAGTTAAATGTTCTCTCCTCCTCAGTCCCATTATATGACATTCCGATGCTG
WI-6474b	76	C T	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANACAGAGGCAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCCAGAAAGTAAAGTGGATTTTGAAAGGCACAGAGAAAGGGGTGTAAGAGGAGAACTATGTAAAGCAGAGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6474	76	C T	---	AAGCAGTAAATCTTCCATCATGCCATGGATGCCAGTGGTAAATGTTATAGAACTTCAGAGGANACAGAGGCAA[C/T]GTTGGTTATAGCAGTCAACGACATCATCAATGAAGACATGACTTGCTTAGAGCCAGAAAGTAAAGTGGATTTTGAAAGGCACAGAGAAAGGGGTGTAAGAGGAGAACTATGTAAAGCAGAGGTATAGAGGAACATAAGTATAAAGAGTGAGCCATAACTTAGGGTACCATAA
WI-6478b	175	T A	---	GAACTCAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTAAGTGTCTATTTACCTCCCAATAGTGGAGATCAGAGT[A/G]CTCCTTGTGAGTGTGCTACAGAGAAGATATACAGGATGGAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6478	175	T A	---	GAACTCAATTAACTTTGCAACACTGAGAAATCGGATTTGGAGATCTGCAAGCTGAGGTTGAGATTGGACCTTGGTGATCCAAATGGGGAATGCCACGCTTCGAGGCTGTCTATATGCTTTATTTTGTAAGTGTCTATTTACCTCCCAATAGTGGAGATCAGAGT[A/G]CTCCTTGTGAGTGTGCTACAGAGAAGATATACAGGATGGAGGACAGCTCCTCGTAGGACCTAGACACAACCTG
WI-6559	149	G A	---	CACATTTTGAATGCAACTGAGAAANTGGTTTNTAGGCTACCTTTATTTAAGAGTACATCTGGCTCCATGTTACCCCAACATGCAAAACATAAGGCAACAAATCTGATCATTTTATAGGNTCCCAAGCCCAATTAGCAATATCTTA[G/A]TCAAAATTTTAAAGAGAACAGGAAATAAGGAAGGCCTAACAGAGGAGTTAAATAATTGTGCAAACTTATCAGTCTTC
WI-6564b	54	G A	---	TTCTTTATTTGGTCCCTACCAATGTGACTCTTTACCCAGGCCACTGTTCTCTATG[C/G/A]CACTGGCTTTGTAGGCATTCACATCATATGTCTGTGCTGAAATCTCAATTAATTTCTCTCCTNCCTATTCCTTTCCATGCTCTGCCTCATTTNCTCAGAAATTGAAGGCATTTGATTATNATTTTTTTTGGTCTGTGTAAAGGTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAGACCAACA
WI-6564	54	G A	---	TTCTTTATTTGGTCCCTACCAATGTGACTCTTTACCCAGGCCACTGTTCTCTATG[C/G/A]CACTGGCTTTGTAGGCATTCACATCATATGTCTGTGCTGAAATCTCAATTAATTTCTCTCCTNCCTATTCCTTTCCATGCTCTGCCTCATTTNCTCAGAAATTGAAGGCATTTGATTATNATTTTTTTTGGTCTGTGTAAAGGTTCTTGGCAGGAGAACATGCATATGACTTTAAATAAGACCAACA

WI-6608b	46 C	---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGTTC/- JAGTTCAGGCAGCTAAAGGGAGGGGATTTCTCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGTATTTTCTAGAGGAAAGAACTGAACTCCAGCACTAG GTAAACTGCAAAAGAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACACAGAAAGGAA AGC
WI-6608	46 C	---	---	CTAATCAGTAGCACTGAACATGGCTCTAGTGAGTGGGCTCAGTTC/- JAGTTCAGGCAGCTAAAGGGAGGGGATTTCTCTCTAGTCTCTCCCTAGAGCTAAATATGCATCTGG GAAAAATTAGGCTCTGGAGCACAGAGTATTTTCTAGAGGAAAGAACTGAACTCCAGCACTAG GTAAACTGCAAAAGAAACACCTGTGCCCAGGCACTAGCTACAAGGCCACACAGAAAGGAA AGC
WI-6666	68 C	A	---	GTTAGACAGTATCCAGCAAAAGGTTATTTATACCTCTACTTTTCCAAACGAGGAAACCTCCCC A/C/AJAAATCCCATCAACACACAGTCATGCTGGAAGGCATTTCTGCTTACTCTGTTGTTTCATGTAA ATGTTTGGGTGACTCATTCGCCCTCTTCTNTTCTCAAGTTCAGGCTTCTTGGGTAGACCAAACTA ATACACAATGTTAGGCACACAAAGAGA
WI-6670b	120 A	G	---	AGATTAAACATAATTACTGGGGCCATTGTAGGTTNGGAGGAGTGTTTTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAAATGAAC/A/GJTTGTAGCCA GCATTGCCATTAGGGCCGGAGTCAGGTTTGTGGGCCAGAAAGTTTAGACAATTTGGGAATTTCTGA AAAAAAAGAAATACAGAAATTGTAACACAGACACAGAAATCTTAGAAGGGAT
WI-6670	120 A	G	---	AGATTAAACATAATTACTGGGGCCATTGTAGGTTNGGAGGAGTGTTTTTTCTATCTGCAGCCAAA CAGAAATACTGTAGTACAGCAAAACCGTCTCAACAGTAAGCACACAAATGAAC/A/GJTTGTAGCCA GCATTGCCATTAGGGCCGGAGTCAGGTTTGTGGGCCAGAAAGTTTAGACAATTTGGGAATTTCTGA AAAAAAAGAAATACAGAAATTGTAACACAGACACAGAAATCTTAGAAGGGAT
WI-6704c	33 T	C	---	TTTGAAATAAATTCATGCACCAATGTTTTAAC/T/CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGNGCA CTATTGCTCTTTAAATATGGTTGTACATGTCTCATTAATCGATTCTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704b	33 T	C	---	TTTGAAATAAATTCATGCACCAATGTTTTAAC/T/CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGNGCA CTATTGCTCTTTAAATATGGTTGTACATGTCTCATTAATCGATTCTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG
WI-6704	28 T	C	---	TTTGAAATAAATTCATGCACCAATGTTTTAAC/T/CACATATATCATACAGTGCAGGATTTATGA ACATACATAAAATCAAAATCATACCATATAAACGTTTACAAATAAGTTTTTCATGACACACGNGCA CTATTGCTCTTTAAATATGGTTGTACATGTCTCATTAATCGATTCTTCTTCCACATGGTTATTT CAATGCAAGANCCGATCAGCATGAAGAGTCTAGTACAAGATAGGCAGACATG

WI-6710	106	G A ---	---	---	CCATGGACAGTTTAATTAGGAAGCTTCGACTTGTTAGAAATAACAGAGGAAGTCCAGTTATCTACCT ATTCCTTAAACACACATTTTGTGAGGCTGGAATGATTCCTC[G/A]TAGTAAACTCAACATCCACACCT GCATAACATCGCCTCCCAAGTGACTATTATTACTGAGTCGACACAGGATGTCACCAAGTGAGCCTC ATCTCCAGTCCAATGGAGGAGTTGACTTAGACCTTCCTTGGACAGGAAGGGTC
WI-6766b	148	G C ---	---	---	AAACAAATGGTGCAATTGCATAATAATTTGGTGCACAGTATAAAACAATACAAATTAGTTCATATAAC ATTGGATATGGACAAAATAACACANGATCCTTTCTTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGGAGGNGAACTTACCCAATCCCAGTTCCCTTCTC
WI-6766	148	G C ---	---	---	AAACAAATGGTGCAATTGCATAATAATTTGGTGCACAGTATAAAACAATACAAATTAGTTCATATAAC ATTGGATATGGACAAAATAACACANGATCCTTTCTTTGTCTACGGAAATNCTGCAGATCCTTATGT GCCACACTTAAAN[G/C]AAAGTCAACGTTTCTCTCTAGGNTCTGCACACATATTTATCACTGA GAATTTGGTCAACACAGTGGAGGNGAACTTACCCAATCCCAGTTCCCTTCTC
WI-6787b	97	A G ---	---	---	ACAGATAAAGTCTTTATTCCTCTGTATGTTAGATAAGAAAGTTCTTTACAGACTTTTTTTATACA ATACCTTGTCAGCAATGTTCAAAATTCAC[G/A]JTTTTACTGCATAAGATATCTTCATGTACAACTGT ATGCTTTGTCTTCTTGGGAAGGACGCGTTAAAGACCTATGATAAACACACATCCACATGACAAAGGA GAGTGCAATAGGCGAGTAGANTACTCACAGGAAAGAGTAAATTCAGGT
WI-6793	105	C G ---	---	---	GAACCCACAGGTCCTGTTATTTTATTAAAGGAGCATTTACATTATGATAGCAAGTTTCAACACATTCA TCAACAAGGGGTCTTCAAAATCAATCAGTCAACCC[C/G]GAGTTAGAAAGTAGAGTCATGAGGAA GAGCTGCTTGGCTGTAGGAAGTAGGTTAATGCCCTCTAATCCCGAAAGGGCAGACTGAAGCCA GAGCCAGANTCCTGGCAATTCACCGATTTCTCATCACAGGTAAAAGGCAAC
WI-6810b	37	T C ---	---	---	CACAATAATAAATCACTCCCTACCTTGAAACTTTAT/CJAGAAGCATTTTTAATTTTACAACACA AAGCTCAACACGNACCTACAATAAGTCTAGTCTGTTACGNGCCAAGGGATAAGGCTGAACAATA AATTAACCCCTTTAAATGTCTATGNACAAGTACAATTTCTTTTGGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6810	37	T C ---	---	---	CACAATAATAAATCACTCCCTACCTTGAAACTTTAT/CJAGAAGCATTTTTAATTTTACAACACA AAGCTCAACACGNACCTACAATAAGTCTAGTCTGTTACGNGCCAAGGGATAAGGCTGAACAATA AATTAACCCCTTTAAATGTCTATGNACAAGTACAATTTCTTTTGGAGTTCTGCAGAGCAATGACC ACTAAGNAATATTTTTAAAGGCTGAACAGAAATCCAGCGGCAATGAAGTTAAT
WI-6817b	145	C A ---	---	---	GCATGATTAACCCAGTGCAGAAAAATACCAAGTACATGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTGTAAATCCAGTTAAGACCATCAGCATATACACATCATCACTAACTCAACAATGTAGCT GCAGGGTAAC[C/A]JTGTGGATACCCCTGTGTGCTCTACTINGCCTCCAAAGGCATTCAGGGGATCATCA AAGATGTTGGACACACCTTGTTTCAATCTTGGTTACGGTGGGCTGTGTCAG



WI-6817	145 C A ---	---	---	GCATGATTAAACCAGTGCAGAAAAATACCAAGTACATTGGGTGAACGATGAGCTAGCTGTTCTAGTA TTTGCTTTTTGTATCCAGTTAAGACCATCAGCATATACAAACATCATCACTAACTCAACAATGTAGCT GCAGGTAAC[C/A]GTGGATACCCGTGTGCTCTACTNGCCTCCAAAGGCATTTCAGGGGATCATCA AAGATGTTGGACACCTTGTGTTCAATCTTGTTTCAGGTGCGGCTGTGCAG
WI-6819b	221 C ---	---	---	GATGAAAGCCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTAC CATCATGTACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTTTCATATACAAAATTTTCTGCTATTTTG CTTAGCAACAGCAATAACTTTTGTTTCTCTATATGACACCTAATATCCAG
WI-6819a	175 G T ---	---	---	GATGAAAGCCATTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTAC CATCATGTACCCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCC CGTCAGTAGTACACATTTCTCTATGGTCTTCAACAGTTT[G/T]CATATACAAAATTTTCTGCTATT TTGCTTTAGCAACAGCAATAACTTTTGTTTCTCTATATGACACCTAATAT
WI-6826b	154 A G ---	---	---	GCAAAAGCTTTATTGGCTCCAACAAATTAATCCCTTTTAAACTCCTCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCAATTTTCCCTAAGAACCATATAAATAC ATGCAAAACCTTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGTGCACTGT TAAGCTGAATTGCAAAATTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6826	154 A G ---	---	---	GCAAAAGCTTTATTGGCTCCAACAAATTAATCCCTTTTAAACTCCTCTCTCTCTCTGCTCAGTG GAACAACACATTTGAATTCAGATTTGCAGTTTATAGCAATTTTCCCTAAGAACCATATAAATAC ATGCAAAACCTTTGTACAT[A/G]GAGCTTAAATAATATCAAAATGCAAAATATAGATTGGTGCACTGT TAAGCTGAATTGCAAAATTATGGCAACACACACTGGACTGGGTATACGTTG
WI-6857a	122 T C ---	---	---	AGTGCAAACTATTTGAACAAAAGTAACTATGAGTCACAGCATTCAGCAAGACATCAGACACGGA AGAGTGAACAATATTCACTAAGTAAATACAGCAGATGAGATGTCTCTCACATGTAT[C]ATTTAAT TATTCATGCTTTTCAATAGTCTCTTAGTCAACTTTTCAGTGTAAATTTCCACAAATATATAGCAGCTCA AACACAAATGCAGGAGCACAAATGGCAAAGTTTGGCAACTGTTTGGGCTAAT
WI-6865	153 G A ---	---	---	TTATAGAATACTTATGGGGCATACNGTAAATGAAGTCAACCTTAAATCTAAACAAACAGCTTG TTTGTTGTTCTGCTGAAATCCTCCCTGCTCACAAACAGCCAGCTACTNGGTTTCTAAAGACGTA ATTTGCAGGCAACTTC[G/A]TAGAGCCATTCTGTGCAGAAAGGGAAGGAGAGCTGTTTGT TTACCTGTAGTATGAAGATATTCTTTGCGCTGTAGAACTGAGCTCATTAA
WI-6909	73 C T ---	---	---	ATTGAAAACTGGTTAGCAACAGATAAATTACATAGAGCTGGATATAAAATGAGAGAAGAATGC AGACTTA[C/T]AAGCTTATAGAGAAAGTCAAAAGGAGCAAGTTT[TG]AAATCAGATTTTATGATAC GGAAAAAAATTTCCCTTTTGGCCAACAGGATTATTTCGAATAATAATCTGCCAGTGCCCAATCAG AAACACCATTTCCACAATAATTTGTCATGCCCTAGTTGCCCTATTTTATACATATC

WI-6910b	163	G T ---	---	CACTCAAAACCTTTATTGATTGATTACAAACTGTACAATAATTACAAAGTTTAGGCATTATCCCA TATTGACATGAATGCTGTGGAGAGTCTAAAATAAATATGTGGCACATAGCTTAATATACACATCAT GGCTCTTTACACTTAAGCCATTACCAATAAGTTGAGATGTATGGAGAAATTTAATGTGTAGAAAA GTCAGAGTGGCTGACCCAGTCCCGACCTTCCATGTGAATGACTCTTCCCTTGGC
WI-6915	144	A ---	---	GCTTGTTTTTTTGTGTTTTTAAAGTGACACCTTGGCCTTGTGGCATTCTTCTTCACTTATCTTACCC AAAGTGCCCTTGGGCCAGCCACTGACTGATTTAAACCCAGAAATGTGGTTTTAAACAATGTGGT CGTGGTGAATTCAGGTGATTTTNAATTTCTATTGGTAGTATTTTTCAGATTTCACAAAGAACATG TATTGCTTTGTAAATTTGAAAAAATAACAACACAGGATAGTAAAGATAT
WI-6928b	175	T C ---	---	CAATCAAAAGTTCCAAAGTTTCAAAGCTGGGATGAAAGCCAGGTCTTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGGTGAGCTAAAGGTTTCTAATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6928	175	T C ---	---	CAATCAAAAGTTCCAAAGTTTCAAAGCTGGGATGAAAGCCAGGTCTTCTGACTTGCACCTGTGCAC ACTGGATTTTNCCTCTGATCCAGCTGCAGCTCCCATAGAAAGTTCACTCTTAATTTTCATGTCCCATG CTTTGCTTGGTCCCTGTGAGGAAAGGGGTGAGCTAAAGGTTTCTAATAAGGATGGGTAGG TATCCTGGCAAGATATTTCTCTGAAATAGTAAACGTGACCTTAGAAGTTA
WI-6955b	79	G A ---	---	TTTTATGAAACATTTGAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAATTCCTAGGTAGTAAAGTATCAAGTTACAAANTAC AAGTGCCGNTAATTAACCTATAGGTAGTATATAAANCAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAGC
WI-6955	79	G A ---	---	TTTTATGAAACATTTGAGATTCCTCATATCACAGCACATCAATAAGCAGTATGTACATAGACTGA CTTTTATAGTAC[G/A]NGTCATGTCCCAATTCCTAGGTAGTAAAGTATCAAGTTACAAANTAC AAGTGCCGNTAATTAACCTATAGGTAGTATATAAANCAAAATGNGTTTTTNGCAATTATGTGAAAT AAGGCTTTAACCAAGC
WI-6957	47	C G ---	---	AACTAAAACCCCTTATTGTCTCCAAGTGTGGCAAAATAGAAAATC[G]TTTCAATTACATTAGG AAATCGGGTGGATAACGGAGTATAGTTATTCCTCACTTAAGAAAGCATTCAGTCAATAATCACAAAA ACAAATTCAGATTGCTTGGATCTTGGTCAATTTATGGCTTGAAGAACTGGATTGAAAACCACTTTAGG CTAAATAAATGTATATGAATAATGCATAGACTGTGTATCTAGAAAATCATGC
WI-6996c	242	G T ---	---	ACTTCTAGTGCCTCTGTTACCAACCTCTAATGCCTCTGGTGGCCGCACTTCTGATGTCCGTAGGCCT TAAATCTGCCCTGGCTCCCTCCCTCTGTCTTCAGCAACCCAGAGGAGAGAGAGCCGGCAGTTCCCTG CAGGAGAGAGGGGCTGTGGACCCCAAGGCTCAGTCCCTCTGCTCTCAGGAACCCCTGTCTGACT CTCTCCTGATGTGGGCCCTCTGTGCTCTCTCTTCC[G/T]GTCCGGATC

[illegible]



WI-7136	58	T C	---	---	TGTGAAGCCACATTTCCAAACATGAGCCTCATGAAGCCAACTAAGTGTATTGAACTGT/CJAAATTC TCTCAATAACTCAGTGTAGCACTTTAAAGTCTGAAGGACAGCAACATGAAGAGCATATCAATGTG GTGGAGAAAGGAAGGGTTGGCTTTTAAATTTATTTCTTCATCTTTTATAACAAGAAAGNNNNN NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTAGCTTTCTATATATG
WI-7146c	210	A G	---	---	GGGACGCCCTGTTGTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTTCCATTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTGTTGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGATGCC AACGC/A/GJTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146b	210	A G	---	---	GGGACGCCCTGTTGTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTTCCATTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTGTTGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGATGCC AACGC/A/GJTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7146	202	G A	---	---	GGGACGCCCTGTTGTTGGCTCAATTTGGGTTTGTGGTCACATGGAGCTCTTCCATTCGTTTAGCTG AATAATGAGTTGTTCTAGAGGAGACAGCCTGTCTCTCTGTTGCCCCAAAGCCCATGCCCTGCCG TGGTGGCAGCTGGGCTGTGGATGGAGGGGTCCCAACATGGATGTGTGGCCCTCTCTCCGATG/A JCCAACGCAGTTTCATGTACAAGGCCCTCTGCAACTGGAGAGAAATTA
WI-7153	161	A T	---	---	ATATTACAACTTGCTTTTAGCTGATCTTCCATCTCCTCAATGACTCTTTTCTTTATATGTTAAACATA TATAAATGGCAACTGATAGTCAATTTTGATTTTATTTCAGGAACATCTGAAATCTGCTCAGAGCCT ATGTGCATAGATGAACNNNNNNN[A/T]AAAAAAGTTATTTAACAGTAATCTATTTACTAATTAT AGTACCTATCTTTAAAGTATAGTACATTTTACATATGTAAATGGTATGTTT
WI-7155	156	T G	---	---	TAGAATAGATGCGGTCAATTTCTTCTTGGCTCTGGTCTTCCAGCCCTCATGGTTGGCATCACATAT GCCTGCATGCCATTAAACACCAGCTGGCCCTACCCCTATATATGATCTGTGTCTTAAATTAATACAC CAGTGGTCTCTCTCCCTGT/GJTAAGACTAATGCTCAGATGCTGTTCAGGATATTTATATTCTAG TCTCACTCTCTGTCCACCCCTCTCTCTCCCAATCCCACTCCAG
WI-7169b	161	A G	---	---	AGCTCCACCAGATGCAGATTTGTGTTTGTGTTTCTGTTATCACTGTCACACAGCTTATAACATGTAT GCTTTTCAGAAATACAGTTGTCTAGCCAAGCCATCAAGTGTCTGAAATTCATATTTGGTTTATGCAAA ACAGCAAACTTTTATTTAAGTAGATTA/GJGGAGAAATATGTTTAAATATTAGGAATCCTAGACCATA TTTTCAAGTCATCTTAGCAGCTAGGATCTCAATGGAAGTGTATATATA
WI-7175b	194	C T	---	---	CTCCTAGACTAGTCTTTACCTTTATTAATGAACGTGTGACAGGAAGCCCAAGGCAGTGTCTCACCA ATAACTTCAGAGAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAAATCACTATAAACCATC AGTTACTGGTTTCAGTTGACAAAATATATAATGGTTTACTGCTGTCAATTTGTCCTATGCCTA/C/TJAGAT AATTTATTTGTATTTTGAATAAAAAACATTTGTACATTCCTGATACTGGG

WI-7175	194 C T ---			CTCCTAGACTAGTGCTTTACCTTTTATTAACTGTGACAGGAAGCCCAAGGCAGTGTTCCTCACCA ATACTTCAGAGAAGTCAGTTGGAGAAATGAAGAAAGGCTGGCTGAATAATCACTATAACCATC AGTTACTGGTTTCAGTTGACAAATATATATGTTTACTGCTGTCAATTGTCCTATGCCTA[CT]TAGAT AATTTATTTTGTATTTTGAATAAAACAATTGTACATTCCTGATACTGGG
WI-7178b	273 G A ---			TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGCTCACTGGCTGGCTCTAGGGGAACAGACAGCCAGTGACCCAGAAAGCATAACACCA ATCCCAGGGCTGGCTCTGCACCTAAGAGAAATTCACCTAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCTCAAGCCAGTGAAATGTGAAGGAA
WI-7178	273 G A ---			TGTATCAGGTCAGGGACTTGGACAGGAGTCAGTGTCTGGCTTTTCTCTGAGCCAGCTGCCTGGAG AGGGTCTCGCTGCTCACTGGCTGGCTCTAGGGGAACAGACAGCCAGTGACCCAGAAAGCATAACACCA ATCCCAGGGCTGGCTCTGCACCTAAGAGAAATTCACCTAATGAATCTCGTTCCCAAGAACTACCC CCTTTTCAGCTGAGCCCTGGGACTGTTCCTCAAGCCAGTGAAATGTGAAGGAA
WI-7182b	116 A C ---			GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACCAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCTCTGCAACCCACTCTGAGCCTA[CT]CTCTCTCTCTATTT TACTTGAGGCTGCCAATTACAGCCCCAGGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCTGAAGCCTAGTACCCCAATT
WI-7182	106 C A ---			GCATATTTGGCAGCTTATTGCTTCGAAACCCAGCTGGTCAACCAAGCTTGATATACAGAGAAGAAG AAGGCTCAAGAAATTTATTCACAGTTCTCTGCAACCCACTCTGAGCCTA[CT]CTCTCTCTCTATTT TACTTGAGGCTGCCAATTACAGCCCCAGGTTTCAGCTCAAGAGATGCCTTAAGATAATTATGTGAGG CCACTTGGTAGCAAGAATGGCAGCTATTTCCTGAAGCCTAGTACCCCAATT
WI-7191b	273 T A ---			ATAATTGCTTGTTCAGCCTGGCAAGATATTTTCATAAAGAGGGATAACAATGCTGATTACTAC CTTTTAAATATTTAGATAAATGCACAGCACACAGCACCATCTAAGCATTAGTGATGGGTAGC TGATGTCAGCTTCATGTGGATTTAAGCACTCTAGAAACAATGAAGCTTCTTGGCATAATTTAAGGAG CTCCCAAATGTGTACCTATTAAATTGTAACCTCAGCAAGTAGAAGACCAATT
WI-7199c	112 T C ---			CCCAGTGTGAACAGAACCTCCCAAATTTGAGTTGCACCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTGCTTGACCTATGAGCTTCJGGGGCCTGACTAGGAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTTGTTTGGTGTCTCTGAATTTCTTCTTATTAT AGTCCCTATAGTTTACTCCTCAGTTCCTCACCATCATCATCTTGCTAA
WI-7199b	112 T C ---			CCCAGTGTGAACAGAACCTCCCAAATTTGAGTTGCACCTTCCCTGTGGCCTTATGAGCTCAGCCTC GCTTTGAGGTACCCACCGTCTGTGAGCTGCTTGACCTATGAGCTTCJGGGGCCTGACTAGGAAAGT TGGGAGTTAAGGAGGAAATTAGCATTCCTTAATGTTTTGTTTGGTGTCTCTGAATTTCTTCTTATTAT AGTCCCTATAGTTTACTCCTCAGTTCCTCACCATCATCATCTTGCTAA

[illegible]



WI-7233b	213	C T ---	---	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCCGGTCTTGTGTACATTCATTTCATTGTTACA GATGTGAACCTTTATTCCTTGTCACATAATTATAATTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTCTTCTTCCACCTTTTGTGGCAATATTAAGTGAAGTGAAGTGAAGTGA GTGTAAGTATCTGTGCACAAACCACTGCCAGATAACAGAGGGGCTG
WI-7233	211	T C ---	---	CGATCGTACTGCCAGTAGCATTGTCTGTCTGTCCGGTCTTGTGTACATTCATTTCATTGTTACA GATGTGAACCTTTATTCCTTGTCACATAATTATAATTAAATTAATTTCTAGGAAGTCAAAAAATATAA TAAAGGTTGAGCCCTCTACTTCTTCTTCCACCTTTTGTGGCAATATTAAGTGAAGTGAAGTGAAGTGA GTGTAAGT/CJACGTGCACAAACCACTGCCAGATAACAGAGGGGCTG
WI-7238	128	T C ---	---	GCGTCTACAGACAGCTCACCAATTTTGTCTGTATCTGTAAACACTTTTGTCTTAGTCTTTTCTTG TAAATTGATGTTCTTTAAATCGTTAATGTATAACAGGGCTTATGTTTCAGTTTGTCTT/CJCCGTT CTGTTTTAACAGAAATAAAGGAGTGTAAAGTCTCTTTCTCATTTTCAAGTTGCTACCAGTGTAT GCAGTAATTAGAACAAAGAAACATTTCAGTAGAACATTTATTGCCTA
WI-7252f	520	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGCTGGAGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGACGCCCTAGAGCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCCA
WI-7252e	552	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGCTGGAGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGACGCCCTAGAGCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCCA
WI-7252d	540	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGCTGGAGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGACGCCCTAGAGCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCCA
WI-7252c	552	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGCTGGAGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGACGCCCTAGAGCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCCA
WI-7252b	540	T C ---	---	CCACAGGATCCAGCCCAAGCGGCCCTCCGCCCCCTCCACTCGCAGCAGACGCCGGGACAGAG GCCTGCCCCGGCGCCAGCCCCGGCCCTGGCTGGAGCTGCCCCGGCCCCCTGGTCTCTGGTCCG GACACTCCTAGAGAACGACGCCCTAGAGCTGCTGGAGCGTTTCTAGCAAGTGAGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCCA

WI-7252a	520	T C ---	---	CCACCAGATCCAGCCCAAGCGGCCCTCCCGCCCTTCCACTCGCAGCAGCGCGGGACAGAG GCCTGCCGGCGCGCCAGCCCGCCCTGGCTGGAGGCTGCCCGCCCTGGCTCTCTGTTCCG GACACTCTAGAGAACGCGAGCCCTAGAGCCCTGCGCTGGAGCGTTTCTAGCAAGTGAGAGATGGGAG CTCCTCTCCTGGAGGATGCAGGTGGAACCTCAGTCATTAGACTCCTCTCTCCA
WI-7265m	252	T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTCACCCATTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTGTTTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGTCCTTT/
WI-7265i	231	T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTCACCCATTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTGTTTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGTCCT
WI-7265k	121	T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTCACCCATTCTGTGTTTCATTGTAGTA GTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGTCCT
WI-7265j	174	T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTCACCCATTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGTCCT
WI-7265i	227	T C ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTCACCCATTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTGTTTATATTATGTAATAATAACGATCTCTT AAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGTCCT
WI-7265h	80	T A ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTCACCCATTCTGTGTTTCATTGTAGTA GTTAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGTCCT
WI-7265g	170	T G ---	---	AACTTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAAAAGGCATGCTATGTGTACGTGTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTCACCCATTCTGTGTTTCATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTGTTTATATTATGTAATAATAACGATCT CTTAAAAATACCACAGTTTGATTTTCTTTAAGGAGTAAAGATTGTCCT



WI-7265f	231	T A ---	---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTTCTGTGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAACGATCTCTT AAAAATACCACAGTTTGTA TTTTCTTTT/AAGGAGTAAGATTGCGCT
WI-7265e	227	T C ---	---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTTCTGTGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAACGATCTCTT AAAAATACCACAGTTTGTA TTTTCTTTT/CCTTAAGGAGTAAGATTGCGCT
WI-7265d	174	T A ---	---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTTCTGTGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAACGATCT CTTAAATAACACAGTTTGTA TTTTCTTTTAAAGGAGTAAGATTGCGCT
WI-7265c	170	T G ---	---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTTCTGTGTTCAATTGTAGTT TAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAACGATCT CTTAAATAACACAGTTTGTA TTTTCTTTTAAAGGAGTAAGATTGCGCT
WI-7265b	121	T G ---	---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTTCTGTGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAACGATCT CTTAAATAACACAGTTTGTA TTTTCTTTTAAAGGAGTAAGATTGCGCT
WI-7265a	80	T A ---	---	---	AAC TTGGTTATGTCAGTTCCTGTGTGTAGACAGTAAGGAAAGGCATGCTATGTGTACGTGTTT TTCCAGTATGTTTATTTGCCACCAAAAGTAATGCATTTTACCCCATTTCTGTGTTCAATTGTAGTT GTTTAAAGGAAACCAAGCATATAGATGCATTAGTGATTTTGTATATATGTAATAACGATCT CTTAAATAACACAGTTTGTA TTTTCTTTTAAAGGAGTAAGATTGCGCT
WI-7281b	183	C ---	---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTCTGGCAAAACGGAGTCCGAGGCCGCGAG GTGTTGTGAAGACCACCTGTTCTGTGGTTGGGTCTCTGCAAGAAGGCTCTC
WI-7281	171	C A ---	---	---	GATCACCCAGCCACAAGCCCTTCGAGGGCCCTATACCATGGCCACCTTGGAGCAGAGAGCCAAAGC ATCTTCCCTGGGAAGTCTTTCTGGCCAAAGTCTGGCCAGCCTGGCCCTGCAGGTCTCCCATGAAGGCCA CCCATGGTCTGATGGGCATGAAGCATCTCAGACTCTCTGCAAAACGGAGTCCGAGGCCGCGAG CAGGTGTTGTGAAGACCACCTGTTCTGTGGTTGGGTCTCTGCAAGAAGGCTCT



WI-7282b	159	G C ---	---	TGTCACCTGGCACATTCAATTTCTCAGTTGAAGAAGAGAAATTTGAAAATGTCCTTATGCTTTTAGA GTTGCAACTTAAGTATATTGGTAGGGTGAAGTGTTCCTCACTCAAAATATGTCAACTTNNNNNNNT AGGCCCTTTTCATAAAACCAAACTG/CJTAGCAAGATGCAATGCATGGCAATCTGTGCGTCTCCA GTTGGTTATCTGAATAGTGTACCAATTCACCAAGACAGTGTGAGATTGG
WI-7292	92	T C ---	---	CTTGATTACTTCCACTGAGGTGGAGCATCTCCAGTGTCCCAATTATATCTCCCCACTCCACTAC TCTCTTCCCTCCACTTCAATTTTCCTTCCTCTCTCTAATTCAGTGTTTGGAGGCTGACTTG GGGACAAACGTATTATTGATATTATGCTGTTTCTCTTCCCAATAGAAGATAAGTCAATGGAGCC TGAAGGGTGCCTAGTTGACTTACTGACAAAGGCTCTAGTTGGGCTGA
WI-7301f	133	A G ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTG A/G]CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCA ATCAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301e	94	T G ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTG/GTGGAGGATATGATGGTTACAATGAAGGAGGAAATTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301d	138	A G ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGT/A/G]GTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301c	211	A C ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTATGGAC/A/C]CATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301b	182	C T ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGATATGGTGGCGGTGTGGAGGATATGATGGTTACAATGAAGGAGGAAATTTTGA CGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG
WI-7301	88	G T ---	---	AACTATGGCAGTGGTCTGGTTATAGTAGAGGCGGGTATGGTGGTGGACCAGGATATGGAA ACCAAGGTGGTGATATGGTGGTGGGAGGATATGATGGTTACAATGAAGGAGGAAATTTT TGACGGTAGTAACATATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAA TCAAATTATGGACACATGAAGGGGGCAGTTTGGTGGAAAGCTCGGGCAG

WI-7301	205 A C ---			AACTATGGCAGTGGTCTGTTATAGTAGAGGGGGTATGGTGGTGGACCGAGGATATGGAA ACCAAGGTGGTGGATATGGTGGGGTGGTGGAGGATATGATGTTACAAATGAAGGAGGAAATTTTGA CGGTAGTAAGTATGGTGGTGGGAACTATAATGATTTTGGAAATTACAGTGGACAACAGCAATCA AATTACJGGACACATGAAGGGGCAGTTTGGTGAAGAAAGCTCGGGCAG
WI-7314c	49 G A ---			CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA(G/A)TTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCCTTTTCAGCAGTGTAAATAAGTCAATTAATAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTTATTAAACAAACTTGTTTTT
WI-7314b	49 G A ---			CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAAATTTGGGAGGTCA(G/A)TTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCCTTTTCAGCAGTGTAAATAAGTCAATTAATAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTTATTAAACAAACTTGTTTTT
WI-7314	36 A G ---			CTCTCCTTTTCTTCAGATCTGCTCCTGGGTTTAA/GTTTGGGAGGTGAGTGTGTTCTACCTCACTG AGAGGGAACAGAGGATATTGCTTCCTTTTCAGCAGTGTAAATAAGTCAATTAATAACTTCCCAGG ATTCTTTGGACCCAGGAACAGCCATGTGGTCTTTCTGTGCACTATGAACGCTTCTTTCCCAGGA CAGAAATGTGTAGTCTACCTTTATTTTTATTAAACAAACTTGTTTTT
WI-7321b	199 C T ---			ACTCAGGGAAGGATGCCCATTAAGTGACAAAGGTGGGTGGGACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGAGTGTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGTGGCACACCCATC[C /T]GTTGCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7321	199 C T ---			ACTCAGGGAAGGATGCCCATTAAGTGACAAAGGTGGGTGGGACCATGGCATGAGGAAG AAACAAGGTCCCTGAGCAGGCACAAAGTCTGACAGTCAAGGAGTGTGGCATCCAGGGCTCCA GTCACCTCACTGCCATACATTAGAAATGAGACAATCAAGNNNNNNNAGGTGGCACACCCATC[C /T]GTTGCTGGGTGTGGCAGCCACATCCAAAGACTGGAGCAGCAGGCTGGCCA
WI-7336b	248 A C ---			AGACATTCTCGCTTCCCTGAAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCCCTGGC TCCAGTGAAACTTGGGCACATGCTCAGGCTACTATAGGTCCAGAGTCTTATGTTAAGCCCTGGCAG GCAGGTGTTTATTAAATTCTGAATTTTGGGATTTTCAAAAGATAATATTTACATACACTGTATGT TATAGAACTTCATGGATCAGATCTGGGCAGCAACCTATAAATCA[AC]CA
WI-7338c	221 A G ---			CTCTTCTCAGCACATTGATGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAATATTGGCAAAGGTGCTTTACCTTGAGC CATTATTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAAGACTATCTGCAGCTA GTGTGTTTCTTCTTACACAC[AG]TATACACACAGACATCAGAAATTCGT

WI-7338b	125	A C ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACJCCTTG AGCCATTATTGTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAGACTATCTGCAG CTAGTGTGTTTCTTTACACACATATACACACAGACATCAGAAATTCTGTT
WI-7338	125	A C ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACJCCTTG AGCCATTATTGTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAGACTATCTGCAG CTAGTGTGTTTCTTTACACACATATACACACAGACATCAGAAATTCTGTT
WI-7338	221	A G ---	---	CTCTTTCTCAGCACATTGATGGGCAACTAGAAATTACAGCAGTTTCAAACTCTACCATGGATAATGCA AACAAACCGAAGCTACATGCCAATGATAGGTGCAAGAAATATTGGCAAAAGGTGCTTTACJCCTTG CATTATTGTGTGTCAGAGAACAAAGAAACAGAAATCAATATATAAATTCAAGACTATCTGCAGCTA GTGTGTTTCTTTACACACAGGTTATACACACAGACATCAGAAATTCTGTT
WI-7384c	146	T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAATTTTAAATAATAATAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATAGATTGTATTTCATTGTGAACAGGATTTCTTCA CAGATCTCATTTT/AJAAATTTCTTAATGATTATTTTATTACTTACTGTTGTTAAAGGGATGTTA TTTTAAAGCATATACCATAACACTTAAGAAATTTGAGCAGAAATTTAAAGAA
WI-7384b	146	T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAATTTTAAATAATAATAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATAGATTGTATTTCATTGTGAACAGGATTTCTTCA CAGATCTCATTTT/AJAAATTTCTTAATGATTATTTTATTACTTACTGTTGTTAAAGGGATGTTA TTTTAAAGCATATACCATAACACTTAAGAAATTTGAGCAGAAATTTAAAGAA
WI-7384	145	T A ---	---	CCTATGTCAATGAAATGCTAGGGGCCAGGGAACAAATTTTAAATAATAATAAATTCACCATAG CAATACAGAAATAACTTTAAATACCATTAATAGATTGTATTTCATTGTGAACAGGATTTCTTCA CAGATCTCATTTT/AJAAATTTCTTAATGATTATTTTATTACTTACTGTTGTTAAAGGGATGTTA TTTTAAAGCATATACCATAACACTTAAGAAATTTGAGCAGAAATTTAAAGAA
WI-7388c	106	A T ---	---	TGAAATCCTGGTCTCTTGGCCTGCTGTAGCTGGTTATTTTACTTTGCCCCCTCCACTTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACTTATTAAGGTTTTTGAATTCAGATTTAA ACCAACTTATAAGCATTGCAACAAGGTTACCTCTATTTTGGCACAAGCGTCTCGGGATTGTGTTGA CTTGTGCTGTCCAGAACTTTTCCCCCAAGATGTGTATAGTTATTGG
WI-7388b	106	A T ---	---	TGAAATCCTGGTCTCTTGGCCTGCTGTAGCTGGTTATTTTACTTTGCCCCCTCCACTTTTT TGAGATCCATCCTTTATCAAGAAAGTCTGAAGCGACTTATTAAGGTTTTTGAATTCAGATTTAA ACCAACTTATAAGCATTGCAACAAGGTTACCTCTATTTTGGCACAAGCGTCTCGGGATTGTGTTGA CTTGTGCTGTCCAGAACTTTTCCCCCAAGATGTGTATAGTTATTGG



WI-7388	94	T A ---	---	TGAAATCCTGGGTCTCTTGGCCTGTCTGTAGCTGGTTATTTTACTTTGCCCCCTCCCACTTTT TGAGATCCATCCTTTATCAAGAAAGT/AJCTGAAGCGACTATAAAGGTTTTTGAATTCAGATTTAA ACCAACTTATAAGCATTGCAACAAGGTTACCTCTATTTTGGCCACAAGCGTCTCGGATTGTGTTGA CTTGTCTGTCTCCAAGAACTTTTCCCCCAAGATGTGTATAGTTATTGG
WI-7438	64	A G ---	---	TTAGATTTTAATTGGCAACCAGCAACTCACTGCCACCATTCCACTGCAGATCTNCTATTCCTGG[AG] GTTGATATGACAAGGAACCTATTGGAAACCAAGTCTTCAGATTGTNCCATGTGCAGACAGGCTCCT TGCTGTAGGTGTAGTAGCATGTACACTGTACTGTCTCACTGTAAACATAGTTTGTNCTGGTATTGTTA TTGGAATGAATATCGCTTCCACTGACTTTTACCA
WI-7454b	152	T C ---	---	CCATGATCCCCTCCTTGGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCTGATAGCAGTGTCTGAATTTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTGTTTAAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAATGTTTTTGACA
WI-7454	152	T C ---	---	CCATGATCCCCTCCTTGGCCAAATGGAGGAAGCCTGTGGATGGTACCAACAACAAGCCCCAAACC CAGTACAAACTGAGAAATGAGAGAACCTGATAGCAGTGTCTGAATTTGCCAGGAGCCTCCAAGGCTAA TCCTACCCCTGGATTCTT/CJTGTGTTTAAAGTTATTTCTAGCCACCACAAGAGGGTACTGCCCAA CAGACTCATCCTTAAAAAATCCCATTTGTCTACTTCTCAATGTTTTTGACA
WI-7464c	177	G C ---	---	AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACATGCACTAAATTACTATTATAATTTCTATGTA CAACAGAGCCACAGCACAAAGAGGGTGGGCATAAGCAGTTGCCA[G/C]CCAGAAGAGCTTTCAGTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGGAAGCAAGTTTACCAACAATTAT
WI-7464b	168	C A ---	---	AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACATGCACTAAATTACTATTATAATTTCTATGTA CAACAGAGCCACAGCACAAAGAGGGTGGGCATAAG[C/A]AGTTGCCAGCAGAGAGCTTTCAGTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGGAAGCAAGTTTACCAACAATTAT
WI-7464a	103	C A ---	---	AATTTGAAATCTGAAAAAAGTGCATAAGCAGAGAAATGACACTTATTCCAAATAAATAATTGT CCATTTTTCAGTCAGTCCATCTTAACCATGTACATG[C/A]ACTAAATTACTATTATAATTTCTAT GTACACAGAGCCACAGCACAAAGAGGGTGGGCATAAGCAGTTGCCAGCAGAGAGCTTTCAGTCAT GAAAGAAAGCCCTACAAATAGGCCCCAGGAGGAAGCAAGTTTACCAACAATTAT
WI-7499b	134	T G ---	---	CAATTCCTCAATCCAACCTAGTCTGTGTTGCCCTAAACCATTCAGAGCAAACTTCCACTTCGAAGTTT AATGCATAAGTCAGATAGCAATCCTTCAGTTGCCCCAGAGGCACATCAGTTCTTTGATGCTTCAT /GJTATAGTCCCTTTCATTTAGCAATCAGTGAGGCAATACACTGGCATCATGCCCTTTTITTAGGA ACTCTGTACAAATTCCTTTGAAAATATAAATTTTGGAAATGAGTGATGA

WI-7499a	33 A G ---			CAATTCTCAATCCACCTAGTCTGTGCTTAAGJCCATTCCAGACAACTTCCACTTCGAAGGTT TTAAATGCATAAGTCAGATAGCAATCCTTCAAGTTGCCAGAGGCACATCAGTTCTTTGAATGCTTC ATTATAGTCTCTTCAATTAAGCAATCAGTGAGGCAATACACTGGCATCATGATCCCTTTTITAGGAA CTCTGTACAAATTCCTTTGAAATATAAATTTTGGAATGAGTGATGA
WI-7506b	118 A C ---			TGGGAATAGTAAGAGAAAGATGGGAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGTAGTCTGGTGTGCTGATTGCCCTAGCAGCAGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAATATTTAAATATTGGACCACTCTTGTCTACCATCCCTACCCACT
WI-7506	118 A C ---			TGGGAATAGTAAGAGAAAGATGGGAAGGTGACCAAAACAATATAGAGGCAGAGGCCAAGTGAAT GCATCCAGCAGCAGACCACTTNAAGTAGTCTGGTGTGCTGATTGCCCTAGCAGCAGAGAGTTGAG TGCCACAGGTAAAGATGAGTGAAGAGGAAATCATGATGTCATGTATGCAGTAATTACTATGTCA GAAGAAATATTTAAATATTGGACCACTCTTGTCTACCATCCCTACCCACT
WI-7534b	143 C T ---			TGTGAATTCCTAGCTCTGGAAGGTGTTTATGCCTTTGGGGTTCTTGATGTGTCGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAACACATCCCGGTGATAGAAATGCT AAATTGTCTGTGAATAGGTAGAAATTTCTTAAATATGGTTTCTTATTCGTGAAATTCGG AGAGTGTCTGCTAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7534	135 T C ---			TGTGAATTCCTAGCTCTGGAAGGTGTTTATGCCTTTGGGGTTCTTGATGTGTCGAGTGTACCCCA AGAGTCAGAACTGTACACATCCCAAAATTTGGTGGCGTGGAACACATCCCGGTGATAGAAATGCT /CJAAATTCGTGAAATAGGTAGAAATTTCTTAAATATGGTTTCTTATTCGTGAAATTCGG AGAGTGTCTGCTAAATTTGGATTGGTGTGATCTTTTGGTAGTTGTAATTT
WI-7543b	162 G A ---			GGGAAAGAATAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCACTTGAAGGAAGAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTTGTCTTGAAGAACCACTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCTCTGGCTCTGGATGTAGTCAGTTA
WI-7543	162 G A ---			GGGAAAGAATAAATTAGCTTGAGCAACCTGGCTAAGATAGAGGGGCTCTGGAGACTTTGAAGACC AGTCCTGTTTGCAGGGAAGCCCACTTGAAGGAAGAGTCTAAGAGTGAAGTAGGTGACTTGAAC TAGATTGCATGCTTCTCTTGTCTTGAAGAACCACTTGCAGTGACAGCTTGAGTGGGTT CTCTGCAGCCCTCAGATTATTTCTCTGGCTCTGGATGTAGTCAGTTA
WI-7555c	60 T C ---			GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGGTTCTCTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGCTGTTAAGCCACTTGGGTC ATAAGAGGGAAGTAAATGAAGTCTGACTAGAAATTTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTGATGTGCAATTTGAATTCAG

WI-7555b	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGG[T/C]CTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGCTGCTGTTAAAGCCACTTGGGTC ATAAGAAAGGGAAGTAAATAATGAAGTCTGACTAGAAATTTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTCAG
WI-7555	60	T C ---	---	GGTGATCAAGATCTGTTCCACAGGGCTAATGCCACCATCTCCCTCAAAATTTGTAGAGG[T/C]CTA AAAAGAAAGTGGTATGTTGTGTGATGATCAGCACTAAGTCTGCTGCTGTTAAAGCCACTTGGGTC ATAAGAAAGGGAAGTAAATAATGAAGTCTGACTAGAAATTTCTATTGCAGAGGCCAAGTACATTTAGT ATGGCATTGAGTTGTGATATAGTTTTCATTTGATGTGCATTTTGAATTCAG
WI-7567b	290	G T ---	---	TGAGCCATCACTAGAAGAAAGCCCATTTTCACTGCTTTGAAACTTGCCCTGGGTCTGAGCATGAT GGGAATAGGAGACAGGGTAGGAAAGGCGCCTACTCTTCAGGGTCTAAAGATCAAGTGGCCTTGG ATCGCTAAGCTGGCTCTGTTGATGCTATTTATGCAAGTTAGGGTCTATGTATTTAGGATGCGCCTAC TCTTCAGGGTCTAAAGATCAAGTGGGCTTGATCGCTAAGCTGGCTCTGTTT
WI-7569b	63	T C ---	---	AATGTATCCCTTTTCGGTCCAAACAGGAACCTGACTGGGCGAGTGAAGGAGGATGGCA[T/C] AGCGTTATGTGTAAATAACAAAGTATCTGTATGACAAACCGGATCGTTTGCAAGTAACTGAATCCAT TGGACATTGTGAAGGCTTAAATGAGTTTATGATGGGAATAGCGTTGTTATCGCCTTGGGTTTAAATT ATTTGATGAGTTCCACTTGATATCATGCGCTACCCGAGGAGGAGGAGTTTG
WI-7574c	216	A G ---	---	GCCACAGCAGAAATGGAGCGGTGTGAGGAAGGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCTCAGTAAATCATTTTG TACCACCTACATTTAGGCTGGGCAAGCAGCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC[A/G]TCTGCTGGGCTGACCCAGTTACTCATCCCCGTTA
WI-7574b	216	A G ---	---	GCCACAGCAGAAATGGAGCGGTGTGAGGAAGGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCTCAGTAAATCATTTTG TACCACCTACATTTAGGCTGGGCAAGCAGCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC[A/G]TCTGCTGGGCTGACCCAGTTACTCATCCCCGTTA
WI-7574	216	A G ---	---	GCCACAGCAGAAATGGAGCGGTGTGAGGAAGGTCCCTTTCTCTGTTTGTGTTGCCAAGGCCAAAC TCCCACTCTGCCCCCTTTAATCCCTTTCTACAGTGAGTCCACTACCTCAGTAAATCATTTTG TACCACCTACATTTAGGCTGGGCAAGCAGCCTGACCTAAGGGAGAATGAGTTGGACAGTTCTTG ATAGCCCAGGGC[A/G]TCTGCTGGGCTGACCCAGTTACTCATCCCCGTTA
WI-7576c	168	A T ---	---	AATGATGATGATAATGATGATGACGACGACAACGATGATGCTTGTAAACAAGAAACATAAGAGAGC CTTGGTTCATCAGTGTAAATAATTTTGAATAAGGCGGTACTAGTTCAGACACTTTGGAAGTTTGTGT TCTGTTTGTAAACTGGCATCTGACACAAATAAATGTTGTTGAAGGCCCTTATCTACATTTACCTAC TTTGTAGTGAGAGAGACAAAGCAAGCAANNNNNNNNAAGAAATAAAC



WI-7576b	168	A T ---	---	AATGATGATAATGATGATGACGACGACGATGATGCTTGTAAACAAGAAACATAAGAGAGC CTTGGTTTCATCAGTGTAAATAATTTTGAAGGCGGTACTAGTTCAGACACTTTGGAAAGTTTGTGT TCTGTTTGTAAACTGGCATCTGACACAAATAATGTTGAAGGCCCTTATTCTACATTTACCTAC TTTGTAAAGTGAGAGACAAAGAACAAANNNNNNNNAAGAAATAAAAC
WI-7577q	77	T C ---	---	AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCATTC/CAAAATCGTCTCTCATTACTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAGAGAGAACATCAAAAGTGAGATATGTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577p	50	GC ---	---	AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA TAAATAATGCATCAAAATCGTCTCTCATTACTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAGAGAGAACATCAAAAGTGAGATATGTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577o	157	GA ---	---	AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAGTTTCATTTTGGTTTACAC/ATAGGAAGAGAGAACATCAAAAGTGAGATATGTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577n	48	AG ---	---	AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA TAAATAATGCATCAAAATCGTCTCTCATTACTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAGAGAGAACATCAAAAGTGAGATATGTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577m	84	GA ---	---	AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAGAGAGAACATCAAAAGTGAGATATGTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577l	93	T C ---	---	AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AAAGAAGTTTCATTTTGGTTTACACGTAGGAAGAGAGAACATCAAAAGTGAGATATGTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577k	154	CA ---	---	AACCATGTTCCCTTCTTCTTAGCACCAAAATAATCAAAACCCCAACATAAGTGTTGCTTTCCCTTAA AAATATGCATCAAAATCGTCTCTCATTACTTCTCTGAGGGTTTGTAAACAGTAGGAGTTAAT AGAGTTTCATTTTGGTTTAC/AC/ACGTAGGAAGAGAGAACATCAAAAGTGAGATATGTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC

WI-7577j	117	A G ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCACACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAAGACAGTAGGAGTTAAT AAAGAAAGTTTCATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577i	77	T C ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCACACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577h	50	G C ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCACACATAAGTGTTGCTTTCCTTTAA TAAATAATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577g	157	G A ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCACACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTTCATTTGGTTACACGAGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577f	48	A G ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCACACATAAGTGTTGCTTTCCTTTAA TAAATAATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577e	84	G A ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCACACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577d	93	T C ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCACACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTTCATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC
WI-7577c	154	C A ---	---	AACCATGTTCCCTTCTTCTTAGCACCACAAATAATCAAAACCCACACATAAGTGTTGCTTTCCTTTAA AAATATGCATCAAAATCGTCTCTCATTTCTCTGAGGGTTTAGTAACAGTAGGAGTTAAT AGAAAGTTTCATTTGGTTACACGTAGGAAAGAGAGAGCATCAAAAGTGGAGATATGTTAACT ATTGTATAATGTGGCCTGTTATACATGACACTCTTCTGAAATTGACTGTATTTC

WI-7577b	117 A G ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTATTACTTTTCTCTGAGGGTTTAGTA/GJACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGCATCAAGTGAGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7577	107 G A ---	---	AACCATGTTCCCTTCTTAGCACCACAAATAATCAAAACCCACATAAGTGTTGCTTCCCTTTAA AAATATGCATCAAAATCGTCTCTATTACTTTTCTCTGAGIG/AJGTTTTAGTAACAGTAGGAGTTAAT AAAGAAAGTTCAATTTGGTTACACGTAGGAAGAGAGAGAGCATCAAGTGAGAGATATGTTAACTAT TGTATAATGTGGCCTGTTATACATGACACTCTTCTGAATTGACTGTATTTC
WI-7619q	106 C G ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCAATCCCTCCCTAACGAGACTTCGTTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAAATGGGGCCTCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCT CTCTCGCTTTCTTCTTACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619p	150 T C ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTT/CJCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619o	228 A G ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619n	237 G C ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTCTCT CGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619m	99 C T ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG TGGCAGGAAGAAATGGGGCCTCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTC TCTCGCTTTCTTCTTACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619l	189 T A ---	---	ACAAGGCGACTTGAAGAGGACGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACGACAAAGAC AGAGAAGGGCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAATGGGGCCTCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTTCATCTTTTTCCTC TCTCGCTTTCTTCTTACACAGAAACATACACATACCGAGAAACCTATTTC



WI-7619k	90	C G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGCCCAATGGGGTCAATCCG/C/GCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCT CTCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619j	206	T G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC CAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT CGCT/GTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619i	106	C G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCT CTCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619h	150	T C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC CAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT TCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619g	228	A G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC CAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT CGCTTTCTTTTACACAGAAACAT/G/CACATACCGAGAAACCTATTTC
WI-7619f	237	G C ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC CAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT CGCTTTCTTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619e	99	C T ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC TGGCAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT TCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC
WI-7619d	189	T A ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAAGCACAAGAC AGAGAAAGGCCCAATGGGGTCAATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC CAGGAAGAATGGGGCTCTAAGGGAGTGTTGGGTCTGTCTCTCCCTTTTCCATCTTTTCTCTCT TCTCGCTTTCTTTACACAGAAACATACATACCGAGAAACCTATTTC

WI-7619c	90 C G ---	---	ACAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAGAC AGAGAAAGGGCCCAATGGGTCTATCC/C/GTCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTAC ATGGCAGGAAGATGGGCGCTCTAAGGGAGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCT CTCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619b	206 T G ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAGAC AGAGAAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCGCTCTAAGGGAGTGGGTCTGTCTCCCTTTTCCATCTTTTCCCTCTCT CGCT/GTTCTTTCTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7619	189 T A ---	---	ACAAGGCGACTTGAAGAGGACGCGAGGCTTCCAGAGGACAAACCCCAATACAGGAGAACACAGAC AGAGAAAGGGCCCAATGGGTCTATCCCTCCCTAACGAGACTCTCTGTGCTGGGGTGCTAATTACATGG CAGGAAGAAATGGGCGCTCTAAGGGAGTGGGTCTGTCTCCCTTTTCCATTTTCCCTTTTCCCTC TCTCGCTTTCTTTACACAGAAACATACACATACCGAGAAACCTATTTC
WI-7626d	105 A G ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGC/GJTTAAACCACATCATGGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCTGCTGTATTTATAGTAACCATTTTCCCTTTGGACTGTTCA
WI-7626c	155 C T ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAACCACATCATGGACCAAAATGTGCCA TACTAATGATGAGCAATTTAGC/GTJACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCTGCTGTATTTATAGTAACCATTTTCCCTTTGGACTGTTCA
WI-7626b	28 T A ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAGCAACAGCAG TAATCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAACCACATCATGGACCAAAATGTG CCATACTAATGATGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCTGCTGTATTTATAGTAACCATTTTCCCTTTGGACTGTTCA
WI-7626	144 T C ---	---	CCTTTGTATGTGGAAGTATACCTGGCTTTTAAATATATGTATTTAAACAAAGCAACAGTAA TCTATGTGTTTCTGTAAACAAATGGGATCTGTCTGGCATTAACCACATCATGGACCAAAATGTGCCA TACTAATGAT/GCJGAGCAATTTAGCACAAATTTGAGACTGAAATTTAGTACACTATGTTCTAGGTCAGT CTAACAGTTTGCTGCTGTATTTATAGTAACCATTTTCCCTTTGGACTGTTCA
WI-7689c	134 A G ---	---	TCCCATAACCGCTGATTCTCAGGGTCTCTGTGCGCGCCACCCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGAGCGCCACCCAGCAAAAGGTTGTTCTCTAA /GJTAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGTGGTGGCCACAAATAAATGGATTTATTAGAAATTCATATGAC



WI-7689b	134 A G ---	---	---	TCCATAACCGCTGATTCAGGGTCTCTGCTGCCGCCACCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCAGCAAAGGTTGTTCTCTAA[A /G]TAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGTTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7689	121 G A ---	---	---	TCCATAACCGCTGATTCAGGGTCTCTGCTGCCGCCACCAGATGGGGAAAGCACAGGTGGGC TTCCAGTGGCTGCTGCCAGGCCAGACCTTCTAGGACGCCACCAGCAA[A/G]GTTGTTCTCTAA ATAAGGGCAGAGTCACACTGGGGCAGCTGATACAAATTGCAGACTGTGTAAAGAGAGCTTAAT GATAATATTGTTGGTGCCACAAATAAAATGGATTATTAGAAATTCATATGAC
WI-7690	45 G A ---	---	---	TGGAGAACATTCAATCTTGCCGTCACCTATTCATCAATGAAGATTA[G/A]CACTGAGATCCAGAGAGG CTGGATGACTTGGCTCAAGTTCACCAGCATGGTAGTGCAAGAGAGGTCCAGAGTCTGGCCCTTGAT GCCAGCTCAGTGCCACAAAGCTCAGTAGGAGGATGTTCCAGTGGATGAGGGCCACCAGGAAGCAC AGGTCCAAGGCTGGTCCACACTTATCAGCAGCAACAAGTGTCACTTCATCC
WI-7703b	164 T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTGGAAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAAGTAAAT[C]GGTCTCTCAGTGTGTTTATTTAACCTCTAAATTCCT TTCATTTTAGGGTAGCATTTGTGTGAAGAGGTTTAAAGCTTCCATTGT
WI-7703	156 T C ---	---	---	ACAGAAAGTTGAATTTACATGGCTGGAGCTAGAAATTTGATATGTGAACAGTTGTGTTGAAGCAC AGTGATCAAGTTATTTTAAATTTGGTTTTCACATTGGAAACAAGTCAGTCATTCAGATATGATTCAAA TGCTATAAACCAAACTGATGTAAAGTAAATGTGCTCTCAGTGTGTTTATTTAACCTCTAAATTCCT TTCATTTTAGGGTAGCATTTGTGTGAAGAGGTTTAAAGCTTCCATTGT
WI-7743e	106 C A ---	---	---	TTAATGAGTGTGTTGTCAACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCGCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTACCTGCTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCGGTTCAGGA GAGGGCAGAACAGCGCTCTGTCTGCCAGCAGCAGCAGCTCTCAGCC
WI-7743d	275 C T ---	---	---	TTAATGAGTGTGTTGTCAACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCGCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT TACAGAAATTCGTACCTACCTGCTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCGGTTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCAGCAGCAGCTCTCAGCCAAG
WI-7743e	106 C A ---	---	---	TTAATGAGTGTGTTGTCAACCGTTGGGGATTGGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCGCAGCACTAAAGCAGTGGAC[C/A]CCAGGAGTCCCTGGTAATAAGTACT GTGTACAGAAATTCGTACCTACCTGCTGGGGTCTGGGGCTCGGAGCCTCATCCGAGGCGGTTCAGGA GAGGGCAGAACAGCGCTCTGTCTGCCAGCAGCAGCAGCTCTCAGCC



WI-7743d	275	CT	---	TTAATGAGTGTGTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCTCATCCGAGGCAGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCAGCAGCTCTCAGCCAACG
WI-7743e	106	CA	---	TTAATGAGTGTGTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCTCATCCGAGGCAGGTCAGGAGAG GAGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCAGCAGCTCTCAGCCAACG
WI-7743d	275	CT	---	TTAATGAGTGTGTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCTCATCCGAGGCAGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCAGCAGCTCTCAGCCAACG
WI-7743c	106	CA	---	TTAATGAGTGTGTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCTCATCCGAGGCAGGTCAGGAGAG GAGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCAGCAGCTCTCAGCCAACG
WI-7743b	275	CT	---	TTAATGAGTGTGTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCTCATCCGAGGCAGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCAGCAGCTCTCAGCCAACG
WI-7743	106	CA	---	TTAATGAGTGTGTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG GTGTACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCTCATCCGAGGCAGGTCAGGAGAG GAGGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCAGCAGCTCTCAGCCAACG
WI-7743	275	CT	---	TTAATGAGTGTGTTGTCAACCGTTGGGGATTGGGAAGACTGTGGCTGCTGGCACTTGGAGCCAAGG GTTTCAGAGACTCAGGGCCCCAGCACTAAGCAGTGGACCCAGGAGTCCCTGGTAATAAGTACTGTG TACAGAAATCTGCTACCTCACTGGGTCTCTGGGCTCGGAGCTCATCCGAGGCAGGTCAGGAGAG GGGCAGAACAGCGCTCTGTCTGCCAGCCAGCAGCAGCAGCTCTCAGCCAACG
WI-7758	144	AG	---	TGACATTTATTCAAAGTTAAAGCAACACTTACAGAAATTATGAAGAGGTATCTGTTTAAACATTTCC TCAGTCAAGTTCAGAGTCTTCAGAGACTTCGTAAATTAAAGGAACAGAGTGAGAGACATCATCAAGTG GAGAGAAATC[AG]TAGTTTAAACTGCATTATAAATTTTATAACAGAAATTAAAGTAGATTTTAAAA GATAAATGTGTAATTTTGTTTATATTTCCCATTTGGACTGTAACTGACTGCC

WI-7765b	126	G C ---	---	ACAGGGCCTTTGGCAGGTGCAGCCGCCACTGCCTTTGACCTGCCCTTCATGCATGGAAATCCCT TCATCTGGAACCATCAGAAACACCCTCACACTGGGACTTGCAAAAGGGTCAGTATGG[G/C]TTAGG GAAACATTCCTATCCTTTGAGTCAAAATCTCAATCTCCCTATCTTTGCCACCCCTCATGCTGTGTG ACTCAAACCAATCACTGAACCTTTGCTGAGCCTGTAAATAAAAGGTGCGA
WI-7773b	237	C G ---	---	TTAATTTACTGATCCAGCAAGACCAATCATTTGTATCAGATTATTTTAAGTTTTATCCGTAGTTTT GATAAAGATTTTCTATTCCTATTCTTGGTTCTGTACAGAACCTAATAAGTGTACTTTGCCATTAAAGGCA GACTAGGGTTTCATGCTTTTTACCCCTTNNNNNNNNNTTGTAAAGTCTAGTTACCTACTTTTCTTT GATTTTCGACGTTTGACTAGCCATCTCAAGCA[G/C]TTTCGACGTTTGA
WI-7774b	170	T C ---	---	TGCAACCTCTTTTCGTGATGGGAGCCTGCTGTCAGCACTCCAGTAGCGAGAGACGGCACCCAGAAAT CAGATCCCAGCTTCGGCATTGTATCAGACCAACAGTGTCTTTCCCGGGAGGAAACACTTTTTTAA TTACCCCTTTTGAGGCAACCACTTTAATCTGTTT[C]ATACCTTGTCTTATTAAATGAGCGACTTAA ATGATTGAAATAATGCTGCTCTTAGTAGCAAGTAAATGTGCTTGTCT
WI-7785c	165	G ---	---	GCAGAGACCTTCCAAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGTCTGTAATACTGTAAATGCATTGGAATAAACTGTCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAGGCTAATCCAATTATTATTCACATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGTATCTTTGGTGTGC
WI-7785b	165	G ---	---	GCAGAGACCTTCCAAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGTCTGTAATACTGTAAATGCATTGGAATAAACTGTCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAGGCTAATCCAATTATTATTCACATTTACCA TAATTTATTTGTCCATTGATGATTTATTTTGTAAATGTATCTTTGGTGTGC
WI-7785	156	T ---	---	GCAGAGACCTTCCAAAGGACATATTGCAGGATTCTGTAATAGTGAACATATGGAAGTATTAGAAATA TTTATTGTCTGTAATACTGTAAATGCATTGGAATAAACTGTCTCCCCCATTTGCTCTATGAAACTGC ACATTGGTCATTGTGAATANNNNNNNNNGCCAGGCTAATCCAATTATTATTCACATTTACCAATTTA TGATTTATTTGTAAATGTATCTTTGGTG
WI-7789c	84	G A ---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTGATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GOCCTCCTGGTGAATCGGGGCTGTCTCAGACGACTAGCCAGGACCATCT
WI-7789b	84	G A ---	---	TCTCCCCCTCATCCAACTCCGAAAGTCTGAATCTCCCAAGGAGGGCACCATCTTACAGAGACTCTCCC TGACGGTGGAATTTAA[G/A]TTTAGGGTCCCTAAAGCATTTGACACACAGTTGTGATGACTGAC CCAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCCGCTGCCCTAGGATAT GOCCTCCTGGTGAATCGGGGCTGTCTCAGACGACTAGCCAGGACCATCT

WI-7789	73	G A ---	---	TCTCCCTCATCCAACTCCGAAAGTCTGAACTCTCCAGGAGGGCAACCATCTTACAGAGACTCTCC TGACG[G/A]TGGAAATTAAGTTTAGGGTCCCTAAAGCAATTTGACACACAGTTGTTGAATGACTGAC CCAAAATGTGAATGAAGCTAATGTGAATGTGAGTGAAGCTCCCTTCAGGCCGCTGCCCTAGGATAT GCCCTCCTGCTGACTCGGGGCTGTCTCAGACGACTAGCCAGGACCCATCT
WI-7790b	190	C T ---	---	AATTGTCAGTCACCTTCTTCAAAACCTTACAGTCCCTTCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTAIGTGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTTTCTTGAAGTCTC/TTTCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7790	190	C T ---	---	AATTGTCAGTCACCTTCTTCAAAACCTTACAGTCCCTTCTAAGGTTACTCTTCATGAGATTCATCCATT TACTAATACTGTATTTTGGTGGACTAGGCTTGCCTATGTGCTTAIGTGTAGCTTTTACTTTTATGG TGTGATTAATGGTGATCAAGGTAGGAAAGTTGTGTTCTATTTTCTTGAAGTCTC/TTTCTATACTTT AAGATACTCTATTTTAAACACTATCTGCAAACTCAGGACACTTTAAC
WI-7795b	81	C A ---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACACAGATTCTCTTGGCTCATATTTCTTTCTCTCAT CTTGATGATGATC/AJGTCAATCATCAAGAAATTAATGATTAATAAGCATGCTTCTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTTCCAGAAATAATCTCTTGGAGGAAATAATGTCCAAA TAAGATGAATCACCTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7795	81	C A ---	---	CAGATGTTCTGGTAACTGATTGCTGGCAACACAGATTCTCTTGGCTCATATTTCTTTCTCTCAT CTTGATGATGATC/AJGTCAATCATCAAGAAATTAATGATTAATAAGCATGCTTCTCTCTCTCTCT TAATAAGCCACATATAAATGTACTTTTCTTCCAGAAATAATCTCTTGGAGGAAATAATGTCCAAA TAAGATGAATCACCTTAATACCGTATCTTCTAAATTTGAAATATAATTCTG
WI-7814c	41	G A ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCCG/AJTTTCATTTAGTCATGTGACCACTC TGCTTTGTGTTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGATCTTTTAGAGAAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTAAGAAATAACAGAA
WI-7814b	41	G A ---	---	TTCTCTCATTTTATCCCTCACCTGTAGCATGCCAGTCCCG/AJTTTCATTTAGTCATGTGACCACTC TGCTTTGTGTTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGATCTTTTAGAGAAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTAAGAAATAACAGAA
WI-7814	28	G A ---	---	TTCTCTCATTTTATCCCTCACCTGTAG/AJCATGCCAGTCCCGTTTCAITTTAGTCATGTGACCACTC TGCTTTGTGTTTCCACAGCCTGCAAGTTCAAGTCCAGGATGCTAACATCTAAAATAGACTTAAATCTC ATTGCTTACAAGCCTAAGATCTTTTAGAGAAAGTATACATAAGTTTAGGATAAAATAATGGGATTTTC TTTTCTTTCTCTGGTAATATTGACTTGTATATTTAAGAAATAACAGAA



WI-7830d	150	C T	---			GCAGGAAATAGTCACTCATCCACTCCACATAAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGAACG ATCCATAACTTTAGTC/TJTTAATGTACACATTGCATTTTGATATAAATAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTTGGCTGCACCTTTTACTTTTGGCGTGGA
WI-7830c	54	G A	---			GCAGGAAATAGTCACTCATCCACTCCACATAAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATATAAATAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTTGGCTGCACCTTTTACTTTTGGCGTGGA
WI-7830b	134	G A	---			GCAGGAAATAGTCACTCATCCACTCCACATAAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGGATAGGGGGCAAAATCTTTTCCCTTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGA G/AJATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATATAAATAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTTGGCTGCACCTTTTACTTTTGGCGTGGA
WI-7830	44	A G	---			GCAGGAAATAGTCACTCATCCACTCCACATAAAGGGTTTAGTAAGAGAAGTCTGTCTGTCTGATGA TGATGGATAGGGGGCAAAATCTTTTCCCTTTCTGTAAATAGTCATCACATTTCTATGCCAAACAGGA ACGATCCATAACTTTAGTCTTAATGTACACATTGCATTTTGATATAAATAATTTGTTGTTCCCTTTG AGGTTGATCGTTGTGTTGTTTGGCTGCACCTTTTACTTTTGGCGTGGA
WI-7865e	25	C T	---			CCACTTCCTATCTGATTTTCCAGIC/TJAAATGAGGAGGCAATTCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865d	191	C T	---			CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATTCTAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCTTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865c	25	C T	---			CCACTTCCTATCTGATTTTCCAGCAGCT/JAAATGAGGAGGCAATTCTAGTCTTCCACAAACATCTA GCCATCTAAATGGAGAGATGAATCTTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGG GGTATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865b	191	C T	---			CCACTTCCTATCTGATTTTCCAGCAATGAGGAGGCAATTCTAGTCTTCCACAAACATCTAGCC ATCTAAATGGAGAGATGAATCTTCTACCTATACAAACAAGCTAGCTATTAGAGGGTGGTGGGT ATGCTACTCATAAGATTTGAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAAAAC CTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA

WI-7865	25 C T ---	---	CCACTTCCTATCTGATTTTCCAG[C/T]AATGAGGCAGGCAATTCTAGTCTTCCACAAACATCTAGCCATCTAAATGGAGAGATGAATCATCTACCTATACAACAAGCTAGCTATTAGAGGGTGGTGGGTGCTACTATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTACGAAACCTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7865	191 C T ---	---	CCACTTCCTATCTGATTTTCCAGCAATGAGGCAGGCAATTCTAGTCTTCCACAAACATCTAGCCATCTAAATGGAGAGATGAATCATCTACCTATACAACAAGCTAGCTATTAGAGGGTGGTGGGTATGCTACTATAAGATTCAGGGTGTCTTCCAACTGAAATCTCAATGTTCTCAGTAC[C/T]GAAACCTGAAATCACATGCCTATGTAGGAAAGTGCTATTACCCAGTAAACCCAAA
WI-7867c	92 A C ---	---	TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCAACCCTTCAAGCCTCACTAGTCCCTCTAACAAATTACCTGTCAAGAGG[C/C]GAGTGCAGCTCAGGTGGATTAAATGTGGGTTTAAATATGGCCTGTTGAGTTTAAATGTTTAAATGTTGATTCTTAAAGTAACCATTTCTGTTCTTGTCTATAAATCTATGTTCTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7867b	92 A C ---	---	TTCAACACCTGTCTTCCACCTCCACCATCTGTGCAATCACTTCAACCCTTCAAGCCTCACTAGTCCCTCTAACAAATTACCTGTCAAGAGG[C/C]GAGTGCAGCTCAGGTGGATTAAATGTGGGTTTAAATATGGCCTGTTGAGTTTAAATGTTTAAATGTTGATTCTTAAAGTAACCATTTCTGTTCTTGTCTATAAATCTATGTTCTATATGCTATGCTTAAATTTGGATGATGAAGGCAACTTGGATTTAAGG
WI-7868c	173 C T ---	---	TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAAAGAGGCTTAAACCGGGCTTTCAACCAACCTGCTCCCTGTGATCTCCATCAGGGCCAGATCTTCCACGTCTCCATCTCAGTACACAATCATTTAATATTTCCCTGTCTTACCCCTATTCAAGCAA[C/T]TAGAGGCCAGAAATGGGCAAAATTATCACTAACAGGCTTTTGACTCAGGTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868b	173 C T ---	---	TTGATCGATCTTTTCCACCTGTCACTCAACGTGGTCCCTAGAACAAAGAGGCTTAAACCGGGCTTT/C]TCAACCAACCTGCTCCCTGTGATCTCCATCAGGGCCAGATCTTCCACGTCTCCATCTCAGTACACAAATCAATTAATATTTCCCTGTCTTACCCCTATTCAAGCAACTAGAGGCCAGAAATGGGCAAAATTATCACTAACAGGCTTTTGACTCAGGTCCAGTAGTTCATTCTAATGCCTAGAT
WI-7868	66 T C ---	---	ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTCTGCAGTGATTAGAAGGGGTGGGGTGGCGGGAATCC[C/C]ATTATCAGACTCTGTAATTGAATATAAATGTTTACTCAGAGGAAGTGCAAATTGCCTGCAAAATGAATCCAAATGAGCACTAGATAATTTAAACATCATTACTGCCATCTTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG
WI-7870b	85 T C ---	---	

WI-7870	76 C T ---			ATCTTTGCTCCCTGCAAGAAATCAGCCATAAGAAAGCACTATTAACTACTCTGCAGTGATTAGAAGGG GTGGGGTGG[C/T]GGGAATCCTATTATCAGACTCTGTAAATGAATATAAATGTTTACTCAGAGGAG CTGCAAAATTGCCCTGCAAAATGAAATCCAATGAGCACTAGAAATATTTAAACATCATTTACTGCCATC TTTATCATGAAGCACATCAATTACAAGCTGTAGACCACCTAATATCAATTG
WI-7889c	54 C ---			TTAGGTCTCATGCCACTCCCTCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCTG CAGCCGTGAGGACTCTAGCTCATGAGTGGAAGTCACTACAGGACTGGCCGGCCAGGCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGGAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAGGCTGTCTCTCCAGAGCACAAAG
WI-7889b	54 C ---			TTAGGTCTCATGCCACTCCCTCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGCGCTCTCCCTG CAGCCGTGAGGACTCTAGCTCATGAGTGGAAGTCACTACAGGACTGGCCGGCCAGGCTCT GGCTTCCCTGCCCAATCCTCCCTGGAGGAGGACATGGGAATGAATTGAAATGGGGCGCTGGACACC TACAGCAGCAGCATGTCCCTCCAGGCTGTCTCTCCAGAGCACAAAG
WI-7894c	142 A G ---			AGCCACCCCAATATACTGTTATCCAGAAGCTGTTATGTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCTATTGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAAATTTGCAATTTTATTGAAATTAATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAACCGCTATAGAGTATCCATA
WI-7894b	142 A G ---			AGCCACCCCAATATACTGTTATCCAGAAGCTGTTATGTCTGTTCCATACATGTTTTGTACT TTTACTATATCTACATACATCAATTAACCTTATGTCTATTGTTTGTGAATTTATATTTGCGTATAC ATTATC[A/G]TATGTAAATTTGCAATTTTATTGAAATTAATGTTTCTTGAGATTTATCCACATTG AAACATGGAGCTCTAAATCGTTAATTTTAACCGCTATAGAGTATCCATA
WI-7900e	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGTTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAAGTGAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGTTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAAGTGAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84 C T ---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG[C/T]CCTGCCATTGAACACAGTGATTAAGTTTGATCAAGCCATGTTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCAAGTGAA TATGATGATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC



WI-7900d	128	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900e	84	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TJCCCTGCCATTGAACACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900d	128	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900c	84	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TJCCCTGCCATTGAACACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900b	128	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATGCCCTGCCATTGAACACAGTGATTAAAGTTTGATCAAGCCATGGTGA/C/TJACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7900	84	C T	---			GCTCACTGTGACCCATCCTTACTCTACTTGGCCAGGCCACAGTAAACAAGTGACCTTCAGAGCAGCT GCCACAACCTGGCCATG/C/TJCCCTGCCATTGAACACAGTGATTAAAGTTTGATCAAGCCATGGTGACACA AAATGCATTGATCATGAATAGGAGCCCATGCTAGAAGTACATTCTCTCAGATTTGAACCCAGTGAAA TATGATGTATTTCTGAGCTAAACTCAACTATAGAAGACATTAAAGAAATC
WI-7901c	33	C T	---			AGACTTAGGTACAAATTGCTCCCTTTTATATA/C/TJAGACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTTGGTTGGGTCGCTGGGTTATTGGGGCAGCGCGGTGGTGGT CACACAGTCGCTCTGCATGCTCTCTGTCTATACAGACAGGTAACCTAGTTCT
WI-7901b	33	C T	---			AGACTTAGGTACAAATTGCTCCCTTTTATATA/C/TJAGACACACAGGACACATATATTAACAG ATTGTTTCATCATTCATCTATTTCCATATAGTCATCAAGAGACCATTTTATAAACATGGTAAGAC CCTTTTAAACAACCTCCAGGCCCTTGGTTGGGTCGCTGGGTTATTGGGGCAGCGCGGTGGTGGT CACTCAGTCGCTCTGCATGCTCTCTGTCTATACAGACAGGTAACCTAGTTCT



[illegible]



WI-8021b	57 C T ---	---	ACAACTCAGAAAGGACTGTGCAAGTCAATGAGTCGCTTGTTGAAATTCATCTGGAAAC/C/TJGATCCC ACGTCTTAGAACCTTCACCAAGAGGATTTCTTGTAGTATTCTCAAAGTCTTGGTAGGCATTGGA ACTGGTCCCTTACACTTTGAGATTCTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTTAGGGTGATTGGAATTCGGTGAATTGCCA
WI-8021	57 C T ---	---	ACAACTCAGAAAGGACTGTGCAAGTCAATGAGTCGCTTGTTGAAATTCATCTGGAAAC/C/TJGATCCC ACGTCTTAGAACCTTCACCAAGAGGATTTCTTGTAGTATTCTCAAAGTCTTGGTAGGCATTGGA ACTGGTCCCTTACACTTTGAGATTCTTTCTTTGCGCCTCTTATCAAGTCAGCACACACCTTTTCCAAG GATTTACGTTGCGGCTTGTTAGGGTGATTGGAATTCGGTGAATTGCCA
WI-8024c	206 A G ---	---	CTGAAATTTACTATGCTCTCCACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTTCAGGAGGACAGGAGGATCCAGTGCCACTTCCCATGGGAAGACAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTCATCACCAAAACCAATTCAGCCGCTCTAGCCTCTAA TTCCC/A/GICTCTAGAACAGCTGGCCCTGGTCTCAGTACACAAAGGAAAGAGC
WI-8024b	206 A G ---	---	CTGAAATTTACTATGCTCTCCACAAGAGCTCCCATTTCCACAGACACAGTCAATGTCAGTCA GCTTGATTTCAGGAGGACAGGAGGATCCAGTGCCACTTCCCATGGGAAGACAGAGAGT GGCCCCAGAGATGGAAGGACCCAGTGTCATCACCAAAACCAATTCAGCCGCTCTAGCCTCTAA TTCCC/A/GICTCTAGAACAGCTGGCCCTGGTCTCAGTACACAAAGGAAAGAGC
WI-8077	167 A G ---	---	GAATGAGCCTTCTAGCGCGAGGAGCCTGCTGCTGTTGTTGGCTGCACATGCATTCATGGAATGC TTTTGGCCAAAGCGGGGCACTGAGGACTAAGCTCTGANNNNNNNNNATCTGCCAAACTCCTTCT AAGGAGCTCTGGGTGTCATGCCCTACAAACC/A/GJTAATCTCATCAGATGGATTTTATTAAAGTT GTGATTGTGACTTACTTTCCAATCTGACTCTGGCATAACAAGGGAATA
WI-8118f	114 G C ---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCCTCCCTTGCTAAGGAAGC GTACTTCATGCTGTGGAAACTGGCAATACAGAAATGAGCTTGTTCCTTCTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCCTATTCCTCCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118e	40 A G ---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCCTCCCTTGCTAAGGAAGC GTACTTCATGCTGTGGAAACTGGCAATACAGAAATGAGCTTGTTCCTTCTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCCTATTCCTCCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118d	118 T G ---	---	TCTAGGTTTAATCAAAGCAATTTGCANTTTGGATTTTGGAAATGACCCTCCCTTGCTAAGGAAGC GTACTTCATGCTGTGGAAACTGGCAATACAGAAATGAGCTTGTTCCTTCTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTCTGATTTCCCTGCTCCTCCTATTCCTCCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA

WI-8118c	44 C T ---			TCTAGGTTTATCAAAGCAATTTGGCANTTTGGATTTTGAATGATC/TTCACCTCCCTTGCTAAGGAAGC TATGTACTTTCATGCTGTGGAACTGGCAATACAGAAATGTAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTTCTGATTTCCCTGCTCCTATTCCTTCTCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8118b	88 T C ---			TCTAGGTTTATCAAAGCAATTTGGCANTTTGGATTTTGGATGACCCTCCCTTGCTAAGGAAGCTAT GTACTTTCATGCTGTGGAACT/CJGGCAATACAGAAATGTAGCTTGTTGTTTCTTAGCCTTGAAGA TGACCAGGTAGAGACAGAGTGAGACCAACAGTTTTTCTGATTTCCCTGCTCCTATTCCTTCTCT AAAAATCAGACTCATTTGTGACCAGTAGTCTTGAGGACTCAAGCTGAATGA
WI-8171d	299 C T ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGCTCGGGAAG AGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAACAATCACGGCA
WI-8171c	46 A G ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGCTCGGGAAG AAGAGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAACAATCAC
WI-8171a	46 A G ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGCTCGGGAAG AAGAGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCAC ACATTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAA GGCACAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAACAATCAC
WI-8171b	298 T C ---			TTTTCTCTCTCCGGGGGACCAAGGTACCTTCTGGGGCATACAACATGGCAGCGGCTCGGGAAG AGGGTAGGAGGACCGAGCAGCATTTCTGTAGAGGAAGACAGAAAGGAGACCTCTTGGCACACA TTTATGGAGGTTGTCCCTGAAGAGAAAGGCGAGGTGGGAGAGGTTCCCTGTTACTTAAGAGAAGGC ACCAGTGGGCAAGAGCACAAATGAAGAGGATGATGATAAAACAATCACGGCA
WI-8314b	85 G C ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCATTGCAATTGAGCACATTTCTGGGTCTGT TTCTCTATCTCTAAGGGIG/CJAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCACTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGTAACCCT
WI-8314	78 C G ---			GAGGGAAATGACATCTGGAGATCTAGGTATGTGGCCATTGCAATTGAGCACATTTCTGGGTCTGT TTCTCTATCTCTAAGGGIG/CJAGTCTCAAAACCCAGCTCAAAATACGACACTAACATGATGAACAT GCATGAGCTTTGAAAAGTGCTCTGTAGTCTTATGATGATCTAGAGAGCACTGTCCAATAGAACTTTC TGTGATGATGAAAAGATTCTACTTCTGACCTATTCAATAGGGTAACCCT

WI-8321	178	G A	---			TTTTAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTTGTTTCAAGAGCTGCTGTATATAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGTTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA TTTGCTATGGTTCTAGTTATCAACCTACTTTATTAGCTGAACTGTTGGC
WI-8321	178	G A	---			TTTTAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAGTTACAATGTGTCCAG TGATATACCCAGGNAATCCATTCTTGTTGTTTCAAGAGCTGCTGTATATAGTCTCTGAGAAG TCCCCTTAGATAATAGCTGCCACTTTTCAGTATGTTTCAGAAATG/AJAGTATCTTAGTATCTTTCTA TTTGCTATGGTTCTAGTTATCAACCTACTTTATTAGCTGAACTGTTGGC
WI-8332b	123	A C	---			TATGTAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAGTTACAATGTGTCCAG AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGCAGCTTGAJA/CJACTAAGTAG CAGTACTGTTTGGTGTGTTTGTCTTCCAGCAATGCTACTGCGACTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8332	114	A C	---			TATGTAATATGCCCGTTTAGAGCAGACACAGTCACAATAAAAGTTAAAAGTTACAATGTGTCCAG AATTACCTCTAGATTGTCCAAAGCCAGTCTTCCCTTCCCTGTGCAGCTTGAJA/CJACTAAGTAG CAGTACTGTTTGGTGTGTTTGTCTTCCAGCAATGCTACTGCGACTACTTAGTAACAACACTAG AGGTGGAGGGTNTCCGGGAAGCAGTTAGATGAGTTAAGTGTGATGCACA
WI-8378b	311	T C	---			TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGAGACAGCAGTGGGGATGGCACTAAACCATTAGA AACTGCCCCATGATCCCAATCACTNTCACCAGGCCCTCTCCACACAGTGGG
WI-8378	308	T C	---			TGCGGGCTTAACAGGAAGCATGACTGGAGGCTCAGGAAGCTTATAATCATGGCAGAGGCGAAGG GGAAGCAAGGACCTTCTTACATGGCAGCAGGAGAAAGAGAAGGAGGAGTCTACACACTTTT AAACAACAGATCTCATGAGANTTCCATCGGAGACAGCAGTGGGGATGGCACTAAACCATTAGA AACTGCCCCATGATCCCAATCACTNTCACCAGGCCCTCTCCACACAGTGGG
WI-8426	184	T G	---			TTAGCACATATTAGCATTAAGCCTCAAGGATACAGCAATATGTTACATCTCTGTGAAACAG TTGTTGTAGACTGTTAANNNNNNNAATGTAACTCCGACTTGTGCCTAATAGGATTTGACCNTTAA GAGGNTTCTTTGCTGTGGANGGGGGCTTTGCTTGAACCTTCCATTCTGT/GJGCTTGTAGCTGGTG AGGCTGGGAGTATGGANGGNCOCGGGGCTTGGCNAATGNAATTCAGTGAG
WI-8450h	61	C A	---			TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTC/AJCA TCTTCTATCTTAGTCCAGTTTGTAGTTTCAATCCCAATTATACCAATTCATTGTTATTTTAAAGA AAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTCAT



WI-8450g	55 T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCJACACTCCAT CTTCTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450f	108 T A	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCJTTTAAAGA AAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450e	125 T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCJTTTAAAGA AAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450d	125 T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTCJTTTAAAGA AAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450c	108 T A	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTCCATCTT CTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450b	61 C A	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATACACTTCJAJCA TCTTCTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8450a	55 T C	---	---	TTGAGCCTCCACAAATAATGCAACCAAGTTTACATTTTAAACAGCCCTTCTACATTCJACACTCCAT CTTCTCTATCTTAGTTCCAAGTTTAGTTTCAATCCCAATTATACCAATTCCATTGTTATTTTAAAGA AAAACCTTCCAGTTATTGTCAGAAACTATGATTAGCTTACCCCTCCACTACCCAGCAAACTAC AGAGAGGATGGGAGTGTATATGAGCAGTACAGAGTCTTAATGCAATTTCAT
WI-8458b	60 A G	---	---	CAAGGAAAGCTGTCAGTCTTCATAAAGTTTCAAGAGTTACAAATAACGTATTTTAAJAJGJCTA CAATTCAAGATTAGCATCCAAACCTACAAACATGATGTAGATTGTCACACACCATACAACTTCAC ACCTGGCTACAGCAATGTTGACTTACATCACCATGTTTATAGTTGTGAAAACTTTATTGTGCACAGT GACATCCATTCCGCCAGACTTAATGTTATAAAGCAGCTGAGCAGAGTTCTCA

WI-8461c	105 A T ---	---	---	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATATACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCATTTT[A/T]NNNNNNNNCCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461b	38 T C ---	---	---	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAAT/CJATAACTACAACCTTACAAATGCCAA TTAGACAAAGAGANTAAATGATATAATAATCATTTTNNNNNNNNCCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	38 T C ---	---	---	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATATACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCATTTTNNNNNNNNCCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-8461	105 A T ---	---	---	CTTCCTCCTCCAAAATCTACATGAATACTTGAAGACAATATACTACAACCTTACAAATGCCAATTA GACAAAGAGANTAAATGATATAATAATCATTTT[A/T]NNNNNNNNCCCTTGCTTATTACACAT TCAGGGAAGTCTAGCACCAAGGACAGTNTTAAACAACATTACAANTTTNTAGAAAAGTTATTACTTA AAACATCTGTGTGACCTACATCAAGAGAAAANTCAAGGATTTGCAAAAAGGGGG
WI-9438	77 A G ---	---	---	AATAACATGTTATGAACAAGCTGGTTACAAGTAGTAGTACCTTAATTTTGATAAAAAAT TAAAAAGCAT[A/G]AACATGCATATAAAAAATTAGATTATGTACAAAATACCAACAGTATTACTTC TGCTCAGTAATTAATAATCTCCCTTGTTTGTCTTTTAAAAACATTATTTCTGAAAAAAA ATCAGAAAACATGATCGTGGAGAGATTATT
WI-9439b	101 C T ---	---	---	ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAATCCAGTCTGTGAGCTCAGTACCTGTTC/TJGTGCACACTGTACCATCTCAGTCCACTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCGAGGGTCTGCGAGTTAATACCTTGAGATAGTCTA CAGTTTTCATAGTTGTGTGAGCTAGAAAACCTGTACCTGTAAACAAAG
WI-9439a	76 C T ---	---	---	ACAGAAATTGACCTTTATTTGTGTACTAAAGCCTGTTTAACTTTTGATACAAAGTAACATTTTAGTA CAGAAATC/TJCCAGTCTGTGAGCTCAGTACCTGTGTGTGCACACTGTACCATCTCAGTCCACTCT GCCTGTAACCTTAGAAAACAGCCCTACCCCGAGGGTCTGCGAGTTAATACCTTGAGATAGTCTA CAGTTTTCATAGTTGTGTGAGCTAGAAAACCTGTACCTGTAAACAAAG
WI-9446b	75 T C ---	---	---	GAAGGCTTGATTAAAGGAGGNTTTATTGTATGTNAACCTTACCATTCCATAGACTATAAAGANCATT TAAAAAAAT/CJCCCTCTAAAGNGACACATGCCCCCAAATGACCANGNCATAAGCAACCTTTTAAAT TACTCATCTTTCATATGTGTGTTGTGTCCTACTNTTATCACTGTGCTCTTGTGCTTGTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATTGT

WI-9446	75 T C ---			GAAGGCTTGATTAAGGAGGNNTTATTGATGTNAACCTACCATCCATAGACTATAAAGANCATTA TAAAAAAAT/CJCCTCTAAGNGACACATGCCCAATGACCCANGNCATAAGCAACCTTTTAAAT TACTCATCTTTTCATATGTGTGTTGTGNCCTACTNNTATCACTGTGCTCTGTCTTTTGCTACCTA TGNGAACTGCACACTATCTGTGGCAATATTGT
WI-9497b	185 A ---			ATTAAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTCTAGATTCAGGCTTTCTTCTAGATGTAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAGTATGTTAATGTCACCTT GGAATTCTACATGGAAAGCCCAACAAATAACTAAACTTGACTAATGAAG
WI-9497	185 A ---			ATTAAATGTCAAGGTTTCATGTTTACATTTCTTATATCAAGTACAATGGTATATATACTTTTTTT GAGATAATTATTCTAGATTCAGGCTTTCTTCTAGATGTAGTNCCTAAAGCTTATAGTTTACATTGA TATCTAGACATATATCTTAAACAGTCTCCAAATTTNCTTTAATTAATCAAGTATGTTAATGTCACCTT GGAATTCTACATGGAAAGCCCAACAAATAACTAAACTTGACTAATGAAG
WI-9523b	193 C A ---			GTGAAAAGTTTCTATTCTATCCATCATAATAGATTGTGCTAAGGATCATTTTGGAGAATGTG CAGCATTGAGAGTTGTATCTCATCATGCACTCAGCAGCATTTTATCTAAAGTACGTGCACA GACTCAGACAATTACAACTATTTTCAGCCATGATCTATGGTGATTTTCCACACATTTGTA/C/AJAGTG AAAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCAGACTGCATGCACATATAT
WI-9523a	47 G A ---			GTGAAAAGTTTCTATTCTATCCATCATAATAGATTGTGCTAAG/C/AJATCATTTTGGAGAAT GTGCAGCATTGAGAGTTGTATCTCATCATGCACTCAGCAGCATTTTATCTAAAGTACGTGCA CAGACTCAGACAATTACAACTATTTTCAGCCATGATCTATGGTGATTTTCCACACATTTGACAGTGA AAGCTCTTCAGCTTGGAAACAACCTTGTCAGGCAGACTGCATGCACATATAT
WI-9554	202 T C ---			AAAAACAAGTTTTCATACATCACAAAACCTTCCATTATAACACAGAAGTGATTATTACCAGAC AAGCATCAGTGATGTATCTGCTTTNCTAGTTGTTATTGTACAAATGCTGTAGATAATGCAGCCCATG CAATACACCCAAAGAACACTAGAGTCTACACCCAAAGTACAATATGATAAAGCAGCCCTCTGCAAGTG GTT/CJGCTGGATACCACTAAGAAAGTCTACTGCAGCCATGTTGGTTATGATTTT
WI-9555	97 G A ---			CCAAAAGCCAAACCATTCATATGTATGGATTTCATAAACATTTATTGATCCTTTTGGGTAAGTAT AAATACCTTTACATGGCTAACCTTCTAAC/C/A)CTTGAAAATCAATTTCAAGGGACTCTTTAATCA GTTAAATAATCTGCTTTAGAAGGCACAAATGATCATACTTCAGATTAAATACAGGTAAGTATTCAG GGNTAAATGGTACAAAAGGCTGTAACCTTTTNCCTTCACATTGATCACA
WI-9625b	172 A T ---			TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAATCTGCAAGTAAATCAATCATTTT TAAAGCAATAGCTACCATATATTTGTATCTNCTCCTTGGGAAAACCTTTGGAAAAAACAACGCACA TAAGTATCAATACTGAGGTTGTGGACAAGTTACTTCTTATGTTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAACAACACTGACAAATCTTTTC



WI-9625	172 A T ---	---	TTGAACATTTAATGAATGACAAAGACATAACATCCTCTGAAAAATCTGCAAGTAAATCAATCATTTT TAAACAATAGCTACCATATATTGTATCTNCTCCTGGGAAAAACCTTTGGAAAAAAACACGACACA TAAGTATCATAACTGAGGGTTGTGGACAAAGTTACTTCTTATTTACCAATTTTATATTGACATAA AGTAGCACAGACTAGTTATTTCATTTAAAAAACACACTGACAAATCTTTTC
WI-9647	144 C T ---	---	TTTTCTGAGATTCAAAGAGCTACATTTTGGTTAGTGTATGCTACTATACCTTTTTCATCCTTTTCA ACATCTTTTGTACATTTTAGGTGATGCTCTTGTAAACAGTGTATTGCTAGACCTAAAAATCCAAAGCT TACAACTTC/TGTCCCTTACCTGATACATTTATTCATTTACTTTTCACTTTGGATTTTAAAAATGTTA ACTTAATACGTCTCTTCAGATGTCCTGCTTTTATGTTAATTGTTT
WI-9676n	114 A G ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTGTTTGTTT
WI-9676m	184 G T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTGTTTGTTT
WI-9676l	84 A C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTGTTTGTTT
WI-9676k	202 C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA C/TTCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTGTTTGTTT
WI-9676j	92 C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCCTGCC CCCATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTGTTTGTTT
WI-9676i	173 T C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCATATGGCAAAGATGAAGAAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGTACGGTCTTTATAATGCAGAGCAAGATGTGGCTTCTCCTGCC ATTTACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGGAACTCTATGCATTGTTTGTTT

WI-9676h	134	C A ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCCQ C/AJATTTCAOCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676g	202	C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCCQ ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGAGG C/TJCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676f	184	G T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCCQ ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676e	173	T C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCCQ ATTCACCTCAAGGCATCTTCAGCAACCCACATGGCTTTCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676d	134	C A ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCCCCQ C/AJATTTCAOCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTG AGGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676c	114	A G ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCAOCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676b	92	C T ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCAOCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT
WI-9676a	84	A C ---	---	GGCCACTGTCCAAAGTCTGTACAGTCTCCCATATGGCAAAGATGAAGAAATTGGCAATCTTTTAA GGGTACCAAGGNTCTGAGTTTGACGGTCTTTATAATGCAGAGCAAGATGTGGCTTTCCTGCC CCCATTTCAOCTCAAGGCATCTTCAGCAACCCACATGGCTTCCCTCTGTGCGCATGAAATAACTTGA GGCCAGGGTCTCTCAGCTTTAAAGCCTTGAATCCTATGCATTGTTGTTT

WI-9738b	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACCTCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACACAGTAATGACTCCACATTTTCCCTTT GAGTCAACAAAGACTCTGCTTGTGCACCTTGCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCACATGTCTGTATTGCTGTCC
WI-9738	40	C A ---	---	TGGACCAACACAGACAGATGATTCCTGGTGCCTGTGTA[C/A]ATTACAACCTCATTGATCACATGC AGCAACATCAACATCTCAAGGAGTCCATTGTTCAAACACACAGTAATGACTCCACATTTTCCCTTT GAGTCAACAAAGACTCTGCTTGTGCACCTTGCTGGAGCGGGTGGTTTTCACATATGTGAGTATCTA TCTTTTATTCTGTCCCTTATGTTGGTGGCACATGTCTGTATTGCTGTCC
WI-9756	47	A -- ---	---	ACTGAAATGTAAATGGCCAAGGCACCCAGGACCTTAAAAATCATAAGAAGTTAATCTGTGGGAAA GAGTAACACAAAGCATCTAAACAAGAGCAGGATGTGATGTAATGTGTCCCTTATCAGCTTTAGTC AGTAAGATAAGAAAGCCCTGGTGAGTATCCACTCCACAACACACAGATATACACTTTTGGAAAG ATTCCACTTAACCACCTTGATTCTTCACTTTTATGATTTAAACTCTCCGTGG
WI-9758	135	A G ---	---	GATGTCCCTTAAGGATTTGCATTGGTTAATGGGCAGACTGGTGCAAAAGAGGCTGAATTGAATAAT TAGGAAACTGGGAGAAATCAATTCAAAGAAGAAATCTTGTTCGCAAGGTCAATTTTATATACTATT A[A/G]TAAATAACTCTGGTAGGTTCTATAGCAATGCTAAGTAAAGTAACCGCTGGTTTCTAAATT ATTACG
WI-9778	127	G A ---	---	ATTTAAATCCAGGCAGCGGGGAAATGGATACCTTTTCATATGTCTGTACCCAACTATAAAGCTTTTG GTTCTCATGCACCATTTTCATTTTGCTTCTCACTCCAGTACCAGTATTTTACCAATTTG[A]CTCTC ATAATTGACTTTGCTACTGGAAGAACTCTTGAATGTTGGAATTTCTCTATTACACACTTTTGCCTCA AAGATGTGTCAGTCAGGACTAAAGGCAATAGTCTCAGGGCAGACAGCC
WI-9832	116	C A ---	---	TCTCCCTTTGCCCTCCTCATGCCACTCCCTCAGCTGCACAGAGCGTTTCTCCAGTGTAGTCTGGT CCATCTGCATCAAAATCACCTGCAGGACTTGTGACAAATGCAGTTT[C/A]TGGATCCACCCAGGA CTCAAAAACCTAGGAATTGGGAGAAGAGGACCTGGAATCGGTGTTGCTAGCAAGCCCCCAGGTGG TTTGTAAAGTGACTAAAGTTTGAGGACCAGACATGGAAGTTGGCTTTGGC
WI-9841	101	A G ---	---	TGGAAAATAGCTTTTATCAATCTCTGATATGCTACATATGTCATGGAGAAATGCAGAAATGGCATGA TATGAAATTCATTTTGAATGAATAAATATAC[A/G]TGTGTATGTATATATACTTATTAACTT AGGATTATACACACAATAAAACGCTGTGAAGGATAAACTAAGGTTCTATCAGTGGGAAATGAGA TTGAAAGAGGGGATGTGTTACTTGATATGCTGTTG
WI-9880c	222	G A ---	---	GAACTAACACCTTTCTTGCATGGATTTTCTTGATTATTGGCAGTTAACAATAAATGTTATTAGATC ACTGGTCTTCTGTGGGTTGAGTTTTTATGATATCTCTCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTCTACATCCTTGGACTATATAAGATCCTCTTTAAATATATTTTATATAAGCACATGAA AATGGAATGAAATAATGA[G/A]TTGACATAGGAATTACCTACATATTTTG



WI-9880b	157	C A ---	---	GAACAAACACCTTCTTGCGATGGATTTTCTTGATTATTGGCAGTTAACATAAAATGTTATTAGATC ACTGGTCTTCTGTGTGGGTTGAGTTTTTATGATATCTCCTGTAGACCCATAAGGGAGGCTGTGA GTTGTTTTCTACATCCTTGGA/C/A/TATATAAGATCCTCTTTTAAATTTATATTTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-9880a	108	C T ---	---	GAACAAACACCTTCTTGCGATGGATTTTCTTGATTATTGGCAGTTAACATAAAATGTTATTAGATC ACTGGTCTTCTGTGTGGGTTGAGTTTTTATGATATCT/C/TCTGTAGACCCATAAGGGAGGCTG TGAGTTGTTTTCTACATCCTTGAGCTATATAAGATCCTCTTTTAAATTTATATTTTATATAAGCACAT GAAATGGAATGAAATAATGAGTTGACATAGGAATTACCTACATATTTTG
WI-10183	127	C T ---	---	ACACTGCAGGCACTCCAAATCCTNACAGACATATGCACCTTCGGAATCAACTCAGGCATGCACAGCAT CCCTGTGCTGGAGTTTATTTTAAAAACAACGCCAGTTATCACAGTTTCTNTTTTGT/C/T]CACC ATTTTCCATAACAAAAGAAGCTACACAAAATTNGGGGGAGANACTCTCTTTGGAGACTGACACATT TGCAGAGGGTCATGAATAATGATTCCAAA
FB25G10b	109	A G ---	---	TCCCTCAATGACAGATGAACATAAATTTCTCTTGGGTAAGAAATACCTTATGTCCATTGTGATTAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAA/A/GT]GATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAAGAACCTATTTTGGATATCC CGGAC
FB25G10	109	A G ---	---	TCCCTCAATGACAGATGAACATAAATTTCTCTTGGGTAAGAAATACCTTATGTCCATTGTGATTAA AAGTCAGATTCAAGACACTGCTTTATGTACAAGAAATGGAA/A/GT]GATTTTAGATCCTCCCCCAG TGACAAAGTAACTGAACCTGACCATAATTTATACATAAAATGGAATGTAAAGAACCTATTTTGGATATCC CGGAC
IB3071	102	C A ---	---	ACAACGCTGAACCTCCATAACAGTCAATGGTACAGTCAACATCACATGTACAGAACACACAATTTA GATGAACGTGAATTAAGNTAAATAAAATAAAATC/A]CAATTTTCAGNAAACAAAATCAAAAC ATTAAGNTCCCTGNNATATTCTTAACCCCTAATGAGATTTCACTGGNCTCAAGTCATTTTGTAGTGA GGCATTCACAATATGACCCCTATTAAACCAGTCTAGGGATTCTG
NIB551	161	C T ---	---	CGTCCCTTTCCTTTTGAGATTGCAATTAAGTAGATAATATGAGAGAACTGACAAATGGGTTGTCCC TACTGAGCTTGGGCCAGGTGTGTACTTAGGAACCCCAATCCACCAGAGAGACTCATCTATGTTA ACACTAAGGATGCCCTGGAGGAGGT/C/]T]TGACCACATACATCGGCCATTGGTTGATTTCAGCTTT GCAAGCAGCGTAGTGAGAAACCAAAAGCTTGTCC
S72904	51	G T ---	---	AGCATAGAAAGTGATTTATATTTTAAATGGTTTCAAGTGAAGTTCCTTTG/]AATTTGTGAGTTC ATTCCTGGAAATCTTTTGAGTTAAATAAGGATCCTAGGACAGCACCTCGAACTACAGGCCCTAAA GAGAAATTGCCTCAAAACCACAAGTGCTGTAACTTCTCCTCCCTTCTGTCAATGGTTGTCTTTAAATA TTGCAAAAGTCTGATGCTAAACAGTATTTGGAGTGTTCAGTGTCTGTA

UTR-00481	115	CT	---	TATCTTTTATCCTGGGCCACAGTTCTTGATTAATTCCTCTTGTTAAAGACTGAATTTGTAACCCATTGATATAATGGCAGTACTTTAGGACACACACAAACACAGAGCTTACACCTTTTGATATGTAAGCTTGACCTAAAGTCAAGGGACCTGTGTAGCATTTTCAGATTGAGC
ESTC1	33	---	---	CCCTGTAGCAGTCTTCAGCCTCCTCTACCCCTACNAGATCTGGAGCAACAGCTAGGAAA
ESTC102	37	---	---	GCTACTACACGGCTGCTTCGTTTGGACAAAATAACNAGGAGGCATCCACGGGATTAGTTA
ESTC103	21	---	---	GCCATCAAAATTTCTTCACANTCAATACTGTTGAACACACAGATAACACATCTTCTTGCTCATCCC ACTTGAA
ESTC107	20	---	---	TGCTGGCTCACTTCTCACANGCTGTATTACCTTTTCAGAGCTGAGTGAGGCTGTGCT
ESTC109	35	---	---	AAACCAGGAAGGCCCTGCCCGCAGAGGCACATGNACAGGGCAGTGACAGTGACC
ESTC110	23	---	---	AACTCACAACAGAAAAGAGGANAACACTCAGAAATGTGATTACAGATTAGGCA
ESTC113	37	---	---	AAGGACACAGTGTGCTGACAAGGTGACACTGAACANACAGTTTTCTTTAATTGTAAAGCGGG CATCG
ESTC117	24	---	---	AATTGGCTCTTCTCCACATGATACNTAAGTTCAAGGTCCAAAGTTCTCTATCACAATTTACAAAAGC CTCCA
ESTC119	24	---	---	TGTCAAGCAGATCTTGAGGGTTATNGTTAAGCCTGATAACAGCCTCTTT
ESTC122	34	---	---	GACAATAAACAGCTAAGCTACTGACATAAAATATNCAATAAATTTATGAGATATAAGGTACAGATG AGAAAAATCTGAAA
ESTC123	21	---	---	GAAGCCAGTATGTTGTGGCAANATTCGAGAAAACACACTGAAAAA
ESTC128	42	---	---	GCAGAGGCATCAGATAAGGCCTCAGAAAAGCCAGGCCATCATNTCCATGGACCGGCTGGCTCAA TGTTGGAACCTGG
ESTC129	20	---	---	AGTCACCATGCCAGCCTAGNATGAGTTTAGTAAGATTGGTTATGCTGGGAG
ESTC13	46	---	---	GTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAGNAGCAGGTGCCGAGGGTCTGGA TCAGAAA
ESTC130	49	---	---	GCCTGCTCACAAGGTAGACAAAACATAAATCTTCAGGAAAATGAAACANGAGAAGCTGAAACAAT CTACACCTGAATG

ESTC132	30	---	---	---	GGTAAAGTCTAAATTACTGCCTTAGCAAACNCTATGTTGTCAGGTTTTCTGCTGCA
ESTC137	21	---	---	---	CCAGTTTGGCTTCTGTCTCCANAGTCTCTCTCCATGTGGCAAACA
ESTC139	45	---	---	---	AGGAGCACAGCCTAAGGACATGAAGGTGAGAGTTTCTCAGAGAGNGGGCTGGTCCCTGAGCTAG GAGGAGG
ESTC14	20	---	---	---	CCATTGTGTCACAGGAAGNAGAGGAGGCCACGTTCTTACTAGTTCCCTTGCCATGGTTTAGAAAGC TTGCCCTGGTG
ESTC142	72	---	---	---	CCTAGGCTCATAACAATACAGTCTCAATACAAAGACGTAATAATCTATTTTATTCATTTTAAATC AAAGANACCATTCCATTTCCTAACAAACA
ESTC143	29	---	---	---	GTTTACGAAAGTACTGAAATGCTATTANTAGCTGAATTTGIGATTTCCTTTIG
ESTC144	26	---	---	---	AAATCCATATTTTCTTGACATGAGGTCCTTTTACGAGCATTTCCGG
ESTC146	20	---	---	---	CATGTCCAGGATAAGGAGCANACACGAGGATTTATACCGTGGCAGCG
ESTC148	42	---	---	---	TCTTTGGTTGTCTACACAGACACTTAAGTACTGTATCGCTGTATGCAGCGCCTGTGGAGGCCCTG GGGTGGCTGGCCTGTGTCTGAG
ESTC149	28	---	---	---	TCAGTTCATTTATTGCTTTAAGAGTTANATACCATGAGACACACAGTTCTGG
ESTC15	28	---	---	---	GGATTGTAATATGCCAGCTTTGTAAAGNCATTAAAGCAGAGTTTCTTCAGTGATCTT
ESTC150	20	---	---	---	CCAGGAAACAAAGCACACANACTTATAGAATACTTTGGTTTAAAAATTATTCAATAATCAATATT AAACCTGATGTTTAAAGAACCTAATGAGA
ESTC151	49	---	---	---	GAAGCTAAGGCCCAATTTTCTTTTAAATACAAATCTACTGGTGCTNAAACTCAGAGCTTAGGA AACACAGCC
ESTC155	37	---	---	---	TTTTTAATTGACAACTCAATCTCTACATACAGTNTTGCACGAATTATAAGTGGATCAACAATT ATATTATTGATACAACTCATGAGCATTTACA
ESTC156	32	---	---	---	GCAGCATTTGTGACAGAGAGCGCAAAACAAANCCTGGCTGCCCTGGGATGGAGCGGGGGCCCTCA CCACCACTGCAT
ESTC158	35	---	---	---	ACCAAGCCCTGGGATTACTGTCTTGATGACTACANGGCTTTGCACAGTCTGAGATGCTTCAGTGTGC AA
ESTC159	31	---	---	---	AGCTGGCAAGAGACTTCCTGAGGCACATCAGNTACGTTGGTCAATTTAGGGCACGGTCTGTTCTGCA GCTTTGAAAGG



ESTC16	23	---	---	---	---	CACTGAATGCTCTGCCATGAGCCNCAAGCAGCAGTGATCATCACCACAAGGACAGGTT TTCTAGCATTGCTGTGCAGTGGGGCCTGAGCTGGGNGCAGTGGCAGTGTCAGTGGGCCGTTTG GGACTGGGTTGA
ESTC160	38	---	---	---	---	
ESTC162	36	---	---	---	---	CTCTCGTCCGTTTGCAAGTTGCTGTTTGTTCAGNTACACAGTCAGAGCTCCACAG TCATTCTCCATAGAATATTGGTTTGTAAACANCGAATACAATCCAATATATAACATTAAACAATCC GATACATACCA
ESTC164	31	---	---	---	---	
ESTC169	22	---	---	---	---	GTCTCTGTGTGCAGGGAATCANTTTGCTGGATTAGAGGAAGGTGCCGCTGTCTTCCATGACTT
ESTC176	23	---	---	---	---	CACCTCCTCCCTGAGCTACCCANGTAGTGTCTGGGAGCTGGCA TGGGTGGCTCTTTAAATACCTTCCATTATATTTCAAATTTTNCCTTATTCTATTAATAACCTTTTAT TCCTTTTATCCCATAAAAGGCAACCAA
ESTC177	42	---	---	---	---	TCAGACACTGGCGACATCAGCATTGTCTCNTGTACAGCTCCCTTCCCTGCAGGGCGCCCTGGGAGAC AACTGGACAAGA
ESTC18	29	---	---	---	---	TAGGGATTCCAAAGTTGCCCTGNTTAAATATAATACATATTACAAAAATTACACAGCTCATGCATAC CA
ESTC181	21	---	---	---	---	GCTTGACTAGCGAGGCTACATCACAAATTTATAAAGTGCCAGATNAGTGCTAATTGTCATTGAGCTTG ATTTTTCACCTCA
ESTC186	43	---	---	---	---	
ESTC187	24	---	---	---	---	ACCATGATTGCCCTCACACAAGCATNATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGGCTGG TCTATTAAACAGGGTTATGTACACACCNTGTCAACCTCAACCTCAAAACAGATGATACATCATTGTCTTCCAT CTTGC
ESTC188	25	---	---	---	---	
ESTC189	27	---	---	---	---	AAAGTACAATCCAGTATATGCAGAAAGNTACTCAGCATCACACTCGTGATCA TCCTCAAATACCACCTTTCCCTAACTTATCAGTCTAGTAAGCNTTTCAAAGGAGGAAATGGGTTAC CTTTCAGGGG
ESTC196	42	---	---	---	---	
ESTC197	26	---	---	---	---	ATCTCCAGTGTCTGCTGCTCCTCCNGCAAAGTCTCCACAAGCACA AAGATTAGGACAGACCGCGTATAGTAAGCTCTGNGGAACTCCCAAGAACTAGAGGGGCTGTGGGAA CGCTGCTTAGATC
ESTC20	33	---	---	---	---	TTTGGTGAAATCCCAATATATGAGTTTAAAAAAAATCATTANCATCATTAACAGTACTTTAAAT CAATTACTCCTTTTGGCTGCAACAG
ESTC200	44	---	---	---	---	

ESTC201	35	---	---	---	TCTTACTGGGTAGTTAGCAAACATTTTTAAANCCACATCCAACAGATTGGTT
ESTC202	22	---	---	---	CTGCTGGAGGGAGGACAGACGNCAGGGGCTGGTGGCCGCCAGAAAGGCTGGCGTGATGTT CGAGATGAGCC
ESTC203	27	---	---	---	ACACTTAACAGGTTAAATATCCAAATNAAATTTACTGCAACTTTTGTAGAATTTTATTGTGCTAC AAGACACGTTGCA
ESTC208	43	---	---	---	TATAGCCCATCGCTCTCAGTTATTAGAATCTGAGAGGGATANAGCAATACTATTGTTTAAAGC CTAAGAGTGAAA
ESTC210	29	---	---	---	GATGAAGTGGCTTCCTTGGCGAAGGATNAAGAGTGAGTGACGGTGACCTGTG
ESTC212	27	---	---	---	GGGTAACCTGATGAGGAAGCTCTAGTGNAGAAATTCAGGACGCGTCTTCAGAGCAGAGGGCTTGGT TCAAGTC
ESTC214	21	---	---	---	CTCCAGAGTCCCTCCTCCTCANACCAGGGGCGAGGGAGTTAGGGAAT
ESTC216	49	---	---	---	TGGCAAGAAATTTATTACACTAACAAATTAATTAATCACAGGTATTNTTAGATTGGTCAGAAAA CAAAGACCA
ESTC217	28	---	---	---	TTTGTGAGTAATGAGCAATACACTGANTGGAAATCTGCATGATTAATAACATTAAACAGTTTCAT AACACACCCCA
ESTC219	32	---	---	---	GTACACATCCTGGGGTGAGCACACAGCAAANGGGTGGACGTGCAGAGAGGTATAGGGTAAAG GCAAAGGAAGC
ESTC22	41	---	---	---	TCATTGAAGAAATATGGGTTTATTCTTATTCTAATTGNGAGAATGCTTAATGTCACAGGCTACA TAAGGGCC
ESTC223	27	---	---	---	CTTCTGAAGCCCAAGAGAGGGGCAGAANGTAGTCTTGATTTAAAAACAGAAAGGGAGGAGGA
ESTC224	37	---	---	---	CGAAGGTAGATTCCCTCACATATTACAAAATACACANAAACACACACACACACACACA
ESTC225	20	---	---	---	TGCACTGTTACTCCCCAGACNGAGAGCTTACATACCATATAGAAGAGCATAGTGCTTCAGAAGGA ATGTGTAGGATCG
ESTC23	27	---	---	---	TTCTACTTTATTTCATATTCCCACCACNATAACGACTCCTTTAATTAACTAAAACCATACAGGGT TCCTGAAAGGG
ESTC230	43	---	---	---	GCTTCCTCCCGAATTTGAAAGACATATTGGCTGACCTGATACNTAAGGAGCAGGCCAGAAATTAAGA
ESTC231	24	---	---	---	CAAAGGGTAGTCATATTCCCCANCAACAGCATGATAAATAATTC AAC

ESTC28	23	---	---	---	GAAGAGCTGGGCACGCATCTGACNTTTTCTCTATTCCTATAAAATAAGGAAGCAGAAATCTGC
ESTC3	20	---	---	---	CAGACATGACCTACCGTCCCGCCCTCAATTCATATTTATTTCTTGAGCCGCTTGTCAGGTTTGATTCGCACACTCC
ESTC31	32	---	---	---	ACAGCCCCACAGAACTATTGTAAACAATAATNTCAGTCGGTGATCATTTGTAATATACATAACAAGCAATTTCTCTCAGA
ESTC33	25	---	---	---	AGCACTTCCAGCTCCTTGACGTTGTGNGGACCAGGGAACCTCCGGAA
ESTC39	26	---	---	---	AAGGAAAGGGAACCCACCTGGGCTTNGGTCACAGAACTCAGAGCCTGGGCATTA
ESTC4	23	---	---	---	CCACTGAATCACACAACATGGACNAATCTCAATCATTTATGCTGATGGAAAGAAACCATT
ESTC40	22	---	---	---	GGCATGCTAGACAGAGGCATTANTTTGAAGATCTTTTAAATAATTTTGACTTGTTCCTCCCTTCAC
ESTC45	37	---	---	---	TTTGGAGGTTTGTGCTGGAGTTTGTCTTTGTAACNCTCTCATCATCGAGGCTATATATTAACTGTCCGTGGTGAGCCCTGCGCTGCCATGGGCCAGGAGCCACTGGTGCGGANCCGGGCAGATGTTTACCCTGT
ESTC50	56	---	---	---	GTGCCCTGAAGATTAGCAGCAGCAGCAGCAGGTTGGCAGGAAGNAGTGGAGGGAAGGACACCAAGT
ESTC56	45	---	---	---	AAGTGGCCCTCCAGTCCNCTCTCTGGGCACAGATCCACCAGTCTGCTC
ESTC57	20	---	---	---	GAAACACAAAAGTGTGAGAAAATACTTCTCAAAATNGTTCAGACTTCAGGAAAATGATTTCCACATGGTAAGGCC
ESTC59	38	---	---	---	TCTGCAGCACTTCACTACCAATGAGCNTTAGCTACTTTTCAGAAATTGAAGGAGAAAATGCATTATGTGGACTGAACCG
ESTC6	27	---	---	---	AGTGATTTTGGCTAGGGTGGTTCTCATCTGTGAAATTCACAGCGCAATGACAGCANCCTCTCTCCCACCCACTCAAG
ESTC61	57	---	---	---	ACAGACACAGCATCACACCANAGGCCCCACGGGAGGGTGGGGAGACGACACTTTTCCCTGGGAAAGGCAGCTCTAATC
ESTC63	20	---	---	---	GAGAGGCTAGTCAGGAGGANACCCTCAAGTTTAAATCCCCACACTTACTTACTGCTCATCCGTCACCTTTCGCTAA
ESTC69	20	---	---	---	AGTTTCCCTAGAGCTGTGGGCCAGATAGCTGTCTGAGTTGCANGCACGATGGAGATTGGACACTG
ESTC7	45	---	---	---	G



ESTC72	37	---	---	---	GGGCTTCCAAATGGGTATTGGGGCCAGGAGGCTGGCNTTGGCGTGACGCCTAAAGTGTGAOC AACAAATTCACAGCTACAGGAAATCTAGAACAAATCAAAATATTATCATCANTTGGTTGAAAGTTG GAAGA
ESTC74	49	---	---	---	ATGACTTTOCTGTCCCATCGGAACCCAGAGTTTCCCCAGNGAGCCCTTCTATCTGCGGTTA
ESTC77	40	---	---	---	GGTCAGCACAGGGATAAGANCCCCACTCCGATGTCCCAGAGGGCAGCACTCCAG TTTCAGATGATGGGCTCTGAGATGNTCTCAGGCTGCATCAGCTGCTTCAGTCTCCAGAACAGAAA GAGCCTGAOCCA
ESTC81	20	---	---	---	CAAAATCAAATACACAGATCCAGATATGTGAACCATATATACATATATACANCCATTATTTAGAC TTTCACAAACCT
ESTC82	25	---	---	---	TTTAGCTGTATACCAAGTTTCCATAAANCTGTCTGTGGTTGGGAGGCTACAGCCTGACCACATTG TTTGC
ESTC83	53	---	---	---	ATTGCAAAGGAGTGGAACGTGNTCAAACAGAAATGGTGACAATGA
ESTC85	28	---	---	---	CTGGTCTCTCGTCTGGCATTCTGCTCCTCCTCNGGCCAGTGCTCCACCCAAAGTGCTTCCCCTGATGAT
ESTC89	22	---	---	---	CTCCCCTCCTCAGTTCACAGTGGAGACTANGGAGATTGAGGGCAGGATCC
ESTC90	33	---	---	---	GCACGTTCTTTGTTCTCCTCTTCCAGAAAGTTGNAGACGTCTATTAGTTTGATTATCTGTCG
ESTC93	29	---	---	---	AAATGACTTGACGAAGCTCATAGAAGATTAGCAGGTAGTAGAATAATGACTGCTGACTCTCTAATTCA GTGGATCTTCCCTGGCCACCGTTTGTATTGAGCTGCAATGCTTCTGACTGTTCTTCTCCAC[CT]GCCAG ATTCTTATCAATGATCTTTACCTAAGAAACAGCAAGAAAGATTCTGGCAAGCACACGATCTAGAGATAC ATCTTATTGGGATTTTCACAAATCAAAGAAAGAAAGGCTTAGCTG
DWU-100	127	CT	---	---	TTCCATCCTAGATATCTACTCAAATAATTGAGACAAGTGTCAAACAGAAAGACGCTTGTGCTGAA TGTTTCATGGC[AG]GCCCTATTACAGTAGCCAAACGATGAAACACCCCAAGCTATATATTACCA GATGAAAGGATAAACAAATGTGTGTCATCCATACAAATGGAGTATTACACAGCCATAAAAAGGAAT GAAGCAGTGATCCCTACTACACTGTGGAT
DWU-177	77	A	G	---	CAAAATACCTGGACTATCAACCTTGTGCTTAATCCCTGCAGCATTCAGGTTAATCCATCTAAGTGAC ATTTTGAATTCAGCGGTGCCACCCCAATCATGCCAGCTTCTGTGCATATGATGAGATATACATTT ATGCTGACCTTCCCTCAAGACTGATTTTTCATGTCTGGGACTTACAATATCTCAAGGAACAGCAATG TCAACAGGG[AC]TGGGAAACCAGCCCTATCTGAGTCTTGGCTCCCTCC
DWU-286	213	A	C	---	

DWU-252	94 A G ---	---	AGTATACAAACATTAAAGCTGTGGTCAAGGCTACAGATGTGCTGACAAGGCACCTTCATGTAAAGTGT CAGAAAGGAGCTACAAAACCTACCCTCA/GJTGAGCATGGTACTTGGCCTTTGGAGGAACAATCGGC TGCAATTGAAGATCCAGCTGCCTATTGATTTAAGCTTTCCCTGTTGAATGACAAAGTATGTGGTTTGTGA AT
DWU-330	85 C T ---	---	GAACATTCCTCTGCAGCACTTCACTACCAATGAGCATTAGCTACTTTTCAGAAATTGAAGGAGAA TGCAATTATGTGGACTGA/CJTCGACTTTTCTAAAGCTCTGAACAAGCTTTTCTTCCCTTTTGCAA CAAGACAAAGCAAAGCCACATTTTGCAATTAGACAGATGACGGCTGCTCGAAGAACAATGTCAGAAA CTCGATGAATGTGTTGATTGAGAAATTTTACTGACAGAAATGCAATCTCCCT
DWU-370	231 A G ---	---	GAAATGTTAATTGGGCAGGTGAAAGGGTACAGATGTGCTGTAGCAGACCTTTGGTTTAAAGAGAG AAGCATCATTTCCCAACAGGGCAACTGTAGAAGGCCAGCTGAAGAGTAAAGGAAAGGTCTGAGG ACTGAGCCTGTGGCTGGTGAAGGTGAATGTTGAGGGCCCTTCACTTCCATCACAAGAAAGTC ATTAGACGGTACCAATTCAGTGTCTGTTCTT/GJGCACTCTATTTCCCTCTGTGC
DWU-1537b	89 A G ---	---	CTCTTAACCTCAGTTCCTCATCTATAAGATAAGGGATTGAGTTGTGATCACATAGCTCAGGTAATC CAGGACCAGAAACCCAGGAGC/GJTGAGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAACACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
DWU-1537a	52 C T ---	---	CTCTTAACCTCAGTTCCTCATCTATAAGATAAGGGATTGAGTTGTGATCA/CJTAGCTCAGGTA ATCCAGGACCAGAAACCCAGGAGCATGGGACCTGATCCACAGCTAGAGGATGGGGACTCTGTAGCT ACAGCATTTTCTGAACACACACAGAAATCCAGTAAGCAGCACACACTGGCTGA
ESTD-ADAb	196 C G ---	---	ACCATCTTACTATGGCAGGTAAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTGAGTGGGGTC CCCAGCTCCAGCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCCCTTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCTCGGCACTGAGCTG/CJGAGA CCCGCAGACCAACTCTGAGCTTTCTGGGCTCTGAGTCTGTGCTC
ESTD-ADAb	184 G A ---	---	ACCATCTTACTATGGCAGGTAAAGTCCATACAGAAGAGCCCTCTCTCCCTGGGATTGAGTGGGGTC CCCAGCTCCAGCCAGAGGCCCTGGGAAATCCAGGGTCACTGTTCCCTTCTCTCTCCCTGTGGGAAT CAAGCCAGCTCCAGGCCAGAAAGTGGGACTGTGAGGACATGGAGGCTC/GJAGCACTGAGCTGCAGA CCCGCAGACCAACTCTGAGCTTTCTGGGCTCTGAGTCTGTGCTC
ESTD-ANT1	160 T C ---	---	TCTCCTGTCAATTCCTACTCCATTAGTTCAGGTCAGTGAAGAACTGGGGCAATTAAACCAAGTAATTCA TGGAATGCCCAACTGCGAAACAAGAGGGCCAGTGGAGCAGGAGTATTATGCTACGCGGTTACCTT TTTTATGGAGGACCGAACTGAGGCT/CJGAGCTCAGATGATCCTGT
EST10398 2b	168 A G ---	---	TGCCTGGGTGGCAAGGCTGCAACAAGAGGCAACCCAGGAGGCTTTTATGAAGCGGCCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTTACATTTGGGGCTTGACTTTCCACACGGAGAAG CATGTTTCTTCGGGCCAAGAGGTATCTACCA/GJATAGTGTCTATTAGGCATTG

EST10398	147	C T	---			TGCCTGGGTGGCAAGGCTGCAACAAGGAGCAACCAGGAGGCTTTTATGAAGGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGTTTACACATTTGGGGCTTGACTTTCCAACACGGAGAAG CATTGTTTCTTTC/TJGGGCCAAGAAGGTATCTACCAATAGTGTCTATTAGGCATTG
ESTD-C7	14	G C	---			ATATCGTGGCCTTA/G/CITACCTAGAGCTGGACATCCTGCTGGA
ESTD- D4S95	90	T C	---			CTTTCATGCACGATAGGCTTTCTCTACTAATCACAGAATTTTGAGAAGAGCAAAACAACCTTTCAAGG ATAATGGGGCAATCACCTTTCTTTT/CCTTCTTTAGAGTCTACCGG
ESTD- GPPK2L	38	G A	---			AGTCTTCATCTGGGTGTCCAGGTAGATCCCTTTCAACG/GA/CCGAGAACTGCTCGATATC
ESTD- HRASb	82	A G	---			CTGGGCTGCCCCGAGCAGCTGCTGTCACCTGGACGGCGGCCAGGCTCACTCTATAGTGGGTGG TATTCGTCCACAA/A/GTTCATCTGGATCAGCT
ESTD- HRASa	37	C T	---			CTGGGCTGCCCCGAGCAGCTGCTGGCACTGGACGG/C/TJGGCGCCAGGCTCACTCTATAGTGGG TCGTAATCGTCCACAAATGCATCTGGATCAGCT
ESTD- NRAMP	81	A G	---			GGAGGAGGAGGTGGGAGGGGTCTGTCTGCTCCAGGTCCACAGACAGAGAGGGCTCAGTG TATCCCCACCCCA/A/GTGTGGCGCTGGAGATGAAGAGGAGTTGATGCAGGT
ESTD-OTC	18	A G	---			GTGACCTTCTCAGCTTAA/A/G/AACTTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGC AGATCTGAAATTTAGGATAAAACAGAAAGGAGAGGTATGTAAACA
EST36751	36	C T	---			CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACT/C/TJGATTACTTTTCTATTCAAATCTCTGTA AAATTGAAATATGAACCTTAGTTTCTGATCTATGGTTTCAAGTTAAACAG
EST40562	109	A G	---			CACGTGGAAAGGAGCTATTTTGGAGGCTTTAAGAGTAAAGAACTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAAGTTTCACTGGATGCAATTAATAACAAAT/A/GTTTTACCTTTTGAATAATAA ATGAAGGATTTGACCTGCTTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTTTGAAACAATAACA GATGCTTCCCTGTAGCAGTTTTCAGCCTCCTCTAOCCTA
EST18288	121	C T	---			GCTCTATACCCCTGTGGTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGAGAA GATTGACAGGTTTCATGAGGCTGTGACAGGATGGAAGACTGGCTGCTCCCTGA/C/TJGGGAGCCAGT GTGGACAGCACCCCTGGCTTTCAACACCTACGTCCACTTCCAAGGTAAAGGCAAACTCTCTGCTGGCTC TGGCCCTAGGACTTAGTATOC
ESTD-AK- 168	31	C T	---			GGGAGTGACAGCTAGAGCACCAAGGGGGCT/C/TJACAGCTGTGTTCTCATGGAGGACAGGCTTCT GCTCATTCTGG
ESTD-ALB	180	A G	---			AATCCAGCACTTTAGGAGGCTGAGGAGGCATATCACAGAGGTGAGGATTTGAGACCAGTCTGA CCAACATGGTGAACCCCATCTCTACTATAAAATACAAAATTAGCCAGGCATGGTGGTGCATGCCCTGT AATCCAGGAGGCTGAGGAGGAGAAATCGCTTGAACCTGGGAGGCG/A/G/AGGTTGTGGTGAGCCGA GATGGCACCATTTGCACTCCAGCTGGGCAACAAGAGTAAACTCTGTCTTC



EST70523 3	182	G T ---			TTCCGCGAGCCCATCTTGGACCCCTGGTCCCTCAGGGCCACCCCGGCGACTCACCGCTCT CGCTCTCGGTAAACATCCGGCGGGCGCTCTTGAGCACATAGCCTGGACCGTTTCGGTATAGGAGG ACCGTGAGGCTTCTCTGTCGGGCTTGGCAGGGGCCAGCCCTGTCAGAGAGAGGGGTCCTGT GGTTGAGCTGAACACAGCTGTGGAGTGTCTCCACGTG
ESTD- APOA2	101	C T ---			CCAGGTGTTGTGGCAGTGCTGTATCCAGCTACTCGGGAGACTGAGGCATGAGATCTTTTGAC CGGGGAGCGGAGGTTGCAGTGAGCTGACATCGTCCTGCCACTGCCTCCAGCCTAGGTGACAGAGC AAGACTCC
EST58707 7	112	C T ---			CAGTGTATCTGGAAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATTCGAGAGAC[C/T]CTAGAAGATACACGAGAC CGAATGTATCAATGGACATTCAGCAGGAACCTTCAACGATACCTGTCTGTAGGCCAGGTTTATA GCACACTTGTACCTACATTTCTGATTGGTGGACTCTTGCTGCTAAGAACCTT
EST74167 6	137	C -- ---			AGACCATGAAGGAGTTGAAGGCTACAAATCGGAACCTGGAGGAACAACCTGACCCCGGTGGCGGAGG AGACGCGGGCACGGCTGTCCAAAGAGCTGCAGCGCGCGCAGGCCGCTGGCGGACATGGAGGA CGTGCGGGCGGCTGTGTGAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGGAGGAGC TGCGGGTGGCTCGCTCCACCTCGCAAGCTGGTAAGCGGCTCCTC
EST43211 8	132	C -- ---			CGCTGTGTGAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGGGGTGG CCTCGCTCCCACTGCGCAAGCTGCGTAAGCGGCTCTCTCGGATGCCGATGACCTGCAGAGCGCC TGCGAGTGTACAGGCGCGGGCGCGGAGGGCGCGAGCGGCTCAGCGCCATCGCGAGCGGCTG GGGCCCCCTGGTGAACAGGGCGCGGTGGCGGCCGCTGTTGGCTC
ESTD- ARSB	126	A -- ---			GGAAGAAATGGAGCCTGTGGAAAGGAGCGTCCGAGGGTGGCTTTGTGGCAAGCCCTTGCTGA AGCAGAAAGGCGGTGAAGAACCGGAGCTCATCCACATCTCTGACTGGCTGCCAACACTCATGAAGCT GGCCAGGGGACACACCAATGGCACAAGCCTCTGGATGGCTTCGACGTTGGAAACCATCAGTGAA GGAAGCCCATCCCCAGAAATTGAGCTGCTGCATAATATTGACCCAAAC
EST36770 4	144	C -- ---			TGTAGCCAAAGTCACCTGCATCATATTTGGCTGTGCGAGGCTTGCCAGTTTGCCAGCTATAATCC ATCGAAATGTAATTTTCATTGAGAACACCAATATTACAGTTTGTGCTTCCATTATGAGTCCCAAAT TCAACCTCCCGATAGGGCTGGGCTGACGAAATATAGTGGTTTCTGTTTCTTCTGATCAT TCTTACAAGTTACTCTTATTGGAAAGGCCCTAAAGAGGCTTATG
EST26021 1	137	A -- ---			TAATGTAAGCTCATCCACCAAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTTCGAAACCTGT CCATAAAGTAATTTGTGAAAGAGGAGCAAGAGAACATTCTCTGCGACACTTCACTACCAATGA GCATTAGCTACTTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAGCTTTCTTCTTTTGAACAAGACAAAGCAAGGCC
ESTD- BA511	29	A G ---			GGGCAACATAGTGAAACCCCATCTCTACA[AG]AAATACAAAAATTAGCCAGGTGTGTAGCAAG TGCCTGTAGTCCAGCTACTTGGAGGCTGAAGTGGGAGGATCCCTTAAGCCTGGAGGTGGAGGCTG CAGTGAGCCAAGATGGTGCCACTGCA





ESTD- CB22	119 C T ---			GGCAAGTTTTATTGATAGAGAGGAAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGGATGGACAGACAAATGGGCAGTGCCAACCCATAGGGCTGGGATACAAAAG ACAGGCAAGGAAGGGGTAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCT AGTAACATAATTGTGCTTCATTATGGTCTTCCCGGCTTCTCTCACACAC
ESTD- CB23	136 C ---			TAGAACCATCAAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTCAATTATGTOCTTTCCGGCTTCTCTCTCACACATACAGAGCCCTACAGGACCAGACAGCT CTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAAAACGTGTTCACCCCGA GGTCGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCCAAA
ESTD- CB24	145 A ---			ACCAGGACCAGACAGCTCTCAGAGCAACCTAGCCCCATTACCTCTTCCCTTCCAGAGGACCTGAA AAAGTGTCCACCCGAGGTGCTGTGTTGAGCCATCAGAAGCAGAGATCTCCACACCCAAAG GCCACACTGGTATGCTGGCCACAGGCTTCTACCCGACCACTGAGCTGGTGGTGAATGG GAAGGAGTGCACAGTGGGTGACGACAGACCCGAGCCCTCAAGGAG
ESTD- CB25	146 A G ---			GTTTTCTTCAGACTGTGGCTTCACTCCGGTAAGTGAGTCTCTCTTCTCTCTCTCTCTCTCTCTCT TCTGCTCTGAAACAGGCGATGGAGAAATCACGGACACAGGGCGTGAGGGAGGCGCAGACACCTG TGCACAGGTAGTCTACATGCTCTGTCTTGTCAAGAGAGTCTTACCAGCAAGGGTCTCTGTCTGCC ACCATCCTCTATGAGATCTTGTAGGGAAGGCCAOCCTTGTATGCCGTG
ESTD- CB27	125 C T ---			TTTTCTGTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTTGTTGGGCTGGTTGCATTTCAGGAGTGTCTGTGGAGTTCTGCTCATCTGACCTGACCTGTTCTC TGATTTAGGGAAGCAGCATTCCTTGGACATCTGAAAGTGACAGCCCTCTTCTCTCACCCCAATGCT GCTTCTCCTGTTTCATCCTGATGGAAGTCTCTCAACACCATTTCCATAOC
ESTD- D4S338	59 A T ---			TTTTCTGTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAATATGTA TTTTCTTAAACAATAAAGTTGAAAGTCCAAAATTACTCTTGATCCATGGACTGCAGAAATAAATGTTA TTTTAGCTGTGAGAAACAATACTAATCTTGCATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGTA TTGCCAATAAGCAGTAATAATTTGAGAGGAATCTTGTTCATGCACTAG
ESTD- CYP2D6	61 A G ---			CAGGCCAGCGTGGTCAGGTGTCACCATCCCGGACAGAAACAGGTACGCCACCACTATGCTAGTCA GGTCTCATATTGAAGCTGCTCTCAGGGTTCCCTTGGCTGAGCAGGGCGGAGACATACTCGG
ESTD- D11S1873	40 A C ---			AAAAAACAATTTAACACCTTTTCAATCATATACACCATAA/CJATTTCCATTTTTCACATAAGTCA GTTTGAGCTGAGTTTCCAAATTACTGCAATCTAAATGTCAATACTGATTAATGCAAGTTCAACAG ACAACCTTCCCAAGCATCTACGATCAGAAAGGTCAAAATATTACATACTGGATTAAATTATGCCCA TATCTGCATGTC
ESTD- D17S33b	169 C T ---			CATCCCCAAGCCCATCTCTAGCCACTGGCATTTTTTGGCCGCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGGCCCTACCCCTTGTAGTCCATGGAAAGGCTCTCTGGGGGGTG GGTTGTGTGGCTATGTTGGTGTGTGTAGTGTGGGGCTTGTGTTTCACTGTTGCACTATTGGCTT ATTGCAGATTGCTTGTCTTCCACCTGAGCGAGCCTC





ESTD- DRD1	154	C T ---	---	TCCCAGCCCTATCGGTATATTGGACTATGACACTGACGTCTCTCTGGAGAAGATCCAAACCCATCAC ACAAACGGTCAGCACCCAACTGAACCTCGCAGATGAATCCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGGC/TTCGCTATTAAGAACTAAGGTAC
ESTD- DRD2	144	C ---	---	TCTGCCCTTTGGTGAGGAGGCTGCCGGCAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCACCCGAGAGACCCGTACAGCCCATCCACCCAGCCACCCAGCTGACTCTCCCGACCCCG TCCCACACGGTCTCCACAGCACTCCGACAGCCCGCCCAACCCAGAGAAGATGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	109	C T ---	---	AAGACGATGCCAGGATGAGCGGCAGTAGGAGAGGGCATAGTAGCATGTGGCGGGCCTGGCTGG CACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTGAGGTGGC/TACTCAGCTGGCTCAGAGATGCC ATAGCCAGAGGGAGGTGCGTGATGCCAAGGGGCTTCCTGTGAGGAGA
ESTD- ERB82	93	C T ---	---	TCTTTCAGGATCCGATCTGCGCTGGTTGGCATGCGCTCGTAGGTGTCAGCGGCTCCACCAGCTGG GGTGAGGGGTGTGGTCAAGTGCT/TGGGGGCGGTGTCAGACCCACGCGGGCTGGGAGGACTTCA CCCCGCTCACTCCGTTCTCTGCAGCAGTCTCCGTCATCGTGTACT
ESTD- ETS2	43	A G ---	---	ACTCACAGTCTTTTAAAGTGAAATGGTCGAGAAAGAGGCACCA/GGGAAGCCGCTCCTGGCGCTG GCAGTCCGTGGACGGGATGGTTCTGGCTGTTGAGATTCTCAAAGGAGCGAGCATGTCGTGGACACA CACAGACTATTTTAGATTTCTTTTGCCCTTTTGCAACCAGGAACAGCAATGCAAAACTCTTTGAG AGGGTAGGAGGGTGGGAAGGAACAACCATGTCATTTCAGAAAGTTAGTTG
ESTD-F9	111	A G ---	---	AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTTGAGTTAATATTTGTGTAAGTATGATGTTTA/GTGTCAAACTTCATTTTTCCTCC ATAGGTATGTCCAATTTATCCAGCACAAATTTGTTAAACAAAAAC
EST68787 5	144	A ---	---	CTTCCTATGGGATTTGACTTTATTTCTCCATTTGCTTACCTTTTACAGGTGTTAATATAGTGAAGAAG GAAGCTTGACGCTCATGACAAATTTGAAGCTGACAATTACACAAGAAGGAATAAATTCACAGTCAA AGAATCAAGCACTTTTCGAACAATTGAAGTTGTTTGAAGTGGTGTCACCTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAAT
ESTD- GCDH	200	C G ---	---	CGCAGACCGGTGAGTGGGTGGGAGTGTGGAGGAAGGAGGGAAGGAGGAGGAGGTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTGACAGAGAAAGCGGGAGAACACAGAGCCAACTGGCTAA GTGTAAAGGAGCACTCTGTGTCGACCGTGTGTTCTGCTGCCCTGTTCAGCTGTCTGTCTGCCGAGTTC/ G/GACTCTGTCCCGGAAATTCGAGAGCT
ESTD-GCK	88	A G ---	---	GTTTTATGGATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGCTCACCATGAC AACCACAGGCCCTCTCAGGA/GGCACAGTAAGCCCTGGCAGGAGAAATCCCCACCCACACCTGGC TGGAGCAGGAATGCCAGCGCGCTGAGCCCGAGGAAGCAGGCTAGGATGTGAGAGACACAGTGC ACCTGCAGCCCTAATTACTCAAAGCTGTCCCGAGGTACAG



EST34088 2	62 A T ---			GTGGGGCAACAGTGGGAGAGAAGGGCCAGGGTATAAAGGGGCCACAGAGACCGGCTC[AT] AGGATCCCAAGGCCAACTCCCGAACCACTCAGGGTCTGTGGACAGCTCACCTAGCTGCAATGGCT ACAGGTAAG
ESTD- GNAT2	56 A G ---			GACCTGAGTACCTCCCTAGTGAGCAAGATGTGCTCCGATCCAGGGTCAAAACCAC[AG]GGCATCA TTGAAACCAAGTTTCCGTCAAGACTTGAATTTTCAGGTAAGTGATGGTTCCCTAGG
ESTD-HT2	154 G ---			GGGCTAAATTTCCGAGCAACTTTCATAGACTGTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTACAGTTTGTACAGAGAGAAATAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT5	149 C ---			AACACAAAGCCCCAGGAGAAATTGAACCTCGGACCCCTGGTTTACAAGACCAGTGCTCTAACCCCT GAGCTATGGAGCCCTCGTCTGTTGTTTCTGCTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCCGGCTACCGAATAGGATGTTAGCTTGAATAAATCCAGGATATTCTCTACAAATGAAA ACATTTTCGTGCTGTAAATCCCTCGAAAGGTTCT
EST37382 5	124 A G ---			CTGAGAAACAATTGGCAAAATAAGGAATTTGGCACTCCGACCCCTCTTCTCTCCCTTGGGA CTTTGAGTCAAAATTGGCCTGGACTTGAGTCCCTGAACCCAGCAAGAGAAAGAG[AG]CCCCAGA AATCACAGGTGGGCACGTGCGGTCTACCGCCATCTCCCTCTCACGGGAATTTTCAGGGTAAACT ACCCAGTGGAGCCCGCTCATTGCACGGTCTTGGCAGGAGGTGC[CT]CTGGGAGAGAGGAAGATG TTCCAGGGCACACATAGCTTAGTGGAGACTC
ESTD- IGHV4-6	120 C ---			TTTACTATTTCATGATACAGAAATTGTGGGAGTCACTATATTCCTATGAACAAAATTCAGATTT CAGTGTTAAGTAATGTTGCCCTACATTGTGTGAGTGACGGGCGAGTGGATCCGAGAGTGTGGTGGG TGCACGGACATAATGATTACAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACTGAAAGT ATGTAATACTTCACAAATACTAATAACGGAGTTGAATATAAACCCCA
ESTD-IL1A	110 A G ---			CAAAGTAAGCACCCCAATAATGTTAGCTATTACTATCATTATTATTATTATTTATTTTATTG AGATGGAGTCTGGCTCTGTCAACCCAGGCTGGAGTGAGTGCG[AG]CAATCTCGGCTCACTGCAAGCT CTGCCTCCTGGGTTTCATGCCATTCTCTGCTCAGCCTCCGAGTAGCTGGGAATACAGGCAACCCGCC ACTGTTCCCGGCTAATTTTGTATTTTAGTAGAGACGGAGTTACCCGT
ESTD-IL1B	99 A G ---			CCACTTACAGATGGATAAATGGGTACAATGAAGGCCAATAGCCCTCCCTGCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTTCTCTGCCTC[AG]GGAGCTCTCTGTCAATTGCAGG
EST74082	134 A T ---			TCCAGGTGGCTGGAACCCAGGCCAGCTCTGCAGCAGGAGGAGCTGGCTGGCTGTAAGCATG TGGGGTGAGCCAGGGGCCCAAGGCAGGCACTGGCTTCAGCCTGCCCTCAGCCCTGCTGTGTA TCCCAGATCACTGCTCTCTGCCATGGCCCTGTGGATGGCCTCTGCCCCCTGCTGGGCTGCTGGCC CTCTGGGGACCTGACCCAGCCGAGCCTTTGTGAACCAACACCTGTGCG



EST45311 0	151 C T ---				GCCCTCCTCTTCCAAATCTGTCCCTATAGTTTCCCTCTATTAGTGAACTACATGCATTCTTTTAGT GGATAGATGCACACAACACACAGCCATTATGGGAAGGATCCACGTGTGTGGCCATATTGTAAACA CATTTTCTGCAAAATC/TACCTCTTTTCATTAAACAGCCCTTATTCAATGGCCCTTTTCTTTTTCAGTA GTACATACACATCTGTGTCATTTGTTGAAT
EST65258 8	80 A G ---				TGCCCATCACGGCGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTCAACCAATTAACCAGAAAT CCAGTTATTTTCC/A/GJCCCTCAAAATGACAGCCATGGCCGGCGGTGCTTCTGGGGCTCGTCGGG GGGACAGCTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGT GAGGTTAGGTGCGTGTTCCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	26 A T ---				ATGCAGGATGAAGGTGGACAGGGAGG/A/TGAGGGGCCAACCTGTCAATCCAGGGCCTGCAGATGTGG CTGGACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	149 G T ---				ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATATTAGCATTTGTTTAGCATTAACCTAA TTTTTTCTGCTCCATGCAGACTGTAGCTTTTACCTTAATGCTTATTTAAATGACAGTGAAG TTTTTTTTCTCTG/TAAAGTGCCAGTATCCAGAGTTTGGTTTTTGAAGTACATGCAATGCCTGTGAA AAGAACTGAATACCTAAGATTCTGCTGCTGGGGTTTTGGTGCAATGCA
ESTD- KRT10b	183 C T ---				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCITTTTGGCAATATT AAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGIC/TJTGCTTTTAAATAGT CTCTGCCAGATACATCTCCCTATATAAGTTATAACCAATTTGATA
ESTD- KRT10a	133 A G ---				CCAAAGTTAAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCITTTTGGCAATATT AAGGAAGAAATGCATTTTAAAGTAACTGCTAAGGTTTTTCCATTAAACCACCTATTACTTCTAIA/ GJGAGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTC TCTGCCAGATACATCTCCCTATATAAGTTATAACCAATTTGATA
ESTD- KRT8b	231 C T ---				ACCTCACCCCTCCCTTAGCCGCTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGATT TGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGCTCAGGTTTACCA/C/TJGTCAACATTGACACA
ESTD- KRT8a	21 C T ---				ACCTCACCCCTCCCTTAGCC/C/TJGTGGGAAGCAGGAAATCTCTCTCCAAATCCATGAATACACATC GGATTGGACACCTTGAGAGTCTTAACAGCAGGGCCTGACATGAGACCTCAGACAGAACTTTCTAGAG TTTGCTAGAGGTCAAGGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCAT GGCTGCCTATCTCTCCGCTCAGGTTTACCACGTCAACATTGACACA
EST75099 6	82 C T ---				CACCTGTGTGTCTAGATCTCTCAGTGGCCGCTCTACTGGGTGACTCCAACTTCACTCCATCTCA AGCATCGATGTCAA/C/TJGGGGCAACCGGAAGACCATCTTGGAGGATGAAAAGAGGCTGGCCCAAC CCTCTCCTTGGCGCTCTTGAGGTGG

ESTD-LF79	142 A G ---	---	GGGTGATTTGAGGGCTCAGTTAATATTTCAAATTTGTAACCGTAGCAAACTGCATTGGTATTTAGA AAATAAAAAATTTCCAATATGTAGTGTGTATACCTGCCTCTGCCATGCAGCATCATAGCCTGT GGGAACCCAGGGAGGGCTTCCCTTACCACCCAGA
EST35878 9	142 A C ---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTTCCCAATCTTGTGGTTCCACCGATG GAACTGCCGGCAAATCCTGACACGTGTGCACCCAGGCTGTACCCAAATTAGTGAACATGGCTTCGAG AGAGTTGACACAGATTCCCTGGAAGACAGCAGCGGGATGGGGCAGGAGAGAGCTGCCCTGGATGA
ESTD-LMP2	35 C G ---	---	A TACACACTTTCCTTACCATTCACTGAAACGACTTCGCGCAAACTGGAGCCTTGTAGGAATGGAGT TGACCTTCCCAAAAGCCACTATGATAAGCTATTTGGTG
ESTD-LPL	113 C T ---	---	TGTCAGTGTCCCTAGGGGCACTCAOCCACTCCAGCTTCTTCAGCTCTGGCCTGTCTGCTGCTGCTGCA AGGGTTTGTCTTAATCTCAATCAATGTCTCTTCATCTTTAGTCAGCTGTGGGTTTGTGTTG TTCTTCTGTTTGTCTTAGTATCTGACTACTTTTAAATAAAGAGATGTATCTAAACAAAATAG AGATTGTTATCAGAAAGTTCACAACATTTATAAAATTTTTCACCTG TTGTCAGGAGTGTGCTGATGCTGCTGCCCTCCAGCTCTGTCCCTAGCTC/TGAACTTCAGGACAACGTGC
ESTD-MCC	45 C T ---	---	AG CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAAACAGCATGCATCCCGAA TCTCAGGAAGTCTGTCTTCCAGGGTTGGTCTAAGTTGCTGATTACCCT/TGGATTTTCTGACCG ATCTTCAACTGCTAGAGCATCTGGTTCCTGTTTAGCATGG
ESTD-METH	118 C T ---	---	ATTATCCAGATGAATTTACAAAACCTA/TGTTACCAGATCCACAGACTGATATGGCTGGT
ESTD-NF1	25 A G ---	---	AACATGGACTTGATATTGTACAAAATAAGTTTATTTCTAAAAAAGAAAAAGAGAAA AAATTTAAGGGTGTACTTATATCCACACTGCACACTGCCCTA/GGCCCAAACGTCTTATTGTGGT AGGATCAGCCCTCATTTTGTGCTTTGTGAACCTTTGTAGGGACGAGAAAGATCATTTGAAATCT GAGAAAACCTTCTTTAAACCTCACCTTTGTGGGGTTTGTGGAGAGGTTATCA
ESTD-NFKB1	107 A G ---	---	TGTCCCTAGGCCCCAGCCCTGTGCTCCCTGCCCTGTATCTTC/TAGTACTGCAAGAGAACACA GACAT
ESTD-NPPA	45 A G ---	---	GTGTTTCTTAATCTTCCAGGAACACAGTGACCATAATTTCTTCTGCAGGCATATAGAAATTTGGT GGGTTTCTTTATGTAGGGTGATATTGGATACTTTTGTGTTGTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTG C/TATTCCTGTGGTTTAAATAAAAT
ESTD-NRAS	202 C T ---	---	GCCACCACCCACCCAGCACACCTCCACCTCAGCCAGACAAGTTGTTGACACAGAGAGCCC TCAGGGCACAGAGAGAGTCTGGACACGTGGGGAGGTGTCAGCCGTGTATCATCGAGGGCGCGGG CACATGGCAGGGATGAGGGAAGACCAAGAGTCTGTGTTGGCCCCAAGTCTTAGACAGACAAAACC
ESTD-PAI1	100 A G ---	---	TAGACAATCACGTGGCTGGCT

ESTD-PAR	120 A	---	---	CTCTCAGGAACCAACAGTCTTCTTACCAACACGACTTATTGCTGTCGAGAGGTACAAACCCGTAGA ACTTCTTCTTAACGTAAATTTAGTTAAAGGAATCGAACTGGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTCATTAGCTCTGTGAGTGTTTCTTTCACCTTTTCTGTGTTCTAGAACGTTTCTTAG GACTGGCAGTTTAAGCTTTCACCTTAGGCTTCTGTATACCCATGCC
ESTD- Per/RDS	74 A	G	---	ACCTACAGAGCTGCTGGATGGTGTCACACCCGAGGAATCTGAGAGCGAGAGCAGGGCTGGCTG CTGGAGA/GGAGCGTGCCGGAGACCTGGAAGGCCT
EST68308	5	29 C	T	GGAAAGAGATTTAAGAAAGCTTGATTTGGA/C/TAAATCTGGTCTTTGAGTGTGGAAGATTGCTG TCTGCCCTGAGTTACACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAAT GGAGAAGTAGACTTTAAAGGTAAGAAAGTAGTATTTTTTA
EST54045	6	39 A	G	GGAAATTTAAATAATTTAAATACCTCCATTTTGCTT/A/GTCTTTTAGTGAAGATGATACCTGC AAAGACATGGCTAAAGTTATGATTTGTCATGTTGGCAATTTGTTTCTTACAAATCGGATGGGAAA TCTGTTAAGTAAGTACTGTTTGGCTTGGAAATGGATTTTAAATGTTGACTTTATCAT
ESTD- PXMP1	88 A	G	---	ATGAACATGGTCTTTAATTTATGATATGTTTGTATAGCTATCTTAAAGGGCTTCTTTTTTTTA ATGCAGAAAGAGGGGAAAA/A/GGAGCGAGCTGTGTGGACAAGGTGTTTTCTCAAGGCTCATAC AGATTCTGAAATCATGTGTCCTAGAACATTTGTAAAGAGGTAGTCTTATGAAATTATAATCTT
ESTD-RDS	127 A	---	---	CCCGAGGAATCTGAGAGCGAGAGCGAGGGCTGGCTGGAGAGAGCGTGCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAGCTGGCAAGGGCAACAGGTGGAAGCCGAGGCGCAGACGCGAGG CCAGGCCACAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCCGAACACTGAGAAATAGTGCACT CCAAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- s14544	94 G	T	---	TTGGGAAGTTAGAGCCTATATAAATTACGGAATTAATAAGGCAGGACACAGAGGCTTAATTGAAA TATCCCAAAGTTGAATGTCTCAGTTC/GTCTGTGTGGGTAGATGCAGGATTTATATGATCCGTTA ACCTCT
EST52908	0	45 A	C	ATCACAGGTCTCTGTCTGGCCATCATTTCTCTGGGAGAGATGG/C/TGGTGGTCTGCAAGCCCTT TGGCAATGTGAGATTTGATG
EST19590	55 C	T	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAAGAATGACATTGATGATGAAGATGTC/TGGCTCAG GATGCCGGAAATGAC
EST76136	39 C	T	---	TGAAGCTTCTGCCAGCTTGCAATTGTTTCTAGGAGAACCC/C/TGGGTACATACCTTTATCTATAGCCTT CCCCTAGGTCTT
ESTD- SPTB	176 C	T	---	TGAACACCCCTGTGTCCGGAGCCAGGTGTGTTTCTCTGGAGCCCTGAGGAGTTTGTGTGTGTG CAGTCCCCCGCGCACCTGCTGTTGAGCTGGACATACACCTTCACTCTTGGCCCGGAGAGAC ATTTACCCACCTGGCCATGTCCCTGGCCTGTTGTGCACA/C/TCCCTCTGTGAAGACCCCAACCCCTGC CTCCCCACCCAAAGCCAGTTTCTAGCAAGGGCAGGAC



ESTD-TAT	224 C	---	---	AAATGGTCAGGACCCCTGATCCACAAGAAGTGGTACCATTTTCATCAGGGCCATCAGTTTCATTAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTACAACTTTTCTCCAGTATGGATGGGATTATGATGGGGGG GAGAAGCAAAATTTAAATAGGACCCATGAGACACATCA
ESTD- THR	125 A C	---	---	TGGGCTTTCTCCGGCAGGTAGACTTCTTACTTGGCTGTGATTTCOAAGAGAAAGAGTCCCAAG CACAGAAACAGAAAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATC[AC]CTTCAT CCACTGGATTGGCCCAACAAGTCTGAGTCCAGGCCAGGACTCAACGGTCCCTGTAGATGGG TAGTGAAGTTTTCATCTCTGTCAGCTTCTGGATTCTTCTCCACCGCAACAAGAGAGTCTATGC CAAGGCAGAAAGCTGGTCTTCATGGGCAAAATCAATGTCTCTCCAGATTTC[GT]ATCCCCAA GCAGTGATCCATTGACACATAATAATGCATCCAGACAAGAGGTCATAAATAATTGATGTCGTTAAA CATGGGTGTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA
ESTD-TYR	122 GT	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGCTAACAATGCCCTACTCTTATGCTATGATATCACAA AACCACTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTTCTTTTCACTTTTATACCTTCTTCT AATACAAGCATATGTTAG[AC]ATTAAAGTTCTAGGCATACCT
ESTD- TYRP1	222 A C	---	---	AGTAGTGGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGCTAACAATGCCCTACTCTTATGCTATGATATCACAA AACCACTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTTCTTTTCACTTTTATACCTTCTTCT AATACAAGCATATGTTAG[AC]ATTAAAGTTCTAGGCATACCT
ESTD- TYRP1	222 A C	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTATTACA GGACACATGGATGCTGGAATCACCAGAGGCCAAGACACAAGGTACAGAGACAGGAACACCAGTG ACTCTGAGATGTCA[CT]CAGACTGAGAACCACCGTTATATGTACTGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTATAT
ESTD- VB12	148 C T	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTATTACA GGACACATGGATGCTGGAATCACCAGAGGCCAAGACACAAGGTACAGAGACAGGAACACCAGTG ACTCTGAGATGTCA[CT]CAGACTGAGAACCACCGTTATATGTACTGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTATAT
ESTD- VB12b	148 C T	---	---	TTCCCAAGGCCTCAATACAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTTTCTTATTACA GGACAC[AG]TGGATGCTGGAATCACCAGAGGCCAAGACACAAGGTACAGAGACAGGAACACCA GTGACTCTGAGATGTCAACCAGACTGAGAACCACCGTTATATGTACTGTATCGACAAGACCCGGGGC ATGGGCTGAGGCTGATCCATTACTATAT
ESTD- VB12a	74 A G	---	---	ATGGGCTGAGGCTGATCCATTACTATAT

EST58607 0	105	A G ---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAGGACAGCCACACAGTGGCGGGGATGGCCGGGGAGTTTC TGTTGGGCCACGGCTGTGGCTGTTGTGAACGGTAGCCCTTTGCGGTTGCGATGCCCTAACCTTTGT TTCTTGGCCAAAGGAGGGCGGGTGCCATGCCCTGAGATGTAGATGGCGCC
ESTD-VWF	36	G ---	---	AGGTAGGAAAAGCAAGAGTTGATTAGTGAAGGAGAGAATGGACCTACCTTCCACACTGTCCTTTGG TCCCTAGAGTCTG
EST71770 6	189	C G ---	---	AGCACCACTCTCACGTCAGCCTCAGCACCCAGATGCTGTTCTATAAGGATGACGTGCTGTTTTACAA CATCTCCTCCATGAAGAGCACAGAGAGTTATTTATTCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAATGTACTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAGTC/GTGTGGTGGTGA AGGAGTGCCAGTCCCAGGGTGACACTGGACAAGAAAGAGGCCATCCAAAG
ESTD- TNFab	152	A G ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGAAACAGACCACAGACCTGGTCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGCATGAGGACGGGTTTCCAGCTCCAGGGTCTACACACACAATCAGTCAGTG GCCAGAAACCCCTCTA/GIGAAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTGATG CTGTGTGCCCAACTTCCAAATCCCCGCCCGCGATGG
ESTD- TNFaa	88	A ---	---	TTCTGCATCCTGTCTGGAAGTTAGAAGAAACAGACCACAGACCTGGTCCCAAAAGAAATGGAGG CAATAGGTTTTGAGGGCATGAGGACGGGTTTCCAGCTCCAGGGTCTACACACACAATCAGTCAGTG GCCAGAAACCCCTCAGAAATCGGAGCAGGGAGGATGGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGCCCAACTTCCAAATCCCCGCCCGCGATGG
EST52418 6	113	A G ---	---	CAATTACAGGGTCAACTGCTATGATGTGTTGGAGCCAGTCACCCCTTTGGTGGCTACAAGATGTGG GGAGTGGCCGGGAGTTGGCGAGTACGGGCTGCAGGCATACACTA/GAAGTGAAAACCTGTGAGTG TGG
EST13586 3	89	A G ---	---	CCCACTCTATTTGCCAGCCCCAGGGACAGAGCTGATCCTTGAACTCTTAAGTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCC/GGGGGCTGGCTTATCAGCCTCCAGCCAGACCCCTGGCTGCAGA CATAAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCGTCTGCTGCTGCC CCGGTCACTC
EST51976 7	123	A T ---	---	AGGCAGAAACTGGGCCCCATGGGGGGGAGCTGGAAGGCCACTTGAGCTTCTGGAGAAGGACCTGA GGGACAAAGGTCAACTCCTTCTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAGAT/CTCTCTC CTCCTGAGCTGGAGCAACAGCAGGAACAGCAGCAGGAGCAGCAGCAGGAGTGCAGATGCTG GCCCTTTGGAGAGCTGAGCTGCCCTGTGTC
EST11458 6	140	A G ---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGTCTCATCTTGTCTCGAGTTT CTCTGCCATGTTGCTATTGCAGGACGGACCTGTCTCCAAAGCCAGATGATTTACCATTTTCCACAGTGGT CCC/GJTAAAACATTCTATGAGCCAGGAGAAAGATACGTATTCCTGCAAGCCGGGCTATGTG TCCCGAGGAGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC

ESTD- AT3aa	60 C T ---	---	AGACCTCAGTTTCTCTCTGTAAAGGGAAGTTTGTCTTGGATCTCCATGGGCCAGCCTTAGCA CTGGTCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACAGGTGGAGAGAAATTTGAAAGGGCA TTGGAATTCAGAGCAAAGAGACAGATATTAAAGAGCTGGGGAATGTGG
EST39852 8	106 C G ---	---	CGGTCTTCTCAGGTATTGTTCAGAAAGGCCGAGATGACCTCTATGTCTCAGATGCATTCCATAAG GCATTTCTTGAGGTGAGTACACCTTCCCACTCTCTTA/C/G/GGTACAGAAAGGAGATGCATGAACA GCAGGAACACGTTGGAAAGGCCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCCTCCACAGGCTGCTAT AATACAGCCCT
EST62448 0	112 A G ---	---	ACCTGGTGTGCTGTGGTGAACCTGGTCTCTTGGCATTTGCCGGCCCTCTGGGGCCCGTGG TCTCCTGGTGTGGTAGTCTGGAGTCAACGGTGTCTCTT/G/GTGAAGCTGGTCTGATGGCA ACCTGGGAACGATGTTCCCGAGGTCCGATGGTCAACCCGGACACAAGGAGAGCGGGTTACCC TGGCAATAT
EST36027 2	120 A C ---	---	AGTGACTTCCAAAGGAATGGCTACCCAACTTGCTTCATGGCCCTGCTGGCCAACTATGCCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTTGCATACATGATGAGGAGACTGG/A/C/AACCTGAATA AGGCTGTCACTTCTACAGGGCTCTAATGATGTTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTAC ACTGTTCTTGTAGATGGTGTCTCTAAAGACAATGAATGGGAAAGACAA
ESTD- COL2A1cc	112 A G ---	---	AGAATGTATATAGTCTCAAACCTGGCCATCTCCATTTTTCAGTCCAAAGTTATACAGCTAGACAACA GTGGTGACATACGTTGCTATTATGCTCTCTTCTCTGTCACCTTTC/G/GGGTGTTCAGGTGGAA GGTGAACAGGGTCCCGCTGGTCTCCAGGCTTCCAGGTAAAGTCAACTCAAGCATATACAATACTGCCT TTGGTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT
ESTD- COL2A1dd	97 C T ---	---	TGAGAGAACACCTAGTCTCCATCCTTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTGGACCTGGAAACA/C/TTGGACTTCTTTCTACTGCAGCAGACAAGACTTA CCCAAGAGAGATTAAATGGCAAAGATATACAATTTTATTGACCAAAACACTATCATGTGAACA GCATT
ESTD- CPT2	150 A G ---	---	GCCGCAATGCCCGGAGTTTCTCCAAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGATGCCCTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGAGATGAAAGCTACCATCACTTCTCATCATGAAAC TGGGAGGCCGGCAT/G/GTGTCTATGCCGTGTATCCAGCATTTTGAGAGGCTGAGCGGGTGGAT CACTTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT
EST12274 0	135 A G ---	---	CCCCAGTTGACAGCCACTGCTCTAGACTAAGTTTCTTCTTCCAAATAGAGCCTTACCAAGTGAT TACATAAAGAAGTCAAGTGGTTTACTCCTCATGACCAATATCTTCCCTCCTTAGGATGAGGTG A/GTGTAAATGACCGATGGGGTCCAGAACTGTTCTCTGTCCCATGGAGGATACTATACTGTGAAGA TAAATTCAAGCCACAGAGCTTGCCAGATC
EST76807	91 G ---	---	ATGCTAAGGGGATCGGACATGAAGGACCCCTGTGAGCCGATTGTCTATCTCCAGCGGCCCTGTCTC CAGCTCACTCATCAATGGGGCCAGTCAGGCCAGGCACTGGGCTCCGGAGGACTCAACACTGCCCT GCTGCCATGTGGACTGGTGCAAGTTGAGGACTTCTTG



ESTD-SSA1	111	C T ---			TTCACTTTGTGGATTGTTTCTTTTGTCTGTCAGCACCTTTTCAACATGATGTATCCCATTTGTCCAAGTTTGTCTTGGCTGCTGTGCTGGGATATTTGAAGAGATC/TJTTTGCCAGTCCAATGTCTCTAGA
ESTD-RYR1	109	A G ---			GAGTTTCCCAATGTTTCTTGTAAATAGTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATT TTGATTGATTTCIGTA
ESTD-WT1	70	A G ---			CTTCGTGACGGGAGGTACGTCTCGGCTCTTTTCATGGACATATGATGATGATGCTGACCATTTTCCC CTGCTGACAGTGATGACCGAGACTTGTCTACTATGAG/GGGGGAGCTGTGTGCACTCATGCC CGTCCCTCTGGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTGCGTGGGGCCAGCC ACTCCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD-F2 EST44438 7	100	C ---			AAGACCTACGTGAATGTTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCAGGATGTG CG/GJCGTGTGCTGGAGTAGCCCGACTCTTGTACGGTCGGCATCTGAGACCAGTGAGAAACGCC CTTCATGTGTGCTTACCCAGGCTGCAA
ESTD-PBDA	103	A G ---			GATAAGTACACTGAGGCCCGCAGGAGTTATTGCCTAGTAGCCCAACTGTGCATGCACGCTTAACCTCT GCACCAATGGCTCCAAGGCCGTAGGGAACTGGGGGATCTAGGGGATGGTGAGGAATGGCCC AGCCAGTCCCGCGGTGCTGGTCCCAACAGAGGAGGCCGTGGAGGAGGACAGGAGATGGGC TGGATGAG
EST12839 3	122	A G ---			GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGCGGACCTCAAGCTCGACTTCAAGGA/C/TJG TCTGTCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGAGGTGGG
ESTD-CTLA-4	48	A G ---			CCTTCTCATGCCCAGATGGAAATTCAGTCCCTTCAGGATCTGCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGAAGGCGAGGACTAATCCA/GJTTCTCTACCCGAGCTTGCTGCGCATACAG ACGGACAGTGTGGTGGCAACATTGAAGCTCGTACC
ESTD-ACE	96	C T ---			TGCAAAACACACAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAG/GJTTCAAGTCCA AGGCCATTGGCTATCTCAACACTGGTGAGTGATTACTTGAGTAAGGGAAACTTGAATGTTATTCAAC TGGATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
EST54419 8	88	A G ---			ATGGCTTGCTTGATTTCAGCGGCACAAAGGCTCAGCTGAACCTGGCTA/GJCCAGGACCTGGCCCTG CACTCTCTGTTTTTCTTCTCTTCACTCCCTGTCTTCTGCAAGCAATGCACGTGGCCAGCCTGCTGT GGTACTGGCCAGCAGCGGAGGCTCGCCAGCTTTGTGTGTGATGATGATCTCCAGGCAAGCCAC GATCAAGCAGTGACACCGGTACGATGGACCACTCTCCACAGTGCACCATGAGATGGGCCATATA CAGTACTACCTGCAGTACAAGGATCTGCC/C/TJGTCTCCCTGCGTGGGGGCCAACCCGGCTTCCA TGAGGCCATTGGGACGTGCTGGGCTCTCGGCTCTGACTCTGAACATCTGCACAAATCGGCTGC CTTCTGCCTAATTGAATGATATTGTTGCTGTGGGACCTGAGCACTTTATGGCACAAATGATCACTA TTTTCTTGACCCCTACTTAC/GJATCCTGGGAGATGTATTTGGGTTTAGCGTGGTGTGTTGTTGCTA CTATAGTCCAAGTGAA



WI-2625	98 G A ---			GGCAGTCCTGGCTGTAGGTAGACAGCACTGAAGGATGGAGGAAGAGAGAAACAGGCAGAA GCACTGTGGTAGTTAACAAAGGCTTATTTAGGA[G/A]CAAAATTGATGATACTCCCTGAGGACTCGCAG AAATTACCAGCAGTGGACAGGGTTATCTGTGTGAATTCAGTTATCCACTTGACAGGAGGAAAGCCA GCCAGCAAAG
WI-2924	54 G A TAGG	TGACCTTCCTA GTCTTCTCTTA	GCCTAAGTGT AATCACAGGG	TCTGTTGTCATATTTCCCTCTTTGACTCTGACCTTCCTAGTCTTCTTTATAGG[G/A]ACCCCTGTGATT ACACTTAGGGCCTACCTGGATTATTTAGAACAATC
WI-2939	72 G T GTGCCTTT	GGCTTGCTCA	CTTGTTGAGGG AAGTCTTG	CCATTGTTGAGGTTGGTGGGTCACCTTGTCATTCCTCGCACTCAACAAGTGGCTTGTCTCAGTGC CTTT[G/T]CAAGACCTTCCCTCAACAAGAATGCTTTCCATGCTCCCGTGTCTTTGAAATTCGACT TTATCCTGAAAAACTCAGCTGCAGTGTATCTCCGGTATAAGCCACTCCTG
WI-3203	99 G A AGACGAG	GGTTATGCCGC	TCAAGTATTGC CTTGTTGG	CTTGCTACCATGCATTTACAGCATACAACCTCAGTGAATGCCGTAAACCCCATTAATAAACAT CTTGCCATCGAAGGGTTATGCCGCAGACGAG[G/A]CCACACAAGGCAATACTTGAAGTGACTTGGA GAATAAGATTTGGATGGATGAAGCAAGAGAGAGATGCTAAAGTGA
WI-3473	101 A G GCCCTAGGGA	AAGCATTTTA GCCCTAGGGA	CCTGATGTCAC CAACATTTTCT	GGAAAAGAAACCTGAAGGATGAGTAGAAGTTAATTGGGAGATAGTTGGTGATAGGCCCTGTTTGGGA GATTGCAGAGAAGGAAGCATTTAGCCCTAGGGA[G/G]TAGAAAATGTTGGTGACATCAGGGCT ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTTGGCTCCOC
WI-1796b	29 A G ---		---	ACACACTTTTCTGTATGCTCTTCATCAAA[G/T]GCAGGCGTCATTTCTGCACATGGTGATATTTAAG CAGGAGAGCATTTGCTTGGCTCCOC
WI-1796	29 A G ---		---	AGTCGTCCATCTTCAGGGTCTAACTCTGGATCTGGCTGCAGAGTAGGAAGAAAGATGGGTGAGT AGTCACATTAGGTATTTCCAAATAAIC/T]AAATGCCTCTGAAAATAATCTCTCCCATGTCCCTGTCT TAAATATAACATTTTCCC
WI-4360	93 C T AAATAA	GTAGTCACATT AGGTATTTTCC	GAGAGATATTT TTCAGAGGCAT TTT	GCTGAGCTTTGTGGCAGAGCCAGGACAATTCAGCTGCCGGATTTTAATAGATTCTGCAGCACTGCAA CAGGAACCAAAATCAGTCTCTGGGTAACTGAGAGTGGTTTTCACACCCAAA
WI-1959b	87 C T ---		---	GTTGTCCCTGTAGCAGACAGAGGCA[G/G]AGAGGAAAAGCCCTTTTGGTCCAGGGGCTTACAC TGAATCCCTCAACAATGCAAGATGAGCTAATGGTCTTAGAGGTATAATCTAAGTGTGAGAAAAACA AAGTATAGGGTTTG
WI-1973b	28 A G ---		---	CTTGAGTATGCGTGGATTTTGGTATACACAGAAATGGGAGAGCTGGAACTAATCCCCCATATACCA AGGACAAATTTGATCTGTCTTCTACAATTATACAGTAGGAGACATTATGTTCCATGACAATGGTAAT TTTTAA[C/T]GACAGTTT]TAATTGAGTGAAATTACCATAAAATAATAATAGTAGCAGCTAATATT TACTGAGCTGTTACTAGGTGCCTATAAATAGC
WI-1980b	140 C T ---		---	



WI-2015b	190 A G ---			TGTCAGATAGTCGCTCTACCTAGGTGCGAGTAGCATGCTAGGAGCTATTAAAGTAGACAATTATGCT ATATATTTATACAATATACAATTACTTGCAGATAGCATGACCATGCTAGTGAACCCACAAAGACTAT GTGTGAATCGTCTATTAGGGTTTGCTATAAACTCTACATGGTGCTTTTCCAACTT[A/G]CATATACTT CTAATACCATAGAG
WI-754b	49 C T ---			GAAGGCACAGGGAGAGATGGCTGTCTATCTACAGCCAGGGAGAGAGAGC[C/T]ACATTTATTGGTAA TCCTATAAAGTGCACTTCTTAAATTTGTATTACTTTAGA
WI-754	22 T C ---			GAAGGCACAGGGAGAGATGGCT[C/G]TCATCTACCAGCCAGGGAGAGAGAGCATTATTGGTAA TCCTATAAAGTGCACTTCTTAAATTTGTATTACTTTAGA
WIR-1b	56 A G ---			AGGCAATCAGACCTACAGAGGAAGAAACCCCAATAAAACTCTGATGATCGTACATCC[A/G]TGGCGTG GAGGGTGATGCCCTCCTGAGGACATGGAGCTTCAITGTTGGAGCCCTCCCTG
WIR-1	56 A G ---			AGGCAATCAGACCTACAGAGGAAGAAACCCCAATAAAACTCTGATGATCGTACATCC[A/G]TGGCGTG GAGGGTGATGCCCTCCTGAGGACATGGAGCTTCAITGTTGGAGCCCTCCCTG
WIR-3b	72 A G ---			TAATTTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTCTCTAAAGGCTAAATAAGAA GAAGT[A/G]TCTAAAGTTATTAGCTCAGAGCCTCACACATTCTCAGTGAATGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-3a	69 A T ---			TAATTTTAAATGGGGCCAATAACACAGTACTTATCTCACAGCATTCTCTAAAGGCTAAATAAGAA GA[A/T]GTATCTAAAGTTATTAGCTCAGAGCCTCACACATTCTCAGTGAATGATAAACAATAAGCA AAGCTGGGTGCTGAGATAAGA
WIR-4	47 T -- ---			GAGCCTTTCTAAATAAGGATTGTGACTAGCAACCTCCTGTACAGATTCCCTGCTCACACATGTGCA AGCAGCAGCAATTTGCCAGCTGCC
WIR-5g	209 C -- ---			CGGGACAGAGACAGAGAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAATAAGACACAGAGAGTGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5f	196 C -- ---			CGGGACAGAGACAGAGAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAATAAGACACAGAGAGTGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5e	194 C -- ---			CGGGACAGAGACAGAGAGAGAGATTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGGTCCCACTGTTAGG TTTTGAAGGGAAGGCAAGGGTTAAATAAGACACAGAGAGTGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG

WIR-5d	191 A	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGTCCACTGTTAGG TTTTGAAGGGAAGCAAGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5c	177 C	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGTCCACTGTTAGG TTTTGAAGGGAAGCAAGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5b	159 A	---	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG TGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGTCCACTGTTAGG TTTTGAAGGGAAGCAAGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACACAGG TTTTACGTCCAG
WIR-5a	37 A	G	---	CGGGACAGAGACAGAGAGAGAGTTCTGCAGCATTCACAAGAGGTTATTAGGACTCAGTTCTGCTG CTGTGAGNCATCCACACTGGAGGATGAGAACACCCAGCTGCAGCCAGAGCCTGTGTCCACTGTT AGGTTTGAAGGGAAGCAAGGTTAAAAAAGACACAGAGAGAGTGGTGGCTCTATGGAAACAC AGGTTTACGTCCAG
WIR-6	63 A	C	---	TAACCCCTGAACCTTTGTCTTCTCATCTCAGGGAGAACACAGAGCTTCATGTTAAGACCCAGAA[VC] CGCAGTCTGGGGTGGGCAG
WIR-7	12 C	T	---	TTGCTGACTATT[C]AAGCATCTGTAGATATGAATACATAGTCTTGAGATTGATC
WIR-8	46 C	T	---	GGCGTCTATGACTATCTGCTGGTCAATTTGACTAATGATTCCTG[C]TGCCCTTG
WIR-2	56 C	G	---	AAACAGAAATAAGAGGTTATAAGGATGGAACTAAAGTTGTCAGAGAGGATGA[C]GCTGAAG AAAGAACTACTCTCTTTTGACCAATAATAACAATTGGGAACACTGGAAACCATGGCTTGATTACT GACAAC
WI-7069	93 G	A	---	TGTCCTTGCTTATGCCCTGCTCTTTCGCTTGGCAGGATGCTGTCATTAGTATTCACAAGAGTA GCTTCAGAGGGTAACCTAACAGAGT[G]AATCAGATCTATCTTGTCAATCCCAACGTTTACATAAAA TAAGAGATCCTTTAGTGCACCCAGTGACTGACATTAGCAGCATCTTTAACACAGCCGTGTGTCAAAT GTACAGTGGTCTTTTCAGAGTTGGACTTCTAGACTCACTGTTCTCACTC
WI-18694	41 A	T	---	GGTCATTTCCCTTTTATCTGTCAGGCAGCCAGCTCTGACTT[A]TCTCTGTTTCTGTCTCTCTCCC CCACATACCAACTCTTCACCATGATGATTATACCAATAATACAGTTCCTTATATGAGGGGCTCTGGA AAATTAGACAGTGAAG
WI-18612	37 A	G	TGC	CACACTGTTACACCTATATTTCAAGTTTGGAATGC[A]GJTATTTGCAAGCAGCAATACAAAAGTA TTCATGAAGAATGCATAATCTCTGAAAATTATGAAAACATCCCT

WI-18517	87 C T	CAGGAATCAG CAGCCTGA	TGTTGGACAA GTGCAACA	TTAAAAATCAACTAGGGCTCACCCCTCAACACCCCTCCATTTGTCAACCTCTACAGCCTGCATGCC ACAGGAATCAGCAGCCTGA/C/TTGTGACCTTGTCCTCAACACAACTGACTGC
WI-18668	76 C T	GGCGAAAAAC TAGGCAAAAA	GCTAAATTAA CTGCACTTTT GC	CGATTGACAACCTTTTATTTTCAACTTAGGTAACAGTCCAAATCAGTGTAGATTGGCGAAAACT AGGCAAAA/C/TTAGCAAAAAGTGCAGTTTAAATTAGCAAGGCTCAAGACAGTATGTGGAAAGGAA GGTGAGATTTCCTCTACT
WI-18680	75 T C A	GCTGTCACCT AGCATCTGGA	CCTCCTGAATA TACAACGGAGC	TAAACATACGAGTACTGTACGCAAGCATGCATCCCTGAGTCTGAGTGAGGCTGTCACTCTAGC ATCTGGAAT/C/GCTCCGTTGTATATTCAAGAGGGGA
WI-18704	99 A C	GGTTCTCCGA GGGTAC	TGAAGGCCCTG CTGG	CACCCAGGCTGTACCCAGGCTTCTGTGCGAGCACACACCAAGGGCAGTTGGCTTGAAGGAGCC CTTGAGGAAACACGGTTCTCCGAGGGGTAC/C/CAGCAGGCTTCAAGCTTAAAGTCG
WI-18673	29 A G ---		---	TGTGGGCAACCTTGTATTTAATTGCAAAAC/C/GJACTTAATTTACAGCACATTCAATAATGAACCAAC AGGAGAGTTGCTGACTTTGTAAACATATGAATATAATAAAATCCCTTGCAATTCAGGTAGTCAAGGTA AAAGCGCATACAAGGAAG
WI-18640	121 T C	GTCGTGGGTG GGG	GCAATACCAC TGAAGAGGAC A	ACCAGTCATGTTTATTTGGAGGTTAATTCCTATTAGGATATGAAGGATTCAGCAACGATTGAGATT GTGTTCTCACGGAGGGCTCGGGCCAAAGTCTGTGGGGGTGCAGAG/C/CJGTGTCTCTCTC AGTGGTATTTGCGGACC
WI-18533b	91 T C ---		---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCAATTTTTTAACTCCCGAGATTTCTCTTTATTT TATATTTTCAATTTTTCATCCTAA/C/TTACTGAAGCCATTTCTTTGTTAACTTTAGA
WI-18533a	59 T G ---		---	GGGAGAGGAGGTAGATTGCCAAATTGAGGCAATTTTTTAACTCCCGAGATTTCTT/GJCTTTA TTTTATATTTTCAATTTTCATCCTAATTTACTGAAGCCATTTCTTTGTTAACCTTAGA
D11734	83 A C TTC	TCATCTGATAC CTTGTTGAGAT	AACCAGGATA AGGCTACAACT ATTT	GAGCATATGCTGCATGAGGACCTTTCTATCTTACATTATGGCTGGGAATCTTACTCTTTCATCTGATA CCTTGTTGAGATTT/C/CJAAATAGTTGTAGCCTTATCCTGTTTACAGATGTGAACTTT
D49493	159 A T	CCTGAAGGAA TCTGGGAATT	ACTTTCAGGCC AGGC	CAGGACTTGTGTGCTGCAGCTGCAGACACAGAGCAGCTCATGGGCAACATCACTGGGGCCAGAGAG AGCTGTCCGCCAGTGCATCATTAGGGGGTCTTTTCAATTGCTAGTACTAGCCCCCTTAAATGCCAGCCTG AGTACCTGAAGGAATCTGGGAATT/C/JGCCCTGGCCTGAAAGTGGCCATCATCATACCCACTGTT CT
EST10030 7	98 T C	CATTTTGTTC TCTCAAGTCCC	GCAGTGGTGGT ATGGATGA	TATTTCATAGAGGAGACCTAGGAGGAGTTGACACAGACACTGCTCAGCAGATGACTTAAAATTT CCCTTAGCCATTTTGTCTCTCAAGTCCCTT/C/JTCATCCATACCACACTGCTGATTG
EST10052 2	24 G A	GCTCACTTCTG GAGGCTG	TGTGGAACCTC AATCTTAGACT TC	TATTTGGCTCACTTCTGGAGGCTG/C/JAAGTCTAAGATTGAGGTTCCACATCTTGTGAGGGCCTTC CTGTTGAGTGCATAACCTGTGTGGAAAGTCATCATGTGGCAAGAGAGAGGGCTACAGAGAGCAAGAGGAA A



EST10605 2	118 C G ---			CTTGGTAATCACAGTTCTGTATTATACAAAACCTTTGTTTTCTCTGACAAACTGTACACATAGA AACAAATTTCCAAATGGACAGGAACCTTAAATTTGTGGAGATGCCCATGTTC/GTTGTGAGACTTAA AAAAAGAAAAGATCCC
EST11048 0	61 T G	CTCTCAAGTAG ATAAGAGGCA TAATCT	GCTAAATTTTC AGAAAGAATT TTGTTT	CATGTGTCATCCCATGATTGAAAAGACATGTTGCTCTCAAGTAGATAAGAGGCATAATCTT/GJAA ACAAATTTCTTTCTGAAAATTTAGCTTATGAACCTATTACACTGCAAAACCAGAGAAGGAGCAC
EST11260 8	101 G T ---		---	TATGGAGGCCAGAGGAAGTGACACTATATGTGGAAGTGCTGAAAGAAATGAAGTGTCACACACAAA TTCTATATCCAGCTAAATATCATTTAAGAAATGAAG[G/T]GGAAATGAAGGCAATATCAGATAAA
EST11349 9	109 C T ---		---	TTTGATGGAGAAATCCGAGGCTGCCAGCATCCCGACAGTAGATTCTTTGGACGAAGAAATCCT TCTGTGGATTACGCTTTACCGCTTTCCCTCATCTGCTGTGTTC/TJTTCTCAGAGCTTTAATGTCCGT CCTGCTCTCCGAGTCAG
WI- 16632a	71 A G	CCAACCTACTT TGGAGCOCT	CTAAAAACTCC T	GAATTTCTGGTATTAATAGCGGTGCCACAGGAGCACATAGGAAGAGCATCCAACTACTTTGGAG CCCT[AG]AGGAGTTTTTAGAGAAAGCTGGAGCCCGAAGACCAGTAGTAGGAGTAGCCAGACCAA AAGGAGGAAGGAGTGGAA
EST11772 6	74 A G ---		---	CCAGGAATAAAGAAAAGAGTCAAGAGGAAACAGTCTTTGATGTTATGAGGCTGAGACACTACTC TTCCCTTCA[AG]GACTATTTCACTTCTGACTATAAGTGAATAATACTATTGAAGACTTCAGGAGCTCA
EST11795 3	82 G A ---		---	CTTGTCATTATTTTGTGCATGTTGTTCTTAAAGGCTTGTGAAAGATAACTTGGAAATGTGGGAAAC ACATAGATCCCAGA[G/A]TATTAAAGGGGCTGGAAGTAGCCTTAAGAC
WI-16644	42 G A TAC	CAATAAGCAG CTCATTTTGAT	ACTTCATGAAT TTTACTTCATG TATACC	AGAGCAATGGTGCATCTCAATAAGCAGCTCATTTTGATTAC[G/A]GGTATACATGAAGTAAATTC ATGAAGTAAATTCATTATACCAAAAGCCTCCACAGAACTTTTCATGCACCCTGAGCTATGTGAAC TGAAAAGTAACAGTGGAT
EST12005 9	56 A G	TTGTATAATA ACACTCAGTA	GGCTGGTCACT TCCCTGGAT	GCCTAGTAATCCAAAAGGAACATGTTGTATAATAACACTCAGTACAAAGTCTGT[AG]ATCCAGG AAGTGACCGCCGACGTGTGCTATGACCCCTCTGAACCTCCCATTTCCATAGTTTTTGAAATC
EST12055 9	32 T C ---		---	GTGGAAAATTTTTTATCTGTACGCTTTCCCT/CJATTATATTATCTTGTCTTGAATTCAGCACCC CACCCGATTTGCAGGCAGTGTCTTCTAACTGTGCCCTGTGAGCTGTAAAAGTCTTCT
EST12492 1b	95 A G ---		---	CCCCTAGCAAATGACTTGGAGTTGTGTCCAATTACCAAGTTACATACTGTGGCCAAAATTAAGCTCIC TTCCCCAGAGGCATTAACTGAGATTAT[AG]GGAAACGCACAGCAAAATTGACGATGCAGCTTTTAA CCTTTTAA
EST12492 4	25 A G ---		---	ATCTTGAGGTTTCTGGCCTGTCAG[AG]AAGTGACATCTTTTACTTACCACAGGTCAGGAACCTAT AAAGAACTGTGTAGAAAAGATATCAGGTCAGACTTTTTTAAAGGGCTTCTTATCAGCTCAATAAA

EST12502 2	52 C	---	ATACTAGGGAGAAAACCAACTGGAGGCAAGTCCACAGGTCCACACTTGTCAIC/GCAGCAAGTAT AAACAAAGTGGTTTCGATGAAGAGAAATGCTCACGGGGGAAATGACCAATTTTAAAGGCCCATGTG GTGTCGAGGCGAGTTAGAGG
EST12619 8	105 T C	---	CCAGAGAAAATAGAAATGATCGGTAAAGAAATAGGAATGCATATTTCAACTCACTGTCACAAA CAGGTGTTTATTATCCCAATGACAGTGTGCTGAGAT/C/GATGCATGTGGCAGACGAG
EST12620 0	67 A G	---	TTTCTCTCTCTCATTATTATTCATTGTTCAAAACACTGTCTAGTACCAACATTGTCCACCGGGCJA /GJTGAGAAATACAATATTGAAGAGAGTCACTGCCCTCTGGAAATCAGAGTATTTGA
EST12817 9a	22 C A	---	TTGGGTTCTCCAGGATTCAGIC/AJCTCGTAGCTGATGTGCATGAGTTCTCATCCATGCTCCACGG GTCTTGGAGTGACCGGATGGGAATOCATGTTGCTTTCGTACTCCATCAGGTCAATTGG
EST12941 8	23 T A	---	TCTCAGCTTCCACCTGACCTGCA/T/AJCAACAGCCAGTTATTTACCAGAAATTTGTTTGGGTTTCA ATGTAGTGTGTTAGCTTTAATACACTGCACCTGTTTG
EST12949 2a	52 A G	GGCTTTAATCA TAACCTAATA ATACTGTT	AGGATTTTCATGAGGCTTTAATCATAACCTAATACTGTAAACACACACI/AGJCTGTCACTTG CAGAGACCCACAGGGACACACATTCTCTCTCCTCACAATAGACTCTGAGGTAGGAGTACACTGGCT AAGGAATAA
EST13067 4	104 C T	---	ATTTTGTGTTTCTTAATGAAGCATAATAACAGTTAAATTTCTCAGAAAATCATCTATAGTTGA GTGTAAACTCCCTAAATCAGTCTTCTAGGGCCACACI/TJGGAGCAGAAAGCAGCTTCCCACCCAAAG CACCTCTGAAC
EST13117 6	66 A G	---	TGCTGTCTGCATCAGTCTTTTAAATTTAATCGCTTTATACAATTGACACCAATAAAATGCACJA /GJATTTAAAGTTTACAATTTGAGAAGCTGACACGCTGCCATACAGACACACCTCATTTTACTGTGC TTTACTG
EST13121 6	44 C T	---	TCTGCTTTAAAGATTCTTCATAGCTGCTTAGGTTTGTCTTCC/C/JAGCATATTCAGCTATAATCA CCTACATTCCCTCCACAAATATTTCTGTGTGTGCGCAGGCCAGTCTCCTCACTGTCCCATGAATAGCC AGTCTTATTTCACCTCT
EST13226 6	74 T G	---	AACTGTTTACTAACAAAGGTGCTTTAATTTGAAAAGCATTGAGGAAATAAATTAATGAATAGTCT GGCCATTT/GJGACTAACCCAGTTCTACAAATTTACATATCCGTCACTCAGATGAGCATATACCAAG TCAGAGGAAACAAACATG
EST13230 6	72 G A	GCTCAGATGTG AGAGACGC	GCATCATCAGCGGCTTTTACTGAACTTACAACCAACTTGGCGCTCAATATGCAGCTCAGATGTGAGAG ACGC/GJATCTCTGTACAGGAGCGGTACTGTCTTCAATCCTTTGCATGCAGGTGTTTACCACAGGCA AACAGTTTACTCCACAT
EST13236 9a	70 T C	ACAAGAGGGTT TGACAAAAGA TCTCAGGCT	AAAGATATAAAACAACTCCCATCAGTAGCAATACAAGGTTATACATTTTACCAGATTTTCTCAGG CCTT/CJTTTGGATACCTTTAGTAGTTAACTCTCTTTTGTCAACCCCTCTTGTATATAACCA

EST13278 2a	51 A G	CTTCACCGAA CAATATTTTAG G	CATATTCTTGG GTGGTGAGAA	TTGCGAAGCGTTTACAGCTCCAAACCTTTCACCGAACAATATTTTAGG[A/G]ATTTGAAATTAT TTCTGTAGTTCTCACCAACCAAGAATATGACAGCTTG
EST13282 0	99 A T	CCACACATTTTC AGTCCAAGA	GATGGAAAATT TGAGGAAGGTT	GCTCACTAGATGAGCATTGACCAAAATATTTAGATAATACCTGTTGGGAAAGTGCTGAATTACTAGCC TGCCTGAGAAATCCACACATTTTCAGTCCAAGA[A/T]AACCTTCTCTCAAATTTTCCATCTCCCATCAGA
EST13290 9	39 A G	CAATTTTGA AGTTGGGTTT G	AAATCATTCA TGGAATTTCA	AGCTCATCTGCAAGCAATTTTAGAAGTTTGGGTTCTT[A/G]CTGAAATTTCCATGAAGTGATTTT TTTTCTGTGCTTAACCTCAGTTACTTAAAGACCTAAAGACAAAGTGGTATCACATCATATTTTGT
EST13518 2	45 C G		---	ATGTGTGGGCTTTTIG GAAACATCCTCCAGTAGTATTGAGGTTAAATGATTCAGCAATTA[C/G]ACTTTTAAAAATTACCTCA ATGTTCTCGGAGTCGTCCATAGTTTAAATGACTTCTGCACCTTCTTATAACCTTGATTG
EST13522 8a	66 A G		---	CAGGTTGGTATTCTCAACTAGGAGCTATTTTGGCCCCCATCCCCCGGAGTGCTGGAGAC[A/ G]TTTTGATTGTCACAACTGCGAGAGTGGTGTCTACTGGAATCACTGGGTAGAGGCCA
EST13568 6	69 T C		---	CTTTAAGGAAGTGAGCCAGATGAATCCAATGACCAACCTGGTTGAGAGCCATTGGTCTAGGAGTAGA AA[T/C]GCACACAAGGAATAAGGGAGAGGAGGTTCCGTTAGTTGAGGGAGAGAAAGTTGGAAGCA TTTCAAGCTAAGTAATGGT
EST13785 0	101 C G		---	AAGATTACGGACCATAAGAACTGCCCCGACCCATACACACACAATTTATAGCAGGTAAAAACCA CTGAAAGGAACAAGTAATGACTTCTTGAACAA[A/C]GTTGATTACGAAAGTGAAAGGCTACAGGG TGATTACTA
EST14038 1	25 A G		---	CCTCAACCATCTGTACCCGAGCC[A/G]CAGTGACCGGGACTTGCTGCTTCCCCATCCAGCCCTCT CCTATCAGCATCCGCTAAGCGTCAGTCAGCAGGTG
EST14083 7	23 A G		---	CAATGGTGTCATGTGAACATA[A/G]ACCTATTTCATAAAGTTAAAAATAATCCCTTCTTGAATCA CAGTGCAAAAGGCATGAGGGTGAAAGTCATCTGCTAAATGACCGAACAGGAGGGTAGGAGG
EST14221 5	42 T C	GCATGCTAGA CAGAGGCATT	GGAACAAGTC AAAATATTTT AAAAGA	AATATCAATGCATTTCTTGGCATGCTAGACAGAGGCATTA[T/C]TTTGAAGATCTTTTAAAAAT ATTTTGACTTGTTCCTTCCCTTCACACTCATTTTAAATTGT
EST14812 2	50 A G	CAAGTCAGCTT CTACATTCTGA ATA	TAAAGATTTAC TTAAATCCCAT TATGTACT	TTCACTTAGTACCAAGGATGCCCTTCAAGTCAGCTTCTACATTCTGAATA[A/G]AGTACATAATGGG ATTTAAGTAATCTTTAGAAAGTCCCGGAGTTTGCCCTTTTCTAACATTTTCATATCAGGTGAAACAAT TTTTTCATATGGGTGAT
EST14815 3	128 A T	CATCACCCACC ATACTGGTT	CGGGAACA GTACCGAA	TTTGCTTCGGCAATACATAGTGGCAATGCAGCGTGAGTTCGGCGCTCCCTCCACTGAACCAATAAT TCACCAAGCAATGGCGCACCACTTAAATAAACTTGCCCGTCACTACCCACCATACTGGTT[A/T]TCC GGTACTGTTTCCCGTA



EST15420 6	109 C A ---	---	---	TTTAAACCCAAAGACTTGTAGATGTCAGGACTCCGATCATTTTCTGCTATAGCTTGGATATCTTA ATCTCTCCCTTTGTGCATCATATAATCATATAGCCAAAGGACTTC/AJGGAAATTTTGGCTGCTTCAAGTCA TTCCAAACCTCTCAGG
EST15700 6	48 G C GGA	---	---	GTCACGAGCACTTTTATTAAAGACGTGAAAGACAAAGACAAACAGAGGA[G/C]JAGCAGAGAATAATA TCTCTGTTTCAGCTATTCCAGGATGTTATGCCAATTATCCAGAGTCCCTTGATCTGATGTAGTA
WI-16739	57 G A CACAAGC	---	---	AAGGATTGAAACATACCTAGATCATATAAATTTGTGAAGGTTTTGCCATCACAAAGC[G/A]JTATAG GGAATAATGAACATCAACTATCTACAGCTAACCTAATGAAGACCAAAATGCTCCAAGGT
WI-16782	96 C T CACTGTAAGG TC	---	---	CTTCTTCTCCTAGACGTGGAATACACACGGATACAGTATCTGGAGATGTAGCAGCTGGCTCTTGAC CATAATGGTGGAGTCTCACTGTAAAGGA[C/T]GATGGAGGAACAGAAAGATAGAAGAAGTTTGGGGT GCTGATGAAATTGTGGGG
WI-16783	64 A G G	---	---	AAAATGTAAACCTTAGAGGTTGCCTCTTTTGTGTCACCTTTCTGAGATGCTTTTACCTGAG[A/G] CTAATAAGGATTGAACCAAGCAGTATTTTTTAAATGGCAAAAGTCCAGATGTAACTCGAGT
EST15948 2	58 T C ---	---	---	CAGGACTTAAGGTCAATTTTGCCTGGAAGACTTTAACTAAAGGTCAGGGCAACATAGGA[T/C]JGTGA CAGCACCACTCGGACCAGGAAGTGTGAAATCGTCACACTAGCGTGCCAGCCCTTTTTCCTGGC TGCTCTGCCTCCAGAGC
EST16088 8	89 G C ---	---	---	GGTTTTGAAGACGCAGCTTTATCTCCACCTGCCACTGGGATCTCATTTTGAGAGCTGTTTGTGACGC TTTTCCAGAAAGGCCGCTC[G/C]GGGTTTTCTGAACCTCTCTATGGGCATTTTAGAAT
EST16089 9	96 C T ---	---	---	CGTCTGAAGTTTTCTTTATCACAAGTCACATCAATCCCTCGGGCCCTGCTCAATGCCACCTCTTC CTGAAAGCCATCCCTAAGTAGTCTCTC[CT]AAAGAGCCATCCCTGCCCTTTCTTTGCT
EST16100 1	24 C G ---	---	---	ATCCAGCTGTGAAGGGACAGGAG[C/G]GTAAACACAGTCCATTTATAAGGGGTGTGCACATTCCCA GGGCTCCAAATAATGCAACATTGTTTCACTCGTCCATGCTGTGATAGTTTCATAGTAAAAAGTC ACTCCAGACAGGTTGCTC
EST16104 9a	83 A G ---	---	---	TTCTTTTAAATAACCCACAGACACCCATGACACTTCCAAATTTACAGAGCAAAAGTGATTTGCAG CTGGTTCTCCAGGGA[A/G]TTGGCCCCGGAAGCTGGCTCAGTTCACCTCCAGGACCTCAGTC
EST16118 0b	119 T C ---	---	---	ATGGTATAACAAATCAGTTCAGGTTTTTTTCTGAACAAATGATCCTTTTGGTCTTTCCCGTGGCATG CTCCTAAACAACAACTAAACAACCCCTCTACGTCTAATCAGTCACCTAAGATA[T/C]CGAGTGGCAAAGT CTTTCACA
EST16118 0a	32 C G ---	---	---	ATGGTATAACAAATCAGTTCAGGTTTTTTTCTGAACAAATGATCCTTTTGGTCTTTCCCGTGGC ATGCTCCTAAACAACAACTAAACAACCCCTCTACGTCTAATCAGTCACCTAAGATAATCGAGTGGCAAAGT CTTTCACA

EST16151 2	53 C T ---			AGCCAATTCAAACGAACCTCTATCAAACACACAAAGGCCTAGAGGAGATTATCTTAATGAACGT AAATAATTCAAGGCAATTTTGTATCTAAAGCATTTTGTCTAGCTCTACAAAGGCATGAATGAGGTGT GGTCACGTTTTGTATAGGA
EST16182 6	54 G A ---			CATTGGTTGGTAGGAAAGATAGTAGTGCAAAATAAATGGTAAACAGCAG[G/A]AAATGGAA TTATAGCTTTCTTTTCATATAGGGAATTGAAATTTATTTACTGAGGTGATAGGCAGAAAGTAGTA
EST16183 2b	59 A G ---			GCAGGTAAACTGTGTTTCAACAGTATTGTTCTTTCATAAAGAAAGAAATATCTAGTTG[A/G]GTAG AGGAAGGCACGTGCTCTCTGGCCCTTCTTCGTTTCATATTTTATGTCACTGTCTAACGTGGGCCGTGT GCAAGAGATCTTTGAGA
EST16198 4a	28 G A ---			AATCTTAGGCTCTTGGCTTTCAAATCA[G/A]TACAGACAGATAAGAGCTTTAAGTATTTTCGCATTT CCCAGAGGAAAGTCAGCATCATAAACCACATGGGTACATGCTCACGCACATGGTGTC
EST16229 2c	52 T C ---			TGTGAACCTCGAATTCGCTTGTCCTCAAGTCTGAGTCACAGTTTCATTTGGGAGT[C/J]CCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTACAGACAGGCAGAGGCTGCA
EST16229 2b	45 T C ---			TGTGAACCTCGAATTCGCTTGTCCTCAAGTCTGAGTCACAGTTTCATTTCTGGAGTCCCTGTGCAGCC CTTGCCAGTTTCCACGAGGCAGGATACTCCACTAGCTGATTACAGACAGGCAGAGGCTGCA
WI-16816	124 A G TGGGTTA	GGAGCCATTGT	GCCTAGATTTT	CAGACTTTTCCCTCACACCTCATTGGCTGGAACTGGTGCACATGCACATCCTTGAACATATCATTGGCAA AGGGAAATGGGTATCAAAATTGCTTAAGGCCAAGCAGGAGCCATTGTTGGGTTA[A/G]ACTGTCC TGAACAAATCTAGGCTC
EST16269 5b	49 G A ---			GCACCTCTCTGTGGCTTGCTCTGTCCAGCTGCTGTCCAGTGCCACA[G/A]TGGTCTAGCCTCATGG CAGAAGCATTTAGCCAACTCTGTGTCTGCTCCACTCTCTCTTCCGCCGCTGGGCTCACCCACC TCTTCTCTCTCAATC
WI-16824b	83 G A ---			GTCACCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTTGTTCTTATGAAGAAGTCAG AAGCTGATAAACGTGG[G/A]CTTACACCTTTAGCACGGATAGTTTCTGGTCCCAGTGGGTGTGGA GCCTTCCATTATGGGAATA
WI-16824a	47 T C CAGCTGT	TGATGGTGTG	TTCTTCATAAG	GTCACCCAGCCAAATGCTTCAGGAATAAATGATGGTGTGCAGCTGTT[C/J]GTTCTTATGAAGAAGTC AGAAGCTGATAAACGTGGGCTTACACCTTTAGCACGGATAGTTTCTGGTCCCAGTGGGTGTGAGC CTTCCATTATGGGAATA
EST16445 3	96 T C ---			TTGCTTTTATTAATCCAGAACGGCATGCTACAGATACTGTACAGCATGAACATTTTATTACAAA AATGGCTTCCAAACCATTAAATGAACTTT[C/J]GGAATAAGAGCATAAACGGAACAGTAACATCA
WI-16857	47 G A A	CAAATAAGCA GCTAATGGCA	TGTGAATTGGG AAGACCAC	TATAATCCATCTCCAAACACACACAAATAAGCAGCTAATGGCAAT[G/A]CTAGTGGTCTCCCAA TTCACAAGACCTGTGCTTCAAAATGTTTTCCTGATAATGTGGAGAAATCTGCTCTTTATGTA

WI-16879	79 C T	GATACAGGC ATATTTCCCA	CAAGGCTTCT AGAACTAGAGT CC	AGACAGGTCAAACAACCTCCTAGGGATAAAGATATAATCCAGCAGCATTTATTCAGATACAG GCCATATTTCCCA/C/TATAGGACTCTAGTTCTAGAAAGCCTTGGGAGAACAGGCCACCCAG
WI-16882	99 A G	GAAATGCCA CGTCTCTGAC	GACACATGTCA GGTAAATCGC	ACATGAATGGCAACCTCTTAGTGGGAGAGACAATTCCTCCCTTTACCCAAAGGTTACTCTGAC AAGGCTATGAATGAAATGCCACGTCTCTGAC/A/GJGCGATTACCTGACATGTGTCTATCTCCCT
WI-16888	70 G A	GCTAACTTTGG GCAGGTTT	AATGTTCTGAA TTGACCAAATT TAA	GTAGTAAATGTTTCATCACTACCCGGGAGAGCAAAAGAACCATGGAACGGTAGCTAACTTTGGGCAGG TTC/G/ATTAATTTGGTCAATTCAGAACATTCCAAAT
WI-16905	75 C T	ACTTGGCCTGT GTTGTTCA	GTCTATACTCT TCTAGGCAGTG GG	TTTGTGTTTGTATTTGGCTCCCAACATCAGAACATAAGTTCCATGAAACAGGAACCTTGGCCTGTG TTGTTCA/C/TCCCACTGCCTAGAAAGATATAGACA
WI-16910	74 G A A	AAGAGTAAAG ATGGCGCTAG	CAAAATGAAG TATCGTTTCTA TAACAGA	AGTTTTCAGTATGTGCTTAAGGAGGTTATATTCGCTATGACTTTCATCTCAGAAGAGTAAAGATGGCG CTAGAA/G/AGTATCTGTATAGAAACGATACCTTCAATTTGGGCTGAACCAAGTGAAGGT
WI-16918	93 C T	CAGCCATTAA CACCAGCAC	TCCTGATACAG AAGTGGCATC	GGAAAGAAAATAAATAACCACTTCTCTGCTACCAAGAGCAGCATAAATCTAGGAATTTGAC TTTACTGCAGCCATTAAACACCAAGCAC/C/TJGATGCCACTTCTGTATCAGGAACCTTAACGTGACAACC ATGAAAGGTCCTCTGAAAG
WI-16947b	127 A C	GGAAAGCAGA CCTGGGG	ATGTGATTGCC CGTGG	TGAGTCAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAGCACAGGATT TGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGAAAGCAGACCTGGGG/A/CJCCA CGGCAATCACATGAGATG
WI-16947a	58 C G	CATGGAATA GGCCTGGAG	GCCTCAGCCAA ATCCTGT	TGAGTCAAACGATCTTGACGGGAAGCTGTTAGAGGTCTCATGGAAATAGGCCTGGAG/CJGACAGG ATTTGGCTGAGGCTTTCAACTGACATCAGACAAGACTGCAATCAAGGAAAGCAGACCTGGGGACCA CGGCAATCACATGAGATG
WI-16966	43 T C	AAATGCACAC TACATAACAA CCTAA	TGCAAGTTATC AGTATAAAA CTCATATT	CATTTGTTTACTTTAAATGCACACTACATAACAACCTAATA/T/CJCTTAACCTTGGTCCAACTATTT AGTATAACTAATATGAGTTTTTATACTGATAACTTGCAATGCCATTAA
WI-16995	55 T C	GAGCAGTAGA GACTGAGGTA AATAGTATT	CATGTTGATT CCAGCCGT	TTGAGTCCAGACATCAAGCATAGAAAGAGCAGTAGAGACTGAGGTAAATAGTATTT/CJACGGCTGG AAATCAACATGCCTCTTCTTCTGTGAAGTTGTGAGCTGAGCTGAGAAAGGCTGAGTCAATCT
WI-16992b	60 T G	---	---	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAAAGTACACTGTG/AJCCCTCATCTGAGATGTG TAGGACTGTAAAGGGAATGTGTTGGGGTTAGGAA
WI-16992a	46 G A TC	AAGCACCAG AAGTACACTG	CACATTCCTT ACAGTCCTACA C	AAATACATGGTGTCAACCTCAGCTAAGCACCAGAAAGTACACTGTG/AJCCCTCATCTGAGATGTG TAGGACTGTAAAGGGAATGTGTTGGGGTTAGGAA



WI-17010	23	T C	TTCAACAGGA	AATAACGGT	ATGTTTCAACAGGAAAGCCATGTC/JATGACATTCAAACACCGTATTATTAGAAGCTCATTTAAT
EST17127 9b	74	C T	CAAGCCATG	CA	TGTTTAAATGCAGACAAATAAAGGCTAACTAAAGCAGATCCAATGACCCAGTGATCAACCTAGA
			CACTGGCAC	GGGAGGCGAGG	GGTDOCCAG
			AGACAGAGT	GGTG	ATTCCGTCTCAACACAGCATCCAGCGCGGCATCTOCCCCACGATTTTATAACTCGGCACAGA
			AATTCTCTTAT	GGACTATGGCT	CAGAGTC/JJGGGAGCCATGGGGCACCCCTGCCCTCCCGAGGCTTCCTAAGTAACAACT
WI-17040	94	T C A	CATCTCAAGCC	TATTCAGTGAT	CACGCGTTCATTAAATTTGGTACAAAGCATGAACACTCAGGACAGATTGGCACAATACATGCAGTTC
			G	G	GAGAAATCTCTTATCATCTCAAGCCAGTC/JCATCACTGAATAAGCCATAGTCCCAGTCTCGTTTCC
			GCCAAGGAT		AAATCTTTCTCATATTGT
			TAACGTATAG	GGGATCCCT	TTGTTTGTGTTTGTCTCTCTCTGCAAGGATTAACGTATAGGTC/JTCTTAAACAAGGGGATC
WI-17044	47	G T G	G	TGTTAAGA	CCCCACTTATAGCTGACAGCAGCAGCTGCAACCACTGACTCTCTCTGCAGAAATGGCAGGGAATCGAAT
			TGGACTTGTCA		CAAAAGAAAGCAAGTG
			GCCTATAACT	TGTAGAGTTAG	GCATGTGTTGGAGCAGATCTCCATGTGTAGCCAAAGTGAGCTTGTGAGCCTATAACTACTCT/JAG
WI-17021	62	T A	ACTC	TGGCAGCTGC	CAGCTGCCACTAACTCTACAGGCACAGTAACACTTATACAGGAGCACATGCCAAAGTGCCCTGG
			CCAGAAAGGA		GAGTGCCCAATAAATCAA
			AAAGCATAAA	CCCAAGAGAC	TGTAAAAATGTAGACATGGGGGAAAAACATTCGTATCAACATGTGCTGTTTCTACTTCCGGTA
WI-17065	90	T C	CTT	AATGAAATCCT	CCAGAAAGGAAAGCATAAACTTTC/JAGGATTTTCATTTGCTCTTGGGT
			TGTACAGCCA	GAGATGTTGAA	
			ACATCACTGTT	AATGTTCTGGA	TTCATAAGGTTGTACAGCCAAACATCACTGTTTTC/JATTCCAGAACATTTTCAACATCTCAAAAGA
WI-17066	32	A C T	A	A	AACTCTGCACCCATTAGCAGTCATTCCTGTAGCTTCCCTCATAGGCAATGGCAACTGCTGATC
WI-17074	86	T G	---	---	TGCTGACTGTCATGACTTAGTAAGGCCATCACAGGTTGCCAGAACATCTACTCACTGTTCCAAAGCAT
					AACCTCCTACACAGGCCCTTC/JCTACATAGGAGTATATTTGGCCAAAGACTCACCACTAGAAAGTGATT
WI-17104b	108	T C	---	---	CAGATGAGAACTCATGCTGGCTCATCTGCAAGCTTCTGATGCTTTGCGAGCTTCCCATTCATTCCA
					AATCAGAAAGCAGTCAGTGGCCCGTGGTTCCAGACGGCTTC/JCTCTCTTTGTTAAGAAATTA
WI-17114a	37	T C	TTCCATCAAG	TTGTATTAA	AGCGTCCAACAGATGTTTCCATCAAGGACTTGTGTTTTC/JGTCTCTTCACTCTGCTATTATAATAG
			GACTTTGTTT	ATAGCAGAGTG	AAGCTACCTCCCAAGGCCAGATGCTCTAAGTGCTAAAGAAAGAACTGCAGCCACAATCAGAGTTACAT
			GATGAAATTC	AAGAGAC	GGGA
			AGATAGTCTTC	TTCTCAGAATC	
WI-17150	76	T G	CTCTT	CTGGAAGATAT	CGTGGCTGGACTAAGTGCTCTTTCCATGTGGACACATCTCCACTGAACAGGATGAATTCAGATAGTC
				G	TTCTCTTTTC/JCATATCTTCCAGGATTCGTGAGAAGGGCCCTCCTTTGTCTGCTCTAAATTT
			CATTCTTTGT		GAAATCGAATACGTCCATTCTTTGTAAATAACAATAACGTTTC/JAAGGCCAAAGCAAGATTCTG
			AAAATAACAA	CAGAATCTTGC	TAAACCAACATTGGAAAGGGGACACAGGGGAGGGGAAAGGCCAGATTTTCAACGGTTT
WI-17163	43	A G	TAACGTT	TTTTGCCTT	CCTCCACATCTGCAGACAA

WI-17178	127	T C	GGACTCCCTCA	CCCTCAATTTT	AGCAATGTCCCTCCAATTTCAATAGCTATGAGGATTATCAGTTTCATTCAGAGCGAATTACTGGGCGAGGGGTTTAAATATCTGATGGTTTAAATTCAGTGAGGACTCCCTCATGAGGAGCTTCJAGAA
WI-17180b	81	C G	---	CAACTGCTTC	GCAGTTGAAATTGAGGG
WI-17180a	47	T C	CACAAAAATA TAGAGAATCC	---	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAACTCTGCACTTCCCAAGTCTCGTCGCACAGGCTTCAACAATTACIC/GJAACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACAGATGAGGGAGTC
WI-17156	54	G C	TGTTCTCTAAA CTTTAGATATC	TGCGACGAGAC TTGGG	TCATGGACATCCTGAAGCAGACACAAAAATATAGAGAACTCTGCACTTTCJCCCCAAGTCTCGTCGCACAGAGCTTCAACAATTACCAACATCTTGCCCATTTTGTTTCATTATCCGCACCCACACTGACAGATGAGGGAGTC
WI-17149b	79	T C	---	CAAGAAATAT	TGAGGTAGCAGGGCATTCTTAAGAAATGTTCTCTAAACTTTAGATATCTCCCATG/CJTTCACAGAAATCAAAATATATTTCTTGTTGGAAATTTAAATGTTCTTAACTATCTGCCTACCATCCACCTCAATTAATATTCTTG
WI-17149a	48	C G	CAAGGTTTGA AGGAGGAACA	OCACGCAGTG CATGA	CAGGCAGTTAATGTCTGACATAGTAACAAGGTTTGAAGGAGGAACATC/GJTACATGCACGTGCGTGGAACCCAAATTGTCATGTGTATGAATACTACAAAAGGATGGGAAAGAACACATTTCTCTCACA
WI-17197	67	G A	GCAGAAGTAG CTGGGGCTAC	GGTGAGGTGGT GCATACC	ATTTTGCTATGTTGCCCTGGCTGGACTCCAGCAATCCTCCTCAGCAGAAAGTAGCTGGGGCTACIG/AGGTATGCACCACCTCACCTGCTTATCAGTTTCGTTTAAAGAAATATTGACTTTTAGATGCGCA
WI-17198	38	A C	TCCCTCTGTC CCTAGTTT	TCCATTTGTCC ACTGAGAAATT	TGTATTTTCAGTACTTTTCCCTCCCTGTGCTAGTTTACJTTAATTTCTCAGTGGACAAATGGACAAACCATCTCTGTTTGAATTTGAATACACAGATACATGCAAGATATCTTACAAGAAACAATGCACATCCTTC
EST18753	27	C T	CTACCCAGGCT GGTCTCAT	GGATCGCATGA GCCTGA	TCGCTATGCTACCCAGGCTGGTCTCATC/JTTCAGGCTCATGCGATCCTCCTGCTGCTGCAAGTGGCTGGGATAAGACACAACCTGCCACAGGCTGCCCTAGGAGTAGTCTTAATGCCCTGATGGTGGG
WI-17108b	74	C T	GCCATTACGTC TCAAAGTAAA	AACTACGATTT ATCATATGCTC	TTATTTTAAACATAACCAGATGCACCTTGGTTTACATTTCTGTTGCCATTCAAGTCTCAAAGTAAACACIC/JTGGGAGCATATGATAAATCGTAGTTTAAAGGAAGCCATAGCATTACAGAGT
EST19087	41	A G	---	---	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/JGJGTGGCATTAAAGTACATTCAACTTTTGAGCAACCCGCATCACCATTCATCATCCTCCGTT
EST19087	40	A C	CGTGACCATT AAGGTATAG	AAAAGTTGAA TGTAATTAATG	ACACAAAATTTACCATCGTGACCAATTTAAGGGTATAGTTCA/JCJAGTGGCATTAAAGTACATTCAACTTTTGAGCAACCCGCATCACCATTCATCATCCTCCGTT
EST19125	28	A G	---	---	CTGTTTCTCAGAGATGACACTGCCAACAJNGJTCACAGATTTGCATACAATACAGTTATGTATTGGCTATTACAAATTTACAGTAGTGTTTTCTCTGAAAAA

EST20824 8	115 T G	AGTCGGGAGT GCTGATTG	AAGATTTTATC TTGGACCCGA	GTGTGAAGCCGGAGTTTATTATTCAATCAGTCTCTCTGAAACTCAGGGATTGAGGTTTTTA AGGATAACTTGGTGAGTAGAGGGCCAGTAAGTCGGAGTGTGCTGATTGTT/GJTCGGGTCCAAGATAAA ATCTTAGG
WI-17347	50 A G	ATCCTCAGAA CTTCTCAGCCT	TCAAGCATCCA CTTGTGCTA	TTGGTTAAATGATGCCAGATGGGTACATCTCAGAACTTCTCAGCCT/VGJGTAGCACAAGTGG ATGCTTGAAGAACTCAGTCTTGGAACCTCAGACAGCAATGGAGACGGGATGTGAGTGGACCA
EST21904 b	128 G A	TTCATATGGCC ATTTTAATAA GTG	GGCAGGTGTTT AGAAAGCAT	TGATTGTGGTCTGGGAGCAGGTGGCAGTTTCAGTGAGGACAGAGGAAAGTAGACGCAGTAGAAAT GAGACTGGAATCAATAGAACAGAAAATGTACTAGGCTTTCATATGGCCATTTTAAATAAGTG[G/A]TA TGCTTTCTGAACACCTGCC
EST22111 3	82 T C T	GAAGATCTGT CTGGCATCTT	TGGAAAACA GCCCCAC	CAACAATGTAGACATAAGGGAACAAATTCAGAGAGCTCAAGTCACCATGTTTGCTAAGAGAAGAT CTGCTGGCATCTTII/CJGTGGGGCTGTTTTTCCAAGGCACA
EST22197 2	78 T C	AATTATTCTGC TATTCTGCCA	ACCATGAAGG ATGCGGT	GTTTAATGATCACTCACCAAAATCCACAGAGAAATCTTAAATGTTTACAAGCACCAATTATTCTGCT ATTCCTGCCAT/CJACCGCATCCTTCATGGTAGAGTATCACAAAGTTTCTGGTTGTTTCATC TACTTAAACCA
EST22311 9c	92 T C		---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAATCCACCCTGTAAACAG TAGCATTCAATGGTTTTACTCTA/CJGTGCAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST22311 9b	54 A G		---	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAATATACATAAAATCC[C/A]GCCACTGTAAA CAGTAGCATTCAATGGTTTTACTCTATTGTCAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST22311 9a	41 T C	GGATTAGATC ATCTTTTATT GAGTTATAA	TTGAATGCTAC TGTTTACAGTG G	TTTTCCATGGATTAGATCATCTTTTATTGAGTTATAAT/CJACATAAAATCCACCCTGTAAA CAGTAGCATTCAATGGTTTTACTCTATTGTCAAGCTGGGCAACTATCACTACTATCTAATTCAGAA CACTTTCATCATTCCAG
EST22319	19 A C		---	TCGAGGAGCTCTGAGGAGC/CJACCAAGGACGTGTGCCAGGGCCACCGTCGAGGCAAGTGTG GTCCAACTCCTCTCCCTTTACAAAACCTCCAGCCTCACCCACACAACACTGGCTGACAGGCCCTCT TAAGCCTTTTTAACTGT
EST22433 c	103 A G A A	AAGACATGTT CACCAAGTGA	CAGCTTCAGCT TAACTGACAGA	GATGTTAATGACTTTCTTTGAGATATGATGGAAAAATATTCAGGTACACATGGAAAGACATGTT CACCAAGTGAACCAATCTAACCAAGAAAGCTTTACC[C/A]GTCTGTCAAGTTAAGCTGAAGCTGAAAT CTGGGAGCTTGACATGCTG
EST22657 9	71 A G	AAATGGATCC TTATCTGCACA/T	AGTTTCAGTTT GCATGAATTTT	TATCCATTTCAAGAAAAAAATGACTTAAAAAATACAAATTCTATCCAGAAATGGATCCTTATCTG CACA/CJCCATTGAAGAAAAAAATTCATGCAAACTGAAACTATGCTTT



EST22993 5b	71	T C	ATCCTTTTGT TCTACCCC	TTGCCTGTAA TTTGACTGTAA TG	GCCTTTTATTGTCCTCTTTAACATCAAAATGTTTATAACACACTTGATCCTTTTGTTTCTACCCCCA ATTC]CATTACAGTCAAAATTAACAGGCAATATAATAGGTCTAACAGAATGCTTGCAATTT
EST23021 0	108	T A ---		---	TTATTTCTCAGCTTACCATTGTTGTAATCTCTGTACAAAGGTGTTTTTTCTCCATGGAGAAATG TTAAATCTTTGTGAGGTTAAATTTTATTAAATCTTTGCCTTT/AJATGGTTTGACAGTTTGTCCTTTCT
WI-17387	55	C G	CCTTTCAGAT TGAAGAAAA	GCCTTTGCCTA AGATTAATAGT AACTACT	ACAGAAATTTAACATGCAAGTTTCATTACATTACCTTGCAGATTGAAGAAAAA]C/G]AATATTAG TAGTTACTATTAACTTAGGCAAAAGCCATTTCTTTG
EST23869 1	101	A C	AATGTAAGCT CCAGAGGCAG	OCCTOOCCTOC TGTAAGC	TTTTTGGCTTGTCTGCAGAAATAGATGAAAGAGAAAAATATACCCAGATACTTTTGCTCACTCTCCCA AGTGCACACTAGGCAATGTAGCTCCAGAGGCAG]A/C]GCTTACAGGAGGGGAAGGACGCTGAGGC CAAGAGTGTCTGGCTCACTG
EST23733 9	31	T G TT	GGCTGTTAGTT TTGTTTTGTTT	TGCACCTTAAA TCCCATCAAT	AAAGGCTGTTAGTTTGTGTTTTTTCCTTT/G]TATTGATGGGATTTAAAGTGCATATAACTGAAG GCAAAGTCCAAGGCTAGAGAAAGATATAGGCCCCGAGAGAGAGGCTCAGAGATTCTAGAGGCGGC TGAAGAAATACCCACCTAAA
WI-17470	83	A G CCAG	GTCCCGTCCCG CCAG	CCAGTGACGAG GCGA	CTGACACGTCCCTGTGTGGGGGTGTCCATGTGGCGTGTGTGAGTGAGACTTTTTTACTGCGTCCOC GTCCCGCCAGCCCT]A/G]TCCGGCCTCGTCACTGGCCTTGGTCACTTTGATTTCTGTCTTGGTTGGAAA TACCATCAGCCTTCC
WI-17519	55	T C A	GTGTCCTAGC TAATGAATGC	AATTATTATT TGCAGGCAATA CTC	TTTTTAACGAAATCTCACTACTGCAAAATGCATTGTTGTCCTAGCTAATGAATGCAT/CJAGAGTATTG CCTGCAAAATAATAATTGAGATTCTATTTTAAAGAACTTAGAACAGTACATGGTGCATAG
EST25356 3b	95	C G ---		---	TCCTTGATACAGGTAACCAGTTTGTAAACATTATTTCAGAACTTCACTGTATCTTCAAGTTTGTATAT CAGCATCTCTGTGGAGAAAGCAGTGTG]C/G]TATAATGTCAACATCAGGATTTCTTTTT
EST25356 3a	26	A C ---		---	TCCTTGATACAGGTAACCAGTTTGT]A/C]ACATTTATTCAGAACTTCACTGTATCTTCAAGTTTGTGA TATCAGCATCTCTGTGGAGAAAGCAGTGTGCTATAATGTCAACATCAGGATTTCTTTTT
WI-17581c	99	C T ---		---	GGGTGACGCTCCAGATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAATGATAGAACCCAA]C/T]TAGCGCAATTTACATTGACGGTCATGC
WI-17581b	86	T C	ATTCAACATT ACTACCAGTT ATTGATAA	CGTCAATGTAA ATTGGGCT	GGGTGACGCTCCAGATGGGAGACAAGCCAAATTTGGGAGCAGATTGGATCCAGCTTCATTCAACATT ACTACCAGTTATTGATAAT]C]GATAGAACCCAACTAGCGCAATTTACATTGACGGTCATGC
WI-17596	86	A G C	ACTTCCTTGTG TAAACACTCC	CATTCTTAG CTAGAAATCGA CAATAT	GTGTGCTGTAAATGGATAATAGCAGTCTCTCATCTCTGAAGGGTGGGAAGTAGGAGAAGGCCTACT TCCCTGTGTAAACACTCCCA]A/G]ATATTGTTCGATTCTAGCTATAAGAAATGGGCCACTAAGTGGGTC

WI-17623	46 T C ---			TGTGGTTTAAATTTCCCATATAATTAATGGTGGGCACATTT/CJGCATGTGCTTACTGGGTC ATTTCATATATCTTTTGTGAAGCATCTGCTCCAATCTTTTGCTGACTTTGGAGTTTTTGGT
EST26419 1b	46 T C ---			ATTTCATACAGAGATACAAAGGCAACTATGTGCAGC/AJAACAATCTGATGGGCAGTCCAACTTCT TGGAGGAAGTAAATTCATGGTAAATGTCAATGTGCTGGTTCCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26419 1a	35 C A AG	ATACAAAGGC AACTATGTGC	CAAGAAGTTTG GACTGCC	ATTTCATACAGAGATACAAAGGCAACTATGTGCAGC/AJAACAATCTGATGGGCAGTCCAACTTCT TGGAGGAAGTAAATTCATGGTAAATGTCAATGTGCTGGTTCCGAGGAGAAGGTTCAAAGGAGGTAG AGAGAGGAGACAGAGAATG
EST26780 5	69 GC ---			TCAGCTTTAATTTAAGGGACATGTAAATAAAGATGCAATTTGACAGGACAGCAGACTAGTTCAAGC AG/CJAGGTTAGACCAGTAACAACAACCAAGAAAGCAAGTCTGTTTCCATCTTGGCTTTACCA CACTTACAAACTGATACCC
EST26900 7	39 A G ---			TACTTCAGTTTAAGGCAATTTCCACACAGAGACTGTCTC/A/GJGAGACGGGCACAGAACCCAGACACC GTAGAAACACCACCACCATGCATGACGGGGAAGCAGAG
EST27152 1	101 C T ---			CAAGGATTTTATTTTGTCCCTAAAGTAAATCTAGAAAATAGCAACCCACTGCAAGAGAGTT CTATACTAAACATTTTCAATCATCTCTCTTCT/C/JTTTCACATGGTGACTCTTTCATGTACACAT CATCGGAAACAGACTGA
EST27504 0a	33 G A ATTT	GCACTTTGCAA CAATTTAATA	GCTGGTGTGAT GCTACTGTAAT G	TTTTTGCACCTTTGCAACAATTTAATTTATC/G/A/CATTACAGTAGCATCACACCAGCAGTCAAT AATGCCACCTTAGGCAAAAGCTTTTCAGTATTTCTGTACACATTTCTGTTAACAAGAACCCATACATT GGTAAATTCATCT
EST27662 4	51 C T CTCCAGTCTTG	CACATTCTGTT CTCCAGTCTTG	TTATGGAATG GCTTATGTAAC C	ATCTAAAGGACCATTAGAAAAGGCCAGTCACATTTCTGTTCTCCAGTCTTG/C/JAGGTTACATAAG CCATTTCCATAAATCTATAGCCTTCTTCTTAGAGTAACACACACTCTTGTTTAGGAATGTTT
EST27788 3	100 A G ---			ATTTTATTAGCGGTACAAATTCGAAGTGGTAAGGGTGAAGGAAAGGGAAGGCAGGCAAAATACAT TATTGAGCTGAAAACAACCTTACATTCAAGGAC/A/GJGCTTCCAGACAAAGCCATGTAGAACCAGCAT GCCTGGGACTGTGTGGAT
EST27828 4	58 G A AGAACCCAC	GGAAGTCATC AGAACCCAC	GTGCAGAGAGG TACTCCAAGTA C	TCCTTAAACTTTCCTTCTGTTGGATCCCAGTGACGTGGAAAGTCATCAGAACCCAC/G/AJGTACTT GGAGTACCTCTCTGCACCAAGATAGCTGGCTGATTTTCTGCTCAGTCACAATTTTACTTGAA
WI-18369	58 G A ACAATC	AATAAATTC AATCTGTCAC	TCAAGAAGGCC TTATCCAATT	TAAAAATTTGAGATACATTCCCAATGTAAACAATAAATTTCAATCTGTACACACATC/G/AJAAATG GATAAGGCTTCTTGACAAATTTCTGCCACCTCCGTTTAACGCATCAGAACTCAATCTTATCTC
EST28036 4	37 T C ---			TCCCGCTTCCAAAGCTTTATTGGCAATATGCTCTA/T/CJAAAAGAAATGATCAATCCTGTGCTCT AAGTCAATGGAATGAAGAGCTGTGTCCAGGACACACACCACCGCTGTGAAGGAGACTGCTGTGTG TCCACCTCTTATTCATAG

EST28483 7	31 T A	GGAGTAAAG GTGTTCTTCT	TTTCTCGCATT TATTTTATAC CA	CATTGGAGTAAAGGTGTTCTTCTTAAAT/AJATGGTATAAAATAAATGCGAGAAACATTAAAC GGAGAAATGTACAGACAACAGACGAGACATGAGTTTGTCTGACTGTGACACATTGGTGAAA
WI-17724	50 T C	TGGGCOCTOOC TGTC	TGGGTTGGCAG TGTC	AGAAATTGGTCTAGTAATCGTTTCAGGATTCGGTGATGGGCCCTCCCTGTCTTCJGGACACTGCCAAACC CACAGCTGGAGGGGCACCTTAAGGCACGTCATTTTGTGATTAGA
WI-17730b	68 T C	---	---	TGAGCCTGGGAGAAAGACCACAGAGTGAAGTGCTATTAGTTACATCATACCAAGGTACATACTG TT/CACACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
WI-17730a	39 A C	GACCACAGAA GTGAAGTGCT ATT	TCAACAGCCAT AAATCATGTG	TGAGCCTGGGAGAAAGACCACAGAGTGAAGTGCTATT/CJGTTACATCATACCAAGGTACATATA CTGTTACATGATTTATGGCTGTTGATGTTGACCTCAATAACCTGGCTGATGTAGTATGTGTCA
EST29041 5b	53 G A	GGAACAAACA CATTAAAGCAT CA	GGTATTGTTGA TTTGAGGAGTT AGC	TACTCAGAAATGTGAGTTCATGAGGAACAACACATTAAAGCATCATTTGTCACTG/AJGCTAACTCCT CAAATCAACAATACCCCTTTATTTTAGCCATGAAAAC
EST29128 4	58 A G	---	---	CTTTTAGAAGGACACCAGTCTGTTGGACTTAGGGCCTACCCTATTCAGCAGGTGCC/AJGTTATTT TCACCTTGTTACGTCTGTAAAGGACCCTTCCAAATGAGGTTACAGTACACAGGTTCTGAGCAGACATGA GTTTTGCTGGGGACACT
EST29912 3	103 C T	TCTGCCAGCTT ACAGGCT	GCGTAAGTGTC TCATTCTTCTG T	ATTTATTAGGTATCTGCTGTTGGGGTGGGGAGATTGTTGAGATACTGCAACAGACACAAA AGCAAAGAAAGAAACATTTCTGCCAGCTTACAGGCTTC/JACAGAGAAGATGAGACACTTACGCATG GCCATGATACACAGCAGTGA
EST29936 8	121 G C	---	---	TATTGGTATGCTTAGGGAAGATTCTGATTTAGAGATATTAAATCTTAAAGTTAACTCACCATGAAA TTAAACCTTCTGTACTGGCTTCACTGATGAGGCAGTAACTACATAGGGATAAA/GCJAGCTCAGTA TCTGGAATCATGCTCCTG
EST30223 2	99 A G	---	---	AAATAATACATCATGGGGAATGGGATATCCATCCCTCAAGCATTTATCTTTGAGTTACAAGCAA TCCAATTACACTCTAAGTTATTTTAAATATTC/A/GJGGATTTAATTTCTTCTAGTTCAATCTTGGGA GG
WI-16260b	86 G A	---	---	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAAAGACCAGGA GTTTCACAATATAGGTAGC/AJATAACCAGGCTCCTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-16260a	59 G T	TGAGGTGGATT CAAGAAGAAA A	CTACCTATATT GTGAAACTCTG GGT	CTTTTCCATTGGTATTAAACCTGCTAGAGGTTCTTTGTGAGGTGGATTCAAGAAGAAA/GTJACCC AGAGTTTCACAATATAGGTAGCAGTAAACAGGCTCCTTCCCTTCCGTGAGAACTTCGTGGGAC
WI-17835	30 G A	ACAGGAAATA TTGTGCTTTCT TG	TGGGGTATAGG AACAGGC	AAGAGAAACAGGAAATATTGTGCTTCTTCTG/AJGCTGTTTCCCTATACCCCAATATCATAGAATT GTTGTTGCTTCTATAATGTTTCAGCTTCAAAATCTTTTGCTTAATCAATCCAAATGAATTACCTGAATT TTCTCCTCTTGTCAAAA



EST31951 4	87	C T	GGTTGTCCAG CCAACA	CCACCAAAT CACCTCC	ACAGCCATTATTATGTTTACTTGGTAATATCAGAGACTGAAACATTTTCACTCTTTAGCAATGACA TCGGGTTGTCCAGCCAACA/C/TGGAGGTGATTTGGTGGGAATCTTATCACAATTTCT
EST31968 8b	95	T G	---	---	CGAATTTGTCCTCTTATTTGTGATTTCTAGTAATCCTAAAGATTGGGGGGGGTTACTATAAGT GCATTTTATAATGGGATTTTCTGCTT/GJAACCTGCCCACTGATTCTTACATGGGAAAGGTGCAAG ACAGTGGTACTGCTCCC
EST31968 8a	75	T C	T	TGTAAGAATCA GTGGGCAGTT	CGAATTTGTCCTCTTATTTGTGATTTCTAGTAATCCTAAAGATTGGGGGGGGTTACTATAAGT GCATTTT/CJATAATGGGGATTTTCTGCTTAACCTGCCCACTGATTCTTACATGGGAAAGGTGCAAG ACAGTGGTACTGCTCCC
EST32063 2	103	C T	---	---	TCCATGGATGAACAGACGCTACCATGCCACATCCCACTTCCCTCCGACCAGATGTCGTGGCCAGAGC TGGCTTCCCTTCCAGACCTAGCTGGCTTGTAGTCT/GTTTCAGGCCCATTTGAAATAGCAACGCAC AGTCATGTAGCACCTCGG
WI-16303	65	A G	---	---	AAGGCTTTCCAAGCATTCAAAGGCACCTGGGTGTTGTGCTCTAAGTTTCTGTCACTGCAGCCCC[AG JTCTGTATTAGGGAGCACCCCAAGCCAGTAACAATATGTTCTTGACG
WI-17800	29	C G	GGGAGCACAA GAGAAACTCA	TTTCTACAAT TAATCCCAGTC TT	TGGACATGGGAGCACAAAGAGAACTCACTC/GJAAGACTGGGATTAATTGTAGGAAATATTTACACAG TTTCCACAAGTCAGAAAGAGCTAATCCCAACCCTCTGTATCTGGAACATACACTGCTGCCATTTTCTGC CCATGAAGGGAAATACCC
WI-17857	34	T G	CCTAAAGTCTG GGATGACTTTC	TTGGCTTAGGT TCTACTTGATG T	AACTGTCACTTCTAAAGTCTGGGATGACTTTCCTT/GJATTCTACATCAAGTAGAACCTAAGCCAAT TCAGAAATCAGAAATCCTTTTGTCCATCAAAATCCAGCTAACTCCAAGCTGAATTAATGTTTCTTCT
WI-17860	121	T A	TTTCCAGCAA AGCAAATA	ACTAAGGAGC AGTCAGTCGG	GTATCTGATGTAGTTAACCATGGCCTGTCATGATATATTGCTATAAGGAAGGGAACAAATCTTTA TAGTGTCCAAAGATAATTAATTCTTGGTTAAATCTTTGCCAGCAAGCAATA/T/AJCCGACTGAC TGCTCCTTAGTCTGTGATC
WI-17866	43	A T	TTTATAGCCT ACTTCTCAA	CCGTTGTCAC AATCACACAA A	CAGCAACCTTTTGTGTTTATAGCCTACTTCTCAAAATTTGTT[ATJTTTGTGATTAGTGACAACG GGGGAATCTACATGCTCACATCACAGTAACCTACCA
EST33301 4c	80	G A	ATTGTT	---	GAAAAAAGTCAATGTGTTCCCTTTATGGGTGATGCCACCATGATGCTCACACAAGCATGATC AATCGCCACGAGA[G/A]ACTGGATGCCAAAGAGTATGG
EST33301 4b	63	G A	---	---	GAAAAAAGTCAATGTGTTCCCTTTATGGGTGATGCCACCATGATGCTCACACAAGCAT[G/A] ATCAATCGCCACGAGAGACTGGATGCCAAAGAGTATGG
EST33460 1	44	G A	AGCGTGGTTT CAATACTAAA CA	CTGTATTTATT GTAAATATTT GCATTGTT	CTATCCAAAGATATTTATTCAGCGTGGTTTCAATACTAAACA[G/A]ATGTAAACAATGCAATATT TAACAATAAATACAGTGATTAATAAGCCATGGCATATCCAGTTGATGTAATACITTTGCAA

WI-17904	50 A G	AAAGCATGAC AATAAAATGA ACAC	CGCTTAIGTTA ATAGTAATTCC OG	CAAGTGAATATTGATACATGGCTGACAAAGCATGACAAATAAATGAACAC[AG]TACGGGAATTAC TATTAACATAAGCGATAACATCAAAACATCTGGTAAATGCAGTTAAACAAACACAAATGA
EST34149 5	69 A G	TGCCAAATAC TCAAGTGTGA AT	AACTACTAGCG AGAACAACTA ATAAAATC	GTTTTTCTTTGAGTGACACAGCTTGTTCATTTTGAGAAATGTGTGCCAAATACTCAAGTGTGAA T[AG]GATTTTATTAGTTGTTCTCGCTAGTAGTTTGGTATTCTATGAAAAAAGCAGCTAGTTCAGC TTACAAATCACACAAGT
EST34343 8	95 C A	---	---	TGGGAAACATAAGTTAACTCAAGAATATATCCAGTCTTTATGTTACTAAACATTGTAAATAGTGT TTTTATCAATGATGCCGAGGTCACTGCT[C/A]TACAAAGATTAAAGAACTTACCATCAACACTTC CAGTGCATCAA
WI-17982	98 C T	GGACCATATG ATATATAACT CCTAAAGC	CAGAAATTATG TGATAATAACT CCTTCC	GGTACACAAATTTTAAATGGAAGGAACACAGGTATGTTGAAAGAACATCAGTACAGCTGGAGACAGG GAGGGACCATATGATATATAACTCCTAAAGC[C/T]GGAAGGAGTTATTATCACATAATTTCTGGGC GCTACAGAAGTTTTCATCA
WI-17993	118 A C	---	---	CTCAGTAACTCCGGTGTATAATCTGCCATTATTGATTATTATGATAAAACACCTCTCATTGTGA AAAACAGCTAAGGGTGACATCTCCAGAACCACTGTCCTGTAAATG[C/A]CTGCTGAGAGTCC ACATTTTGGAAATCCAAT
WI-17998	84 A G	GTAGAGGCGA AGGGAACAG	AGGCACATGGG CAGC	CCCATCCAGAAACCCAGTGTGATGTGGAGCAGCATGAAACAAACATCTCCCAGGCTCGCAGT AGAGGCGAAGGGAACAG[AG]GCTGCCATGTGCTCTCTAAAGACGCCACCTCAGGTTGATGT CACCTGTGGAGACCGGGT
WI-17136	33 C G	---	---	ATTCTTTATAAAACACCATGTCCCTAAATG[C/G]ATTCAACATATATGCACACCTTCGATGTAT AGGACACTGATCAAAAAGACAGAGAAATGTGTCCCT
WI-18041	24 A C	---	---	GCCACTGAAAAAGGTGCTCTTCC[AG]GTTTCTAACTCCCTGGACTCCCTCATTGGAACTGAAGCTC ACAGATGTTTCAGCTGGACTAGTTTAGACTTTGCTGTATTTTAAAGGCAGTGTGATGCTCCAGGAT TCAAATACTTAATCA
EST35164 8a	57 A G	CACAGCCCTGC OOC	CCCTCTGGATT CTGAATCTCAA	TTGAACCAAGGCCCTAACAGATGACTCAGCAGGGCCCTCAAGCACAGCCCTGCCCC[AG]TCTTGA GATTCAGAAATCCAGAGGGTGCTCAGTCCCTGGTTTAGGTCCTCTGTGACATTTCTCTTG
WI-18052b	67 A G	---	---	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCT[C/T]GGTTACACATCTT[AG] AGJACAGCAGAGCTGCCCTGAGGAGGGTTGTGTTTAAATGTCGTATGCATGCTCAGCAGAGTGTGGC ATGGCCCATCCATGCTTT
WI-18052a	50 T C	CCTGAGTTCTT TCATGTACGA ATC	CTCAGGCAGCT CTGCTGT	AGCGAATGAAAAATGCTACATAGGCTCCCTGAGTCTTTTCATGTACGAATCT[C/T]GGTTACACATCTT AGAACAGCAGAGCTGCCCTGAGGAGGGTTGTGTTTAAATGTCGTATGCATGCTCAGCAGAGTGTGGC ATGGCCCATCCATGCTTT
WI-18054	46 G A	GGGAGTGGG GAGTAAA	CGTCAOCCCTGC TTCCA	CTGTTGTGCTGAGAAACAGAGGGGTCAAGGGAGTGGGGAGTAAAG[AG/AT]GGAAGCAGGGTGACG CATGCAGGAGTCCAGACAAAGACGGGTGATTTTGCTCAGGTTGGTAGCAACAGAGGTAATG

WI-18064	54	G A	GTAGCTGCTA AGCTGTATTTC	CCAGTGGTATG ATTGTGACATT C	CAGCTGCCAATCATCTCTCAAAACCCTGTGGGTAGCTGCTAAGCTGTATTTTCAGAIG/AJGAATGTCAC AATCATACCACCTGGGAGAAAGAGTAAGCACAGTGCCTTATTAGGTGCCAACTGGGTACCTGGGAG GCAGAA
EST35347 2	97	T C A A	GCATAAAATT TCCAGTTGGT	CCCTGGCAACC TGCT	TTAGCACCATCTTAGTGGAGCAGGATTCTTGATCATGGGTGGAAATTTTGTGTATCTGGGCTTCAT GGGATGCATAAAATTTCCAGTTGGTAAGTTCJAGCAGGTGCCGAGGTCTGGATCAGAAAAAAAGG CAGGCA
WI-18070	28	A C	AACCCACTAC TACTCAGAGT GTGTAT	AAAACTAATA AGAAACTGGA GGTTTT	AAACCCACTACTACTCAGAGTGTGTATTCJATATTAACACATGAAAGATATAATCTTAGAAAAA ACCTCCAGTTCTTATTAGTTTGTATATTTCTGTACTCAGAACGATTTAGGTGCAAGGATATATA
WI-18080c	80	C T	---	---	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCCGTG TTTGACITTTATTC/TTCCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080b	65	G A	---	---	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTTGTAAATTAATCTACTATGCCIG/ ATGTTTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT
WI-18080a	41	T C	GCAAATATCA ATATCAAAC AGTCTCTC	CAATTTACATA AGAGATAAAA GTCAAACA	TGGCATAAAGTTTGCAAAATATCAATATCAAACTAGTCTCTCTTC/TCTGTAAATTAATCTACTATGC CGTGTGACTTTTATCTCTTATGTAAATTGAAGCCAAATGCATGTTAATCCTTCTCCTTTGGTGTAT GTGGCATCCTATAAAGCAGCCATGTGTGAAACAAATGATATGCACAGAAAGCATACCTTCG/A TGGCTTTGTTACACGGTTTCTTCAAGAGGAAGATGACTAGCCCTCCAGCTTCTGCAGICTAGC TTAGGAGAGGTGTIGAA
WI-18086	63	G A	---	---	AACTACATAGTAGTGGTGCCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTAACCTTTGGTATCC TTC/TCTTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115b	71	C T	---	---	AACTACATAGTAGTGGTGCCTGGCTTAGAATCAATGGGTAAAGCCTTTAGTGTAACCTTTGGTATCC TTCTCTTTGGTATGAAAGACAGACACCTCTGCTGGAGGACTCATTACAATGTAAAGAAAGGGTGAG TCAGT
WI-18115a	70	C T	TT	A	TTTTGAGAAGCACCTGTAGGCAAGGATGCATTCAAAAATGGCTTTGAGGATTAACTTCTCTTTA GGTAATTTGCA/GTTAAGAAACAATAAAGCATTTTAAAGTCCACTGCCCTTAGAAACT
WI-18136	78	A G	---	---	GGCAAAATATTTTACATCACACCTGGAATCTGCCAAGTCTTTCCACTATGAAGGCAATCGTAGAG TGTGCAGGAGGAAAGGTGTATCCAAGCAGCCATCTTTCCGGAAGCTC/A/GTGGAGCACAAAGCAGA ACTCGGTGGGTAGGTGGA
WI-18169	115	A G	CCATCTTCCG	GAGTTCTGCTT GTGCTOCA	TGAAAGAAGTCGACACAGCGGACACTG/AJTCATAAGTGGAAACAAGGATGAAGCTAATCATGGAG GCAAGCTCCCTGGAGAGACAGGACAAATCAAGATGAGCTGGAGACATTAATCCTGGCGA
WI-18190b	26	G A	---	---	



WI-18190	62 G A ---			---	TGAAAGAAGTCGACACAGCGGACACTGTCATAAGTGGAAACAAGGATGAAGCTAATCATGGA[G/A] GCAAGCTCCCTGGAGAGACAGGACAGGACAAATCAAGAATGAGCTGGAGACATTAATCCTGGCGA
WI-18181	100 A C CAGATC	AAATATATAC AACACTCCCTT	CGTTTACCAT TTGTTAAGCTT TTG		GACAGTGAACAACATTGAAACACAAATACAAACAACATTAGGAACAAGAAATGTGTAATCCAA TGTGTGAACAATAATATACAACTCCCTTCAGATC[A/C]CAAAAGCTTAACAAATGGTAAACGTA TGTGTTCTTGAAC
WI-18215	78 G A CTGCCCTC	AGCAGAGTTC	CCTCCCTCTCT CCCC		ATTACATAAGCAATTCCTGAGTACAACTAGGGACAGGTATTTACAAAACAATAGAGCAGA GTTCTGCCCTC[G/A]GTGTGCGGGGAGAGAGGGATTTCAGCATTTGGTGGAGTATGTTAATT CCCTCAAGTTAATTCCTTC
WI-18232	60 T A AA	TGGTGTGATT GTGATACACTT	AAATAAAGGT TTTCAGGGGT C		CATTTCCGAAAATCTGATAGTTAAATATCCCGTCTGGTGTGATTGTGATACACTTAAGT[A/GAA CCCCTGAAAACCTTTATTTTGAATTGAAGTTTTTGTCTCAGAAACTGGGCAGAACTTTTCACATTCTG AC
WI-17892	76 T C ACA	GGAAAACCTTG AGTTTGAGATC	CACAGAAGTG AATAGACTAGT GAGACA		TTTAAAATGCTTAGATTTTCTCAGTATTTTATCAATAGTGTGTAAGCTGGAAAACCTTGAGTTTGAG ATCACATA[T/C]CTGTCTCACTAGTCTATTCTACTTCTGTGGCATTTCCGGCAGAAAGTGGC
WI-18242	30 G A AATCGTAACA	CCCCAAATGTT AATCGTAACA	GCTAACACTTC TACTGTAAACAG CTTTC		AATATCCCACAAATGTTAATCGTAACATACT[G/A]GAAAGCTGTTACAGTAGAAGTGTAGCAAAAAT TGGATGCCACAACTTATCTCACCATTCTTCAAGCAAGTGAGGGTCAGAAATGTTTCTTGCCCTATATC TGCAAAAGATCGAACAAG
WI-18266c	119 C T ---			---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATC[C/T]ACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18266b	124 T C ---			---	GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAACTGCACAAATGATGCATGAATCCACAT[T/C]TGAGAC CCGCAACTCCGAGGTACCT
WI-18266a	97 C T TTCAAA	AAATAGGAAA TATGGACTATC	TTATGCATCA TTTGTGCA		GCATCAGACATCACCACTCCTGAAAAAACCTTCTACAAGAAATTGAAAAGTGTTCAGGACCTAATA CTGAAATAGGAAATATGGACTATCTTCAAA[C/T]TGACAAATGATGCATGAATCCACATTTGAGAC CCGCAACTCCGAGGTACCT
WI-18312	73 A G AA	GCTGTCAGCTA TTGTTATTTC	GGAGAAAAGG GAGCAGAAGA		CTGAGCCTCTTGATATGTGGTTTAGTGTCTATCATTAAATTTGGAAAGCTGTCAGCTATTGTTATTTC AAATJA/GTATCTTCTGCTCCCTTTCTCCTTTTCTGGGATTCTCATTTCTGCATGTGTATA
WI-18330b	66 A G ---			---	AAACATCTACAGCTGTCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGAGCTGAGGAACAAGAGG[G] A/GJTATGAGGCAGTGAGTCAGGACTATGCAAAACCATAAAATAAAGAACATAATTTTTTGTGTGAT TCACA

WI-18330a	49	G A	TCCTGTAAGA AATCAGGGAT	AGTCTGACTC ACTGCCTACA	AAACATCTACAGCTGTCTTAGGCCATCCTGTAAAGAAATCAGGGATAAGA[G/A]CTGAGGAACAAGA GGGATATGTAGGCAGTGAGTCAGGACTATGCAAAACCATAAATAAAGAACATAATTTTTTTTGTGAT TCACA
EST37564 5	85	T C	AAATTCAAGC CATCTACAAA AGA	CTATGGAGGCC TCAATGAGA	AAATTAGTTAGCCATAACAGGCTGGAATTGCTGTTAGAACTACTGCATGTTATTTAAGCTAAATTC AAGCCATCTACAAAAGATT[C]TCTCATTTGAGGCTCCTCATAGGCTGCAACACATCAAAAGGCATTAC TGTACTGGAGAGGACTGAG
WI-18327	104	G A	AAACAGCTTT CGTTAGGCTAG TT	CGCATACAATG GCTCAGC	CAAAGGATTATTACCTACAACAAGTAAGGAGGACAGCTGGGGCAGTTTCCCAAAGCAGTACCTC CCAAACAATGGTGAAACACAGCTTTCGTTAGGCTAGTT[G/A]GCTGAGCCATTGTATGCGGAGGCAGA GT
EST37624 6b	102	G A	---	---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCACGCTGATGG CCTGCAGTCTCTGCCGTGCTTGGCTCTCTGACG[G/A]TTTCATTCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
EST37624 6a	58	C T	---	---	GTGGCAAGAGCAGCTAAACACACTCATTTTGCATGAACCTCCAAATACGAACAGTGCATGCA[C/T]GCTGA TGGCCTGCAGTCTCTGCCGTGCTTGGCTCTCTGACGCTTTCATCTACATGGCTGCTGCTTTGCGTCC TCTGACCTCCCCATTCC
WI-18357	89	C G	CCCAGCCCTTA GCATCAA	AAGACTCAA AGACTGAAGAT GA	AATGTTTTAAAAAGTCTACCGTGTGAGGTGGCCATGAAGCCAGCCCATGGAGAGACATTTTCAGA TAATCCAGCCCTTAGCATCA[C/G]TCATCTTCAGTCTTTGAGTCTTCCAGCCAGGTCCCAAGCTT GTGGACCAGAGACAAGCC
WI-18012g	117	A G	---	---	TTTTATCTGGGTGAGTCTCTCTTAATGGCTGAAGGTGATCTCTCTTCAACTTTCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGA[G/G]GTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012f	113	G A	---	---	TTTTATCTGGGTGAGTCTCTCTTAATGGCTGAAGGTGATCTCTCTTCAACTTTCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGA[G/G]GTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012e	112	C T	GCCACTTTTGC CCCTT	TCAGCGTGAT CAGGAAACA	TTTTATCTGGGTGAGTCTCTCTTAATGGCTGAAGGTGATCTCTCTTCAACTTTCAGACTTGGAAAG ATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGA[G/G]GTGTTTCTCTGATACA CGCTGACGTTTCGAGGG
WI-18012b	46	T C	---	---	TTTTATCTGGGTGAGTCTCTCTTAATGGCTGAAGGTGATCTCTCTTCAACTTTCAGACTTGGAAAG AGATCCCGCTGTCCACTCTTAGAATTGAAGCCACTTTTGCCCTTCGTGAAGTGTTCCTGATACAC GCTGACGTTTCGAGGG
EST38390 4	75	A G	GCAAAAAGGA CTCTGCATTG	GCTAAAGTCAG CTGATTAATAA ACTTAA	CATATCATAGCCAGATCTACAACCCAGAGTAATCCCATGGTTATGTTACATGGCAAAAGGACTC TGCATTGT[G/A]GTAATTAAATTATTAATCAGCTGACTTTAGCATGGGAGATTATTCTGGAT

EST38512	91 T	TGACGATGCC	CACTGCACCTCT	TAATAAACTGACCCCAATTGGTAACTGTGTCTGGACTGAGAGAAACAATGAAATCTGTAAAT
7		AATACTTCG	GGAAGC	ACCTGATGAGGATGCCAATACTTCGT/GJGCTTCCAGAGTGCAAGTGAATACTGTTATAGCC
EST38519	24 C T T	CCTGCACCTCC	TCTGTTAGGAC	CCTGCACCTCCCTAAAGATCTTTTC/TTCCCCCAAGTCTTAACAGAAATGGTATATCTCTGGAAAA
0		TAAAAGATCT	TTGGGGA	AGATGAACGTCATCAATGGATTGTGCTCTCGTTTCAGCTTTGATTTTTTTTGTCCTTGAGAACCTTG
EST38575	66 T C A A	GAACATCCCA	AGGGAAGGTA	TCCTCCCTGCTGATTT
1		TGTTTCTGTTT	GTATAACACAT	AGTGGTCAATGTAAACTAATGGGGACACCAAGCCTCAGGAAGAACAATCCCATGTTTCTGTTTAA
EST38616	101 C G C T T C	CCTGCTCGGC	GAGGAATGGAT	T/CJCTCTTATGTGTTATACTACCTTCCCTTCTCTTTCTTATACACATAGATTTTCCCTTAATTGCAGC
9		CTTC	GGTGGC	CCA
EST38652	59 T C	TCTGAACCTGGG	TTGCAAAAATG	CCATCTAGGCAGGCTACCTGAGCTCTCTGTGCTCCAGAGTGGTGGCTCACGCCCGGGGCCCCGTGG
8		CATTTCAA	AAAGGAAAAA	AGTCTCCGGCGGCCCGCCCTGCTCCGCCCTTC/C/GJGCCAACCATCCATTCTCCAGGGG
EST38654	42 T C	AATGGTCATTT	CAGTGATGGTC	TATAGTAGGTACTTCCCTTGTGCTGCAGCAGGAATATTCACTGCTGAACTGGGCATTTCAAT/CJGCGTG
5		TAATATATCA	CTTAATCTTCT	GTAATTTTTCCTTTCATTTTGGCAAGTAAAAAATCAT
EST38707	75 A G ---	GTGTTTACA	ATC	CTCAAGCTGAGAAATGGTCATTTAATATATCAGTTTACATA/T/CJAGATAGAAGATTAAGGACCAT
9			---	CACTGAGGTCACATAGCTCAGAGGCAGAGTTAAGATTTGGACCCAGGAGTTGGTTCCAGCATATA
EST38759	86 A G	TGCTCCCTGA	TCACCATCGTG	GGATCCTCACTCACCTGGGACAGCCTGAGAGGGAGATCCACCAAGACCTACTGATCTGGAGTCCCA
2		GGTGATAGG	GACTTAAGG	CGTTCCCCJAGJAGGCCAGCGGATGTGTGCCCCCTCCTCCTCCTCCCAACTCATCTTTTCAGGAACACGAGG
EST38775	40 T A C	AATCAATAGG	GAATTCAAA	ATTCTTGCTTTCTGGAAA
1		AGAGGATTGG	GGCTTTGCTCT	TGACCTTGATTTCTTCACTAGAGGGGAGAAATCACCTACCTTTTGGATGCTCCACTCTACTTGT
EST38815	91 C A C A	ACCCATTACA	GCTGACTGGCA	CTCCCTGAGGTGATATGGJAGJCCCTTAAGTCCACGATGGTGACCTAACTCAGTTTAAATCTTTGCC
4		CACGAGTAA	CATGCTTT	TAGCAGCACCC
EST38858	98 C T	AAGAAACTCA	GGAGCGAGTCC	GACTCTCAACCAAGAGAAATCAATAGGAGAGGATTGGCTT/AJTTTGAATTCAGAGCAAGCCCT
4		TGAC	AAGGAGAA	CTTACTGAGAGGTGAGCCGCCAGCCCTCCAAATGCCCTTTCATGAGTTAGGATCTCCTAAGTGGTAC
EST38865	72 T C	GCTGTAGAAAT	GGAAGGACGG	AAACAAACCAACATGGTGG
2		TGTGTCGATGC	AGGACACAG	CACCCCATATTTGACCAAGGGATGAAGCCTAGCCATGCTCTTTCACCTTATGTGTGTTCAACAAG
				TGTTTATGAGAAACCCATTACACA/C/AJAAAGCATGTGCCAGTCAGCAGATTCTGTATAA
				TCCTTACTGTGCTTACAACCTTCTCCCAAGTTTGGGGTGGTTTCCATATGTTATTGTTATTATTA
				TTCAACACGAGTAAAAGAACTCATGAC/C/TTTCTCCTTGGACTCGCTCCTCCTCCCAATCTCGAT
				ACCGACTGCACCTGTTG
				CCTTAATGGATTTACAGCTCATCTGAGTCTCTGCTGTGTTCTCTGAGGAGCTGTAGAATTTGTGTCG
				ATGC/T/CJCTGTGCTCCTCCGTCCTTCCCAATGAGCACATATGCAGGCGCAGCAAGAGCATGCTGGA
				TTTGCTTAGTTGTTAA



EST38878 9	47 T C	AAACATCATT ACTAGCCTAG ATCCTAA	CCTTCAATAAA TCTCATGTCCT CA	CCAATGAGAACCAAGTAATTAACATCATTACTAGCCTAGATCCTAAAT/CITGAGGACATGAGATTT ATTGAAGGGAATCCTCAATTAATATGAACATTTCTTGAGAAATGGGAAATTTGAAACATTCCTCC TTATTCAATGTCATCTCACACATCTTTATTTTATTGTTTTCACCTTTCTCAAAATATCGGATTGTTGC TCATGAGAATAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCAIG/CJGCTCCCTGGATAGCTAAAT TTA
EST38882 6b	113 G C	---	---	TTATTCAATGTCATCTCACACATCTTTTATTATT/CJTGTGTTTTCACCTTTCTCAAAATATCGGATTGT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38882 6a	35 T C	TGTCATCTCAC ACATTCCTTTAT TTTT	CGATATTTGAG AAAGTGAAAA CAA	TTATTCAATGTCATCTCACACATCTTTTATTATT/CJTGTGTTTTCACCTTTCTCAAAATATCGGATTGT TGCTCATGAGAATAATGGCTGAGGGAGCTGGCACGGCAGTCTTCTCAGGCTCCCTGGATAGCTAAAT TA
EST38909 5	47 A G	GCACAGCATG GCTAAAACG	GGTATTGTTG ATTCCCATCTT T	GCACTAACTAATTTTCAATTTGTGGATTGCACAGCATGGCTAAACG/A/GJTAAGATGGGAATCAA CAAATACCATTTGAAGATATGGAGCAAGAGAACTCTCACATACACTGCTGGAGGAATATAAAAT AACTGAATGGCAGTGAAAACACTACACATCAAACTTAGGGAATGTGTTAGTGTGGTACGTTGAG GGAACTTATAACCTCAC/A/GJGCTTGTTCACAAACACAGCAGACAGAGATTTCCAACTC CAGCAATGACAGGCTAGGG
EST38911 9	85 A G	GTTGAGGGAA ACTTATAACCT CAC	TGTTGTTTGT GAAACAAGCG	TAAACATTCCTCAATTTCCCTTGGTGGG/CJGGGGGGGTGAGATTGCAGTGTCTCAAGATAAA TATCACAATAATATCAAAACTTCAAAATTGTCTATGCAATTCACACACTGACATGAGCCACAAACATT CCTTCACAGGACTGTAC
EST38955 5	30 G C	TGAATTCCTT GGTGG	CACTGCAATCT CACCCC	CCTGCTATGATGCTGGGCAGATCCCGAACCTTCGGTGACQ/A/CAGGCTCCCTGCCAGGGCTTGG CCCCGACCGGGCTCCCGAGCTCGGCCCTGACTGTGGAGGAGCTGAAATACGCTGACATCCGCAACCT C
EST39002 0	42 G A	GGACCTTGG TGACC	CTGGCAGGGAG CCTG	CACGTGGCCCTAAGTTCCGGGTCTTCCTCAGTCTGGATGGCTGTGTGGAAAGCTTGGTGGTAAG GCCTAAGGAAT/GJAGGGGCAGGGGGCGATGCCGCCAGCGAGATGGTCTGTAGCCCTGTGGGTC AAAGACCTAACTTCTGGA
EST39004 8	79 T G	GGTGGTAAG CCTAAGGAAT	ATCTCGGCTGG CGGC	AAAGATAATGTCATCACACGCAACATATAGAAACATAAAAGAAATAAAGTATCCACCCCTAAAT CCCTATTATCCATGATATTTTCA/T/CJAGCACTAGTATATATCAATATATTTTTCACAAACCAT TCAGTTACAC
WI-16398	90 T C	TCCCTATTATT CCATGATATTT TCA	GAATGTTTGT GAAAAATATA TTGATAT	GGTTGCTTTTCATGTATTTTCTCATTTCTATCAGGTTTCTGGTCTTTGTCTCAATTTTAAACAT T/CJCTTTTATATAGGGAATTAGCCCTTAACTGTGGTACATGCTGCCAAATTTCTCTCCAGTT
WI-16403	69 T C	CCTTGTCTC AATTTTAAAC ACT	TAAGGGCTAAT TCCCTATATAA AAG	GGTTGCTTTTCATGTATTTTCTCATTTCTATCAGGTTTCTGGTCTTTGTCTCAATTTTAAACAT T/CJCTTTTATATAGGGAATTAGCCCTTAACTGTGGTACATGCTGCCAAATTTCTCTCCAGTT
WI-16406	24 C T	GCITTAATGGC TACAGAAAGA AGG	CCAGAACCAG ATGTGTTTAA AA	GCTTTAATGGCTACAGAAAGG/C/TJGGTTTATTCTTTTAAACACATCTGGTTCTGGCAGC AAGTTATATTGCAATTAGAGCAATAGGTGCCCTGAA

EST39236	Ob	57 C	TCATCTGAGA ATAAACTTCCT	CATTATAGGTA CTGAGTCATAC	TTCTTTTATTTCATGATTGTTTCATCTGAGAAATAAACTTCCTGTCTAATTTTCCAA[C/G]ACTATGTT TAATGTATGACTCAGTACCTATATGAGACTGGAAATATATTACCTGGCAAATGAATGAGGTGCTC TTT
EST39294	4	63 G T	CCTGAAACAG GGATGCC	GCACAATTAA ACATAGTACCG AGAA	CAAACAGACCTTTGGTTGAGCTCACCTGGTGACAGGAGACTCCTACCTGAAACAGGGATGCC[G/T] TTCTCGGTACTATGTTTAAATTGTGCTGAGCCAGCAACCTCGAGTTACCCGGCCTTTTACCCACGOC AGCTCTGCTTGCTGCAAT
EST39366	2	72 T C	---	---	AGAAACACTTCTGTCTGATCAGAGGAAGATGTATGTAGAAATCAGAAATCTGACTGAATTCCTAAA ATCTATT/CJACACTGAGAGGAAATGGAAAGAAATGTTTGCATAAAGCTTTTCCCTGACTCTCA GAGGGGTTTCAGA
EST39371	9	86 A G	CATTTGGATTA GGGTGAGAGG	TGATTTGAGAC ATTTCACATTT TT	AAAAAGCTGTAGCTGGCAAGTCAAAGTTTATTTATGTGTGTAAATTTCCAGTTGAGCATTTTTTCAT TTGGATTAGCGTGAGAGG[V/G]AAAAATGTGAAATGTCTCAAATCAAATGCTTCTTCTAAAGATTA GACATTGCCCAACCTGC
WI-17177		23 A G	---	---	ACAAAGTGACATATCCAAACCAACC[V/G]TCCATCCCCACCTGTGCCCCCTATTCTTCTGTGTTCTTT AGAGCCTTTTCAGCTATTCTCTGTGAAGCAAACTGCAGAGGCCCTCCCCGTACTCTCCCTGGAA G
EST39428	8	31 C T	GCTCCCCACA ATTTTGATT	GGTCCCTTATG AAGCCACC	AGGTTCTGTTGCTCCCCACAATTTTGATT[C/T]GGTGGCTTCATAAGGGACCCAGGATTCTGCATT TTCTGGGTGGGCTAGGTAATTCTGTGCTTGGTCCACAGAGCACAAATTAAAGAAGATCAGGTCT GGCTGTGC
EST39430	2	45 A C C	GGCAGAGGAA TAACTGATGTT	CAGGGGTGGG GTATTG	AATTTAGCAGAAACAATGAAGTTGGCAGAGGAATAACTGATGTT[C/V/C]CAATACCCCGACCCCTGA CCCAGTAOCTTTCCCTCAGGCCAGGCTCCGGTGAGGATGTCCTGGG
EST39446	7b	117 C T	CTACTGACAT AGGGAATTCA GAGTAA	TCCTGGAAAC TGACATAAAC	AAAGCCCTGTAAACTGAAGCTAGACAACGTCAACTTTGGAAGAAATAACAGGAACCTATTATAT ACGTAAATCACTTTTCATACCTGCCTACTGACATAGGGACTTCAGAGTAATA[C/T]GGTTTATGTCAGT TTTCCAGGATTGTTCTCCC
EST39465	2	80 A G	AATGCAGGAG GGTGGC	CAATCTGGGC CCTCT	ATGGTGTCAATTAGAGGGCCACAGGGGATGGGGAGTAAATAAACATAACGAACTGAACAGAAA TGCAGGAGGGTGGC[V/G]AGAGGGGCCGAGATTGGGTGTTTCAGGGCAGAGAGGTGGAAGACCAG
EST39501	0	81 A G	AAAGATTCT GTAGACATCT AACATTAG	CACTTGCAATT CTGAAGGCT	TGCTTACAACCCATAACCATAGGCCATGTGTTTCAGACATTCTTGACCAAGCCTAAAGATTCTGTAG ACATCTAACATTAG[V/G]TAGCCTTCAGAAATTGCAAGTGCAAGTTCAAGTCAACCAATTTC
WI-18387b		84 A C	---	---	CACAAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTTGGTGACCCCATACATTTGTGGTCA CATGCTTTAGCCATAC[V/C]CATGGTAACATTGACTATGGAGTCTTGTGAAAGTGAATGTGCGGATG GCTATGTAGACATAAAGA

WI-18387a	57 A G	CCTTACTTTGG TGACCCCAT	GCTAAAGCATG TGACCACAA	CACAAATGGGACTGCTGAAGAGTGGACAGTTGGACCTTACTTTGGTGACCCCATACAGJTTTGTCG GTCACATGCTTTAGCCATACACATGTAACATTGACTATGGAGTCTTGTGAAAGTGAATGTGCGGATG GCTATGTAGACATAAAGA
EST40601 9	78 A G	GGTGGAACCT GAAACAC	TTCTTGGGAAGA AAGGCGTC	TCCCAGGATGGTTATTCCAAAGCTGTGGACGGTGAACATTAAGACGAAAGAGGTGACTCGCGTGGA ACCTGAAACACAGJGACGGCTTCTTCCAAAGAGGGCTGTGGCGATCAGGCCACTCAAGG
EST41935	32 A G	AGTGTATCAC ATCTTCAGGAT AGGT	GCACACCCTTC ACACTGTTA	TCCATTGAGTATCACATCTTCAGGATAGGTAGJATAACAGTGTGAAGGGTGTGCTCATTTTCTTC AGCTGTGAGTAGAGGAGTCTTCCCGAGAGTAGCAGTTGTGA
EST43091	28 C T	CATTCTGGTCT TTATTTTGGGA CA	AAACTGATTT GTTAAACATG CTAC	ATGTCATTCTGGTCTTTATTTTGGACAICJTTGTAGCATGTTTAAACAATCAGTTTTTCATAGGCAA CCTTTTGAAACATCAAAAGAAATACAATATATTTTTCACAAATTTCTCATCAGTGAATTTCA
WI-18420c	108 T C	TTCCATTAAAC AGGAAGTTTC C	AAATTCTCAGC ATTGCTATAAG C	AGAGAGACAACAAGAAGAAATAAGGAAATGGGAAGAACAGAGTGAATTAAGCAAATCTTTGGA TTCAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATTCJGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18420a	38 C T	GAATAAGGGA AAATGGGAAG AA	CCAAGATTTGC TTTAATTTTAC TC	AGAGAGACAACAAGAAGAAATAAGGAAATGGGAAGAAJCTJAGAGTGAATTAAGCAAATCTT GGATTGAGATTCCATTAAACAGGAAGTTTCTCAAAAAAATCAAAATGCTTATAGCAATGCTGAGAA TTTCATAGGTACTTCATGGGA
WI-18425b	101 T C	CACCTGTGCT AGACAGATTTC A	--- CCTCCTGTTGT TGTTGCA	AGCTGATCAGCTGCTGTTACTGTGTTTATGTGTGGCCAGGAAAGCCAAAGATCAGACACCTGTG CTAGACAGATTCAJVCJTGACACACAACAACAGAGGTGGGGTCAACGGGCGGAGAGCCAAAGAC TAGGGC
WI-18425	81 A C	CTTTTGGCTCT AAGTGGGACT A	CTCCCCTGACT GTATCCAGA	AAATTGAGGTCCGGGTGGAACATAAAAGGAAAGGAAGAGAAGTAATCAAGGGAGGCCAAAGTG GGAAGCTGTATTGCTGATCTAACGTGCTGTCCAGTTCTTCTTTGGCTCTAAGTGGGACTAICJTTTC TGGATACAGTCAGGGGAG
WI-18449	129 C T	--- CCACAATGGC AGAGGTGA	--- TTTAGGCTTTG AGATGGTTTCT	ATCGCTTCATTGAAGCCTGCTTAATTTCTCTCAGTCAACTGTGCCCCCAAGACATTATTTTATCTT AAATGTCCAATATCTGCCCTGATGTCTGTGTTGTGCACATTGGGGCCACAGJTCJAAATAGGCTAAA AGGCAGTCCCACCTGCT
WI-18457	120 T C	--- CCACAATGGC AGAGGTGA	--- TTTAGGCTTTG AGATGGTTTCT	GGTGCTATAGCTGCTGTACACCACAATGGCAGAGGTGAJGJTAGAAAACCATCTCAAAGCCTAAAA TATTTACCATACATCCCTCACAGCAAAAGTTTGCTAATCTCGGGTTTAGGGACTCCATTGAG
WI-18462	39 A G	GGTGGGGTGC GAGG	GCACGATGGGA GTGACC	TGAGGACGTGTGACAAGCTCCAGCAGGGGTGGGGCCGGGTGAGGGTGGGGTGGGAGGCTJGGT CACTCCCATCGTGCCCTGGCGCTCCCTCCACTCACCCACACCTGCCCCAGTCCAGTTGAGGT
WI-18476	60 C T	--- CCACAATGGC AGAGGTGA	--- TTTAGGCTTTG AGATGGTTTCT	GGTGCTATAGCTGCTGTACACCACAATGGCAGAGGTGAJGJTAGAAAACCATCTCAAAGCCTAAAA TATTTACCATACATCCCTCACAGCAAAAGTTTGCTAATCTCGGGTTTAGGGACTCCATTGAG



WI-18491	109	G A	AACAAATGGT AGGTGGTATT	CGTGTGCATTT TCITGTAAATCC	CTAATGAGATGAATACATGGAAGGCGTTTAGCACAGTGCCTAAACACACAGTAAGTAACCAACAAT GGTAGGTGTTAATACTATTATTAAATCCAGAAATGAC[G/A]GGATTACAAGAAATGCACA OGT
EST50757 b	79	C T	GAGCTCGAGG CTGCTTCT	ACCTTCACCC GCCC	AGCCCCCTCCACTCCTGCTCCACAAAGTCGGCTCCCGAGAGCTCGAGGCTGCTTCTTTTATAT GTGCAGGGCC[C/T]GGGGGGGTGAAGGGTCAGAGA
WI-17675	103	T C	GGACATTGGG ATGTGTGACTT	GGGGAACCAOC CAGG	GATCTTGGAAAGCAGCTAGAACTAAACATCTTCACCAGGTGCTGAAGAAAGTGTCTTCGTTTAAAT TGCCAAAGCAGGATGTGGACATTTGGATGGTGACTT[C/C]CTGGGTGTTCCCATAGATTACCCAT TGCTCTAATGGTGCTA
WI-16543	67	G T	AGATAAACTA CATTGGGTTT	GATTCATCAIT ACAGGGGACTT	GATCCATTACCTAGGGTAAATTTCTCCTGAATGTCAACAAAGAGATAAATACTATTGGGTTTGGT GTTAAGTCCCCTGTAAATGATGAATCAAGAAATCCCTCAAGTCTGTCTTGCCACCCATTTAATACGTATT TTTGTTAAGGCTGAAGTT
WI-17687	107	C G	GCCAAAAGG TTGGGAA	TTACTTTTGT CCGACCAGCA	ATCTGAGATGGAAGAGTTTCATCCCAAACCATCTCCCTGACCCCGAGTCCATGGAAATTTGTC TTCCACAAACCGTCCCTGGTGCCAAAAGGTTGGGA[C/C]GTGCTGGTGGTACAAAAGTAATT G
WI-17690b	79	A G	AGGCATTTTTC TAGCTGTGTTT	CAAGAGTTATG GGTCTGAATC	ACAACATGTGAAGAAGATATGTTGTCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTTGATTT GGCTTCCCTATTA[G/G]ATTACAGGACCCATAACTCTTGTCTCACTCATCTGCTATGCTGCTG ACAACATGTGAAGAAGATATGTTGTCTTTACTCACAGTGGAGGCATTTTCTAGCTGTGTT[G/A]A TTTGGCTTCCCTATAGATTACAGGACCCATAACTCTTGTCTCACTCATCTGCTATGCTGCTG
EST51717 b	128	C T	GCGGAAGACA GTGAGCTGTT	TTGAGGCAATA ATCCAGCTC	GATCCAATCTCAGTGTCTAACTCATCCAGATTATTCTGAAGTGGAAACCCCTCCGACCCCA TGGAACATCACCCACTACCTGTTTCTGGGAGAGGCGGAGAGAGAGAGAGAGTGTGTT[C/T]GAG CTGGATTATTGCCTCAA
EST51717 a	39	C T	---	---	GATCCAATCTCAGTGTCTAACTCATCCAGATTATTCTGAAGTGGAAACCCCTCCGACCC CAATGGCAACATCACCCACTACCTGTTTCTGGGAGAGGCGGAGAGAGAGAGTGTGTTGCGAG CTGGATTATTGCCTCAA
EST53012	97	C T	TGGTCACTTTG GGGC	GGCTCTGCCCA GGC	TTCCAGGTTGACAGGTTTATTCCACCCCTTCCATCCCATGGCCACCCAGGAGGAGAGACAG GTGTGCTGGAGTCTGGTCACTTTGGGGCC[C/T]GGGCTGGGAGAGCCACTGGGTTTACATTCTCTGT GGCAGGTGTGGACAC
EST53349	96	A G	TGTTGAAAGC AGTCACAATG TAC	CATCTGGATAT CTTGTACATTT TT	AACTGCAATAACAAACAAAGAGTCCAAAGAGGCTAAAGTCTAAGCTATAATTACACATG AAGTATATGTTGAAAGCAGTCACAATGTAC[A/G]AAATGTGACAAAGATATCCAGATGTTTAA
EST53389	74	A G	GGAGACCTGC AGAACTTAA CA	GGCCTTTCTAA CAATAAATGCT C	TTTCGAAATGCTCCTCATGACTTGACAGACTGAGAGCCAGCCAGCCAGGAGACCTGCAGAACT TAAACAC[A/G]GAGCATTTATTGTTAGAAAGGGCAAGTCTTACACTCAAAATAGGTTTAAACATGAAC ACATTAAAGGAGATGGCC

[illegible]

EST98276 b	61	A C	---			GAGTCTTGCTATGTTCCAGGATGGTCTTGAGCTCCTGGTTTCAACAATCCTCCTCTCCTTACJAGC CTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98276 a	22	A C	TTTCCAGG	GTCTTGCTATG	AACCAGGAGCT CAAGACCA	GAGTCTTGCTATGTTCCAGGACJTGCTTGAGCTCCTGGTTTCAACAATCCTCCTCCTTAAGC CTCCTAAAGTGCCAGGATTATAGGTGTGAGTCACA
EST98800	53	A T	---			GCCTCCAGCTGCATGACTCCTAAGCCATCATTTCCGAAGATTTGGCTAATTTG/ATTTAGTCTTACAA AGGCAGTCTAGTTCACCAAGCAAGGGGTTTGTGTGGGAAAGCGCTGCTATCTTTGTTTCAAAC TGTAAGCAAGTTCTCTC
J02931	138	G A	GTAA	CAGCATTAGTC ACTTTGAAAT	TTGGAATTGGT TGTAGTACCAT T	AGAGGATAGATACATGGAAACGCAATGAGTATTTCCGGAGCATGAAGACCCCTGGAGTTCAAAAA CTCTTGATATGACCTGTTATTACCAATTAGCATTTCTGGTTTGGACATCAGCATTAGTCACCTTTGAAATG TAAC[G/A]AATGTGTACTACAACCAATTCGAAGTTTAAATTTTAACACCATGGCACCTTTTGCACAT AACATGCTTTAG
L41680	88	G A	A	GAGAAATCGA CTACCAGCTG	TTTAGAGCACT TTGCAGGTATT T	GGATCCAAACACGGCTGGTTTCAGCATCCACCAATGAAGTGAATAAAGACGTTTCATG AGAAATCGACTACCAAGCTGATG/AJAAATACCTGCAAGTCTCTAAATAATTAAATATTTGACTTT AAGGTCCTAGTAAGTGCCACTTCCACTAAGATACAGTTTGAATGTATAATCAGTAGTGTATACAA GATCCAACAGTGCACTCA
M15796a	84	C G	ATATGTAGA	CAAATTTGTA CCTCTAAGTAC	TTGGACTTTAT TCTTTAAACAA ATTG	CTTTCTGTACCAAAATTTGTACCTCTAAGTACATATGTAGATATTGTTTCTGTAATAACCTATTT TTTTCTCTATTCTCT[C/G]CAATTTGTTTAAAGAAATAAGTCCAAAGTCTGATCTGGTCTAGTTAAC CTAGAAGTATTTTGTCTCTTAGAAATACTTGTGATTTTATAATACAAAGGCTCTTGACTCTAAAT GCAGTTT
M20472	103	C T	C	GTTGAGTTCTT TTGGACCAAA	ACAATGAACA ACTCTAAAGAC AAAAA	AGAGCCACCCTGTGGAAACACTACATCTGCAATATCTTAATCCTACTCAGTGAAGCTCTTACAGTC ATTGGATTAATTATGTTGAGTTCTTTTGACCAAAAC[C/T]TTTTGTCTTTAGAGTTGTTTATTGTTG TGATTGCAATGTTTCCCTTCAACTGTGTTCTCCTGGCATTCAAGAGAGGGAGAGGAGGAAGA CCCTCTGACCTGCAGGCCAAGAGCAGAGGCGAGTTGGGAAAGCCTCTGCTGCCATGGT[C/G]GT GTCCCTCTCGGAAGGCTGGCTGGCATGGACGTTCCGGGCATGCTGGGGCAAGTCCCTGACTCTCTGT G
M32315b	129	T C	CATGG	GOCTCTGCTGC	GOCTTCCGAGA GGGACAC	TTCCAGGAGCAGCAAGGGGCTGCTGAGCTCTGGTTAGGTTACAGCTGGAGGTGTGTATATACAA CACACACACGTGTATATACACATATATGTGTATGTATATATATATATATATATATATATGGCTTT[C/T]C AATAACCACTAAATTTTAAACAAAGGTTCTTCTAAGTGTAGAACTTGGGTGGTATTTTACCTTC CTTCT
M33875a	131	C T	GAGGTGTGT	GGTTACAGCTG	AATTTAGGTGG TTAT	
TGR- A003M18 a	29	A G	CT	TTTTTGTAGAG ATGAGGTTTTC	GGCAGACGGAT CACTTGA	TGTCCTTTTGTAGAGATGAGGTTTCTT[A/G]TGTGGCCAGGATGGTCTCGAACTCCTGACTTCAA GTGATCCGTCCTGGCTGCCCAAAAGTGTGGGATTATAG



TGR- A003P30	117	C G ---			ACAAGTTCAAAGGAGAACTTCCTTTGTTTAAATGCAGCTGTGCTCAGAGCCTGTGATTTCTAGGA AACCATCTGGGTTTAGCCCATTAGAAAAATGCAGTTTAAAGCAGTGTCA[C/G]ACTGGCTGCCTGAA GGTACCCTTGGAGATACT
TGR- A004S34	156	C T A			GCTTGCTTTTATGTTTAGGTTGGGGAAAGGAAGGGGCTGACAACCGCAGACATCTGGACACACAGC AAGGTCOCAGGGGAGGTTTGCAGAACTTCTTTTGCTTGGCTAACAGTCTGTGATGTGACAATAGCCA AACCTCCTCATTCCTCTATAAA[C/T]CTTTAACAAAAACAGTTAGCTGTTTACAAAAACAGTTAGCTGTT TACATG
TGR- A004T44b	97	A C ---			AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAGTCAAGGAGATAACCAAAATGAT TGAGTATGATAAAGAAATTTTGTCATGGCGATT[C/A]AAATAGAAAAACCTATAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TGR- A004T44a	69	G A TGA			AACAACAGTGTAACTTTAACAGGGGATGTTAAAGGTAAGTCAAGGAGATAACCAAAATGAT TGA[G/A]ATGATAAAGAAATTTTGTCATGGCGATTAAATAGAAAAACCTATAAATGTAGAAAAAGCA GGTCTGGACTTAGCAAAAGAAACAATATGACTTAGCAAAAGAAACAATATAG
TGR- A004V08	60	T C GGCAATCTCTT			CCTACAATCCTATAATATTGCAAGGGTTGGGAAGGATGCAGGAAACAGGCATTCTCTTA[C/G]GCC TTTTGTGGGAAGGATCAATTTGGTGTCATGCACCTTAGGGGACAAATTTGGGCAGTAGCTGTCAAATTTTC AGTAGCTGTCAAATTTCAA
TGR- A004V26	125	A G ---			TCTAGCTATAAGACCAGATTTTAATATTCTAGATATAGAATTATCCAGAATAATTCTATTGAATTGA CTGATTACAAAAATGTTAACAGCTGGATAAACGGTAAATATGCATTATCTTCACATGA[G/G]AAGGT TTCAGTTTATAAATGCTTAAATACTGTATCTATTGCTTAAATACTGTATCTATIGG
TGR- A004V28 a	29	A G CGATCTC			CCAGGCTATAATGTTGTGGTGCGATCTC[G/G]GCTCACTGCAACCTCCGCCCTCCAGGTTCAAGCAA TTCTCCTGCCTCAGCCTCTTGAGTAGCCGGGACTACAGGCACCCGCCACCGCACCTAACTAATTTTIG TATTTTITAGTAGAGACATTGTATTTTITAGTAGAGACAGG
TGR- A004X20	25	T C GA			TAAGTTTTCCTTCTCTGTAGGAT[C/G]TCTCCATGTTACAGTCAACTATAAACATGGCTCATGT TCACCTGGGCTTCGCTTCAGAGAGTTTGATATTTTGGAGTGGTACCTTTGTTCTGTGTGCTTTTCA GACCAACCGCTTCTTTCATTCTTCAAGGCTTCTTCCAAAGGAGTTAAATCATCATCATGTCCAATC ATCATCATGTCTT
TGR- A004X30	26	T C CCAC			TTTTGAAATCTTAGAGTAGAACCCAC[C/G]ACTCTAGTAATACTTGTATAAAATTAAATAGTTTT AAACACTTCCATAAAGAAATTAGGGGTGCCAGCTCCTTGATTTCCCTAGGGATAAAGATATCCAT GTTAGGGATAAAGATATCCATGTAC
TGR- A004Z04	102	T G ATGCAAAACT			CACGGTATATGCCTTATATATAGGTATATATACAGATCGTACACATATATTAACAGTTTGACATG GGGTCCACAGTACCTTCATTGGGTATGCAAAACTT[G/T]TGCTTTCATGAATTTCTAATTATAAGG ACTGTTGCTTTCATATTTCAATGGACATTATACAAAAATACAGTCTCTTTAGTGATTTAAGACGTC TCTTAGTGATTAAAGACTG

TIGR- A004Z19	85 C T	GAGAACAACT GCAGCAATTTT	AAGATGGTCAT CGGGAAGA	TAAGTGGAGACAAAGTTATTGGAGGAGCTTGACACCCCTCTTCTGCCCTAGCTTGAGAGAACAACTGCG AGCATTTTTTCTTTTTC/TICTTCCGATGACCATCTTTTGGGCTGGGGCCAGGCCCTGGGTGTC TCCATATCGCTGCTTTAGTGAGACTGAGGATCTGGTATAAGGAAACAGATC
TIGR- A004Z42c	89 C T	TTGGGGGAGGT AGGAGACT	CAGGGCTGCOG GTCC	GTCTTAGCAGAGGAGATAACTTTGAGGGACAGCCOCCOCCAGGCCAGGTAGCCTTCAGGGGGGGCA GGGTTGGGGGAGGTAGGAGACTCTGGACCCGGCAGCCCTGGCTCCAGCTTCATCATCTGTGTCTCTT CATCATCTGTGTCTTC
TIGR- A005D17 c	81 T C			TATGGACTGTGTAGAAATATGATTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAGGCT/CJGTCTAGATTCTTCTGGCCTCTCTGTGCAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCTCTCTGGAATGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D17 b	79 G C	GGGGAACCC AGCAAG	GAGAGGCCAA GAAGAATCTAG AC	TATGGACTGTGTAGAAATATGATTGGACAAGAGGGTATGATCTAATAGTAATAGACTGAGAGGGG AAACCCAGCAAG[G/C]GTCTAGATTCTTCTGGCCTCTCTGTGCAGGATTCCTTCTTCTGGGCAC GGGTGGGACCCTCTCTGGAATGGTATCTTACGACAGTCAAACTCTTACGACAGTCAAAACAC
TIGR- A005D44	97 G T	TTAACATTATT GAACCTTAAA CTGTTACAC	TTGTCTATTAT TTAAAGCCAAC AAAA	CATCAGTAACATATACAAATTGGTCACTCAACTGAACCTTGGCTCCAATATATTTCTATACAATACTT AACATTATTGAACCTTAACTGTTACACTG/TTTTTTGGCTTTAAATAATAGACAATGATTTTTG TCTATTACTTAGTGATAGACAAAGTGATTACTTTGTTAGACAAAGTGATTACTTTGTTAC
TIGR- A005E31b	27 G A			GGAGTTCAAATTTATAACCCAGGCTCTG/AJCTCACAGCTGTACTGGCTAGGCAAGCTTCCAGAC ACAAAGCCACCTGCCCTGCCATGTGGATAGTACTCTTGGCTGTGGCCCTACAAAGCCACCTTCTAT TTCATACCAATACCTTCTATTTCATACCAATAAG
TIGR- A005E39	182 G C			CTCAGTGTAACAACTTTGTTTAGGGAAAAAATAATCCAAATGGATATATGGGAAGAGAAAGTG CCAGGCTGGATGGTCTGAGACAGAAATGACCCCTGGGCTCTTTATTTGTTCTTTTCAACAGGAOC CCACAGATATTGCGGTATGTCATGAGGACTGGGATGTCTTCTATTG[C/C]GGATGTCTTCTATT
TIGR- A005E42a	42 A G	AGTAAGGTTA CTGCACCTTAC AGAG	CCTAAATCAGG GGAAATTGAG	GCTGAGTTTTGTATCTTAGTAAGGTTACTGCACCTTACAGAGI/GJCTCAATTTCCCTGATTAGGA AGGCGATGCTAATGGGTATTGCATAGGTGTAAGTATAAAATGTTGTATTTAAGAGAAATCCACAAG CTTGGTATAAGGCAGAAATAAATGGTATAAGGCAGAAATAAATAG
TIGR- A005E46	76 A G	CACCTGACTOG GTGCTTTAC	COCTGGCTGTG AGGTAATGT	ATGACAAATGATGATAGTATTAGCCTACCGTTTGTCTAAGCACCTACTGCGTATCAGGCACCTGACTCGG TGCTTTACI/GJACATACCTCACAGCCAGGGTTGGCAAATGGTCAATTTTGACAAATGGTCAATTTTG ACAC
U20979	24 C T A	GCAGGGGTGA CGTATGTAGA	GGGGAGGACAC CCTAAGC	AGAGCAGGGGTGACGTATGTAGAAI/CJTGCTTAGGGTGTCTCCACAGAGCAGATACTTGAACCG ACTCAATTCCTGTGTAAAGAGACACTTTGTCTGCTTACGGACCTCCCAAGGTGTCAGAGTTCTAT ATAGGATGCTGGATTAGTTCCTTTGATATTGTAAAAATTCCTCCCAAGAGCCGCATATGAAATCTGCC

X57830	106	G C C T	AGT GGAACCA ACGATCATAT	CATTGACAGAA TAAATGAGGC A	GTGGCAACTGTGGAAGGCACACTGAGCAAGTTTTCACCTATCTGGAAAAAATATGAGATTGGA AAAAATTAGACAAGTCTAGTGGAACCAACGATCATATCTG/CJTATGCCTCATTTTATTCTGTCAAT GAAAAGCGGGTTCAATGCTACAAAATGTGTGCTTGGAATAATGTTCTGACAGCATTTACGCTGTGAG CTTTC
X74070b	72	T G T G G A T C	CTTTTAAAGAA ATTTTGTGTTA	GGGCTTAAAAA TATTAGAGATC TAGATT	AACCTGAAGAAGTTACTGGGAGCTGCTATTTTATATTAGACTGCTTTTAAAGAAATTTTGTATTG GATC/T/GJGATAAAATCTAGATCTCTAATTTTAAAGCCCAAGCCCCCTTGGACACTGCAGCTCTTTT CAGTTTGTGCTTATACACAATTCATTTTGCAGCTAATTAAGCCGAAGAAGCCTGGGAATCAAGTTT GAA
Z48804	44	C T ---		---	ACTGCCGAAGTGTAGCGGCCCCCAACCTTGCTCTCATCACCAAG/CJTJTAGAGCTTCTTCCCGAAGGG CCTTTAGGATAGGAGAAAGGGTTTCATGCACACACGTTGTGAGAAATGGAAGAGCCCCCTCCAGAACCACT CTACAGCTGCTAGCCTTAGTTGCCACTAGGAAGTTTCTGAGGCTGGCTGTAAAGTAAGTGAAGG TCCA
D28513b	133	A G ---		---	ATGACCAAGCCACCAACATTTAGAACTTTGGCTGCCCTTGGGAAGTCCAGAGCTGATCTCTCAGCTCC CGCCCCAGAGGGTCAGCACTTTGGACATGGCTCACAAGCAGTTTTTATTGACTGCATGAATGCI/V GJTGCGTGCAAGCATGAACCTTGTTTAAATCAAGAGGCTTACATAATTTTAAACCAGTTCTGTCTTC AGCTGTACATA
D29833b	85	A G ---		---	CCACTCCATCCTGATGCCCAAGTTATCCACAGCCTCCTCCGACCAAGACCCCTATCCACCTGGACC TCCATTTTCCCTGTAA/VGJTTCTCCAACCTGATCCTACCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCAACCAACACAAAAGACACCACTACCTTGTAACTACTGCTTCTGTCTAC
D29833a	21	A G ---		---	CCACTCCATCCTGATGCCCA/VGJTTATCCACAGCCTCCTCCGACCAAGACCCCTATCCACCTGG ACCTCCATTTTCCCTGTAAATTTCTCCAACCTGATCCTACCTCCCTACTCCTGCACCCCAATATGAA CAACTGCAGCAGGTGCCACCAACCAACACAAAAGACACCACTACCTTGTAACTACTGCTTCTGTCTAC CTCCTGCCCTCCTCCTGCTGTGATGCTCCGCTCAACACGCCGAACCTGTCTTGCAATGGGG GAGGGGGCGTTTC/G/AJCTTTCTCTCTTCTGGCTTCTCTTATTCTCCACAACCACTTCTCAATAAA GCCAAAAATCTTCTCTTCTCCCTCAGGCCACCTCCTGTCTCACTCCTGTCTGTGCTGGCTTTT CTGGA
D31762	82	G A ---		---	ATTATCGGAGTGGTTGACCTTACACTTACTCCTTAAATAGCAGTGAGTAATGCATTTGAGCTG/CJ CCCAGGCTCTGTCTCCTCAGCTCATTTCTACTCTCTTTTCTCTATATACTCATTTCTAATAACAT GCACCAAGAGATATGGAGACATAAACCTGTATGAATGAGGCTGGGCTTTTCTGTAAATAAGCTTCC TTT
D37931	64	T C ---		---	



D63807	101 C T	---	---	CAGGCAGGACTTCAGTGCAGTATCCCTGCCTTCAGTCTTCTTTAGAAATCACATCTGTGTTCAATCC ATTGTTTAGAGGGAGTGATTTTCTGTTCCAC/C/TJGAAGAGGACTTTTGTTCACAAATTGGATGCAC AATGCAGAGGAGTCTGTTCTCTCCCGCTCGGCTTCTCGGTGCTGGAGGGTGACCTGTCCACAGATGAC
D90145	21 T C	---	---	TGGGAACATGCGGTGTGACCTC/T/CJACAGCTACCTCTTCTATGGACTGGTTATTGCCAAACAGCCACA CTGTGGGACTCTTCTTAACCTTAAATTTTAAATTTAATTTAATACTATTAGTTTTTATAATTTATTTTGAT TTCACAGTGTGTTTGTGATTGTTTGTCTCTGAGAGTTCCCTGTCCCTCCACCTTCCCTCACAGTGTG TCTGGTG
EST14035 1a	59 T C	---	---	ATTATCACTCTCAAAAATTTGGTGTGTGTGTTAAAGTACTTTCTTATTATGAGCCCCCT/CJGAGGA CCAGACATGTTATTATCAAGCCCCCTTATATACCATCTAAT
EST16868 5	71 C T	---	---	GCATTTTAAATTCACATTTGAATCATTATTTACTATTTATGATGTTTACATAACAATTCAGTATCATTT ATG/C/TJGTAGATTTTCAGATGTAGTCTGTCATCAATACTGAGCACTTATCT
EST16904 7	57 C T	---	---	ACAGACTATCGCCAACCTTATAATGCTTAAACCTTTATGATCAATAGTAATAAATTACA/C/TJGAGATA TTCACACTTTATTATAAATAGGGTTGTGTAGATGATTTTCCCAACTGTAGGTTAAACAT
EST21863 9	49 A G	---	---	TTTTTAACTACCAGGCACTGCTGGAACAGGATGAAAACCTGATACACC/A/GJGTTACTACTTACTC TTCACCTCTTCAAACTGATTCCTTAAAGACTTCTACTTAGCAAA
EST21885 6	80 G A	---	---	GGCTGTAAGTAGAATCAAGGTTAAGAACAATTTTATGCACCTTATTCACAAACATTTACTGAGCATA CTAGGTGCTGGGA[G/A]JGTGACAGTGAGCAAAAACACAA
EST22623 8a	26 A G	---	---	ATTTAGTGCAAAATGACAAAGCCCCAA[A/G]JAGAACAGAGGATCAATAAGATTGAAATGTATTACC TTCTCATAAGTATACGAAGTTTAAACACAAAGTATGGGAGT
EST22644 2	98 A G	---	---	AAATGATTGAATTCAGCAAGTACATTTATGATCTATCTACATTTTAAACAGCACTAAAAATAA AAATTTTAAATGATTATCCATTATTACAG/A/GJAAATGTGGAAAGATGGCTTTTAAACCC
EST23587 1	31 T A	---	---	CCTCATTATTATAAAGACGGACATAAAAA[A/T]ATACAAACAAAACCCAAAGTCACATTTCAG GAGGTAAAAACTAAAAAGTCTGATATGAAAATATGGTGG
EST24246 7	106 T C	---	---	AAAGATCTGGCATTATTCACATCATTTCTAAATATTTTGTAAATTACTTTTCCATGAGTATTTTTTCA TGTCGAAGCATTTTAACTATCATTTTAGCGTAAATACC/T/CJGAATAACCCATAGTTACAGAAATTGG GTCTGTGAACCTCAAT
EST24308 3	45 A G	---	---	TAGTTTAAATTTTCTGAACCTTTGGCTTATAAATTTTCTCAACTT[A/G]CATTTAAAAATGTATCAAT GCACCTTCTTCAGTAGTACCACATGAAAATATAAACCTCGTTC
EST24435 6	73 G A	---	---	CTTGAACTTCTGGTCTCAAGTGGTACGTCCGCTCAACCTCCCAAAATGATCGGATTACAGGCATAAG CAGCC[G/A]JGCTGACCCACATTTTCTTTATCCGATCTGTGTGATGGACATTCAGGTTGTTTC
EST25089 8	25 T C	---	---	TATTGTTGCATTATCAAAATGGTTA/T/CJAGTTTTCAATTTAAACTGTAAATTGATTTCTATGTATAA ACAGCTTTGAAGTTGTAATGTAGTTTCCAATCGTTAGTTAATGCTACATT

EST25476 9	33 G A ---	---	AATGATCTTTATTTTCAGACCTGCTCCTAAAG[G/A]CTTTCTCCTCCTCTAAAAACCAACACACA AGAGGTCTCTTGCTGCTTTCATGACCTGCTGGGGCTGGACTTGGACCGTCTGCTGA
EST26183 2	70 T A ---	---	AGATAATGCATTAGAGCCTGCCCTCATTTGATCTTGATTAACCTTTGTAAGATTGATCTCTAAATAAG ATT[A]ACATTTCTGGGTACTGGGAGTTAGAACAAC
EST27231 1a	28 T C ---	---	AGAAAATAAGGTGCTACCAGAACTCATG[T/C]GATAGCGCTTCTTTTAGGCACATATTATATGCAATT CAGATGAAAGTTCTGTAAATCACACACACACTGTGCTCTAACAAACACGCTGACTCTGA
EST27816 5a	26 T C ---	---	CAACTCAAGGTACAAGACAAATTGCATTT[C]TAACATTTGTTATAATAAAGGAACATCAGATCAAT CATTAAAGGGCTCCAGAGTGAACAGCATCTTCATAAAGTTCCATGTT
EST28588 0	78 A T ---	---	GTTTAATTGGCGTATGGTCCACAGGCTGTACAGAAAGCATGATGGCTTCTGGGAGGCTCAGGAA ACTTACAATCA[A/T]GGTAGAAGGCAAAAGAGAGCAGGCATCTCTCCATGACCACAGCAGGAGG AACAGACAGAGGAGGGGAT
EST30226 5	25 A C ---	---	TACTCACACCGACATACATATCTCA[A/C]GTAGAATTAGCTATACTGCATACTAACTTCATTGTAGT AGGGAATATAAACTACTGAACAAGACAGACTTGTCTAACTTAAACAAGACAGACTCATTTCTTTGA G
EST30935 9a	59 C G ---	---	AGCTATGGTAGAGCAAAATCCAGTGGTGGTAAATCAAGAACTCTAAAGTTCAGTAGAGA[C/G]AGGT GTTTGAATGTCAAGGAAATCACTGAGGTAGATTGGGATTACAATAAGACAGCTGCCCTGTGAGGT CATAAGAGCTTTTGTGAGG
EST32515 7	25 G A ---	---	CCGAATATAAGGAAATAATGGTGGC[G/A]TGCCCTCTAAACCTGTTGAATAGAATAATGGCCAAAT ATTACAGTTTCTCACTTTCCTATGAATACTGGCACCTGTTTATTTTCATGTTTATATGTGAGTTTCTATGC ATAAAATCCCAGTAAGA
EST33274 4	27 T C ---	---	TGCTTTGTTCCCTCCAAATCCTAAAT[C/G]GTGTCTTCAAGAAATTCGTGGAAAGGACTTTTGAA TACGAGTTTGTACCATATTCAGTATTCTTGAATACAGGTTTCAGATAACTATGGAGATGATACCATTT GGACTAGGTA
EST33352 7b	75 C G ---	---	TACACATTATTCAGAGACCCTGACATGCATCTCCTCCGAGAAATACATTCGTCCTCTCTTAGAGA AGTTTAA[C/G]GCACATAGTATTATTTACTAAGAGAAATATCTCTTGGTGCATATCTAGGGG
EST33424 1	126 A C ---	---	ATTTTCCACAGCAGAAAGTATATTATTGTGCTGAAATCAGGTAGCAGGGAATGAATAGCTCTTGG GAACCAGTACAGAAATGTTCAACAAGATTTACAAATCTCAGTCATTACACACTGAGCAAC[A/C]AAA CAAAGGTGTTGAATCCTCTT
EST33488 7	90 A G ---	---	CCTTTGGGGAGTTTTAAGCCAGAAATGTGACAAAGTCACCTTACAGGAAGACTGGAATGTAGCCATAG TTGAACTCTAACATCGTCTATAG[A/G]ACCATTTCCCGTCTCCAGTTAGGTTCTAGGCATACTAAGCT GCTC
EST33508 1b	45 C T ---	---	AAAAACATGCTATTTGAACAAACTTTTTTATAAAGAATAAGTTGA[C/T]TGAAAAGCAGTTTAAAT AACATCAACTCACAAATGACTTTTAGAAGCCAAATAA

EST33508 1a	36 A G ---	---	AAAACATGCTATTTGAACAACTTTTATAAAGA[A/G]TAAGTTGACTGAAAGCAGTTTTAAAT AACATCAACTCACAATGACTTTTAGAAGCCAAATAA
EST33863 4	77 C T ---	---	ACAACATAGGACTGGTTATTCTTGTTTGA AAAATTATGTTGCCACTTCCTATTGTTTAAAAATGA TCATTTAAC[C/T]CTTTGAACACTACAGCCTGAATCCCC
EST34739 3	97 T A ---	---	GAAGTATCCTTCCAGTGGCAGGAACCTGAAGACTCCAGATCAACCAGGTGGACCTTTTCGTTGATGA GCTGATAGCTTCTAGGCTGTGGGGAACCTC[T/A]GGTGCCCTTACAACCTCAACTACTGCAGAATTTCT TGTTGTGCCCTCATAACA
EST34792 6b	104 A G ---	---	ACCTGACTGCTTTAAAGCTCTTTGTAAAGCTGACCGTAGCACAGATCACGTGGCATCCACTATCAATA CTCATAAGTCTAATTTATCCTCAGGATGTTCCCTGA[A/G]GTATTCAGGAATTCCTTAGTCCTATTACA AAGATTTTGTGCTG
EST34835 9b	93 T G ---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTTGTGCTTCTGG[T/G]GGCCTTAAAGAAACAGACAAAATTTGTGCTAAAGAT
EST34835 9a	82 G A ---	---	GGAAATGTTCCCTTTGCAACAAGGTACGTTTATCTGCAACTTAGGAGATAAAATGAGATTTCTG TGGGAGTCTATGTT[G/A]TGCTTCTGTTGGCCTTAAAGAAACAGACAAAATTTGTGCTAAAGAT
EST35230 0	93 G T --	---	CACAAAGGTCACCTTACTTACATGAAGGAACATAAAGGCATGAGAAACAGTCATCTCAATAAATG CAAGACATGAGCATAAAGAGGTTCTC[G/T]GCCCTTCCAGCGTTGTTATTACAGAGAGAAACCT
EST35337 9	33 C T ---	---	TCTTTTCAAATTTTGTAGGCATTTAATG[C/T]TATAAATTCCTGCTTAGGAATGTATCTGCT ATATCTCAGAAGTTTGGGCATGTTGTGTTCCATTTTACTTAGTTCAGAACTTTTCAATTTTCATCT
EST35708 9	32 C T ---	---	CTGCCCCAAATTAACCTTTTAGGCAATGGAA[C/T]AGACTTACTGTATGGGGACATTTTAAAAAG ACAGCTTAGTAATATGTTTCATATGCAGCGTGTGCTTCCCTCTCTGAGGTTGGCACCTTTCTGTTGTG ATGTGCAAGTGTTGGCT
EST35747 9	51 C G ---	---	ATCCAGTGCAGAGTTGTAGCTGGAGACATAATTTCAACCCACAAGGCTCCA[C/G]ATGTTAAAAAGT TTCCCAACATCAACCTAATACAGTGACAGCAACACCTCCCTCCTGCCCCCTTCCAGTAGGGTTGAGATT G
EST35751 9	89 C A ---	---	TGGTCCATTATTA AACTGAGGGAACAACGGTGTGCTGACATGGCAGACATTTATTTCAATGGAGA AGTTCTCTCCCATGAACCAAGA[C/A]CTTGTCCTCATGATAAAGTGGAGACAAATAAGAAAGCCAGGT ATATAATTAAGGCCGTGTA
EST36301 4	93 C T ---	---	CACCTGTTCAATTGGTTCACTGGGCTGCTATCTGTGGGCTGATGCTCTACCAAGTGTCTACGCCTACAGC AGTCAGGAGGCAGCCATGGCCCCCTG[C/T]GCTGATGGAGCTTGTAATTTAGCCCCAAACTGATCTTCA GAAAGAGGTACAACAAA
EST36519 0a	33 G T ---	---	GCCATCAGCCCAACAAGACATGACTACCAACGC[G/T]GGCCCCCTTGACCCCATACTGGCCTCAGCAC CTAAGACTGGACAACCTTTGTACCTAATGACCGCCCCACCTGGCATATACTGGCTGGCCTCTCTCTGT CACAGGGGTCTTAGTCGT



EST36620 6	50 G A ---	---	GAC TTATTAGATAAGGGTTTCGGCTACCCCTCAAGCTCTCAGGACTGG[G/A]GCTAGGGTTTAAGG AAGGCTTATTAAATATGGGAATAAAATACAAAGGGCCACACCCGATGCAAAAGACTTT
EST36690 0a	89 C G ---	---	CCTGTGATGTGCATGGGTCCCTGAGCAGTCGTACTTACTATGCGTCAGACAGCTCAGTATGTCAGGA AAGGAAGTCTGGGATTCCCTA[C/G]JAGGGGACATATCACACATATTCTAAGTCACTGTGTGACTCGG CTTGAGCAAGTCATTCA
EST36729 9	62 C T ---	---	GAGACAGAAGCCATCAGTTAAATGAGGTTAGGCCTCTCCTCTAATACTGATTGACAATG[C/T]A TATTAGCCAGGTAATGCACCTTAGCTACCTGGACATGCTATCAAGTGTGCTGGGAAGGGAG
EST36823 6	103 A T ---	---	ACTGTCTGGCCGATGATTGGAGCTTGAAAAAACTACCATGCCAGATCTCCACCCAGACCAATTAG GTCAGTAICTCTGGGGTGCTATTCAAGCAACAATT[A/T]TCTTTTATGTTCTTAAGCTCATCATGAG TTAA
EST36987 4	126 C G ---	---	ATGATCGCTTATGTAAATTTGAGGGCGACATGGGTAATGGGAGATACCCACAGGACCTGTAATATT TAAATAATATTTAACAGCTGATCAGAGGCTAAATTACAACTGACATTTTGATGCAGTTT[C/G]GTTA GGGAATTAAGACAATGCAG
EST37054 3	88 T C ---	---	GGTCACTCTCTGCCAGGACGGTTTGAACTCTGAGCTCAAGTGACCTCCACCTTGGCTTCC GAAAGTGCTAGGATTACAGG[T/C]GTGAGCCACCACACCTGGTCTTGTTTAAAGTAACCACCTGAA C
EST37269 3b	105 T G ---	---	AATAGTCTATGGCTACGGGCCCGTGGGATGTTAAAAATTGGGATTTTAAATTAGATTGTGAACATG CAACCCAGCAAAATTTCTCAGCTTATATTTTGAAAGTC[T/G]CAGGAGAAAAAATGGGGTCC
EST37284 2	93 G T ---	---	AAAAGACCTTTCTCAAGCAGTAACTTTGAGCAGAGACTCAGATGAAGTAAGGGATGAACCAGGAA GCTCTCTGGATAATGTCACTCTAGGAA[G/T]JAGTAAACAGGTGTTAAACCCCTGAGATAGCAACCCCT CTTGGCTTGCTTGAGGAATA
EST37315 2a	90 A G ---	---	AGATGGGCTTGTGCTAGCTTGGCTGGGCTGAACCTAAAGATATCCTCTCAGCTCCAGCTCCAGGTAGT TGGAACCTATAGTAGGAGTATCT[A/G]CCCTGCCCTGCTAGAACTTCAAGTTTGTGATGGGCAAAATCCA CCCCAGAGGACAGGACAA
EST37374 1	45 C T ---	---	CCTGCCATGATAATGTTAAACATATCAAGATCCTCCTCAAACTT[C/T]JAGGGTGAAAGCATAACC ATCCATTTTAGTTGAATATTCCTTCACATAGCCAACACATTTTTCAGGCACTCTAGCTACTACA GGA
EST37376 8b	101 G C ---	---	GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAG[T/C]JTGAGCGCTGGGGCTGAAGTCAGACT CTCTGGGTTCAAAATCACAGTGCTGTGTCTCTGCA[G/C]GCTGTCTCTCAGGCAAGTTGCTGACTTCTCTG TGCCAGG
EST37376 8a	41 T C ---	---	GTGACATCATGTCTCTTCAATGCCCTTTCAATTAATAGTAG[T/C]JTGAGCGCTGGGGCTGAAGTCAG ACTCTCTGGGTTCAAATCACAGTGCTGTGTCTCTGCAGGCTGTCTCAGGCAAGTTGCTGACTTCTCTGT GTCCAGG



EST51340	51	G A ---	---	GATCAAACTGTATTGCCAGGCCAGCTCCTGAAGAACTGTGAACATATGAAC[G/A]TCTCAGCCTAGA AGGATAATGTGACCTTCAATTGGACACCATCCATTGTCTCTTCAAACTAAGAGCCTCTCTAAGCTA GATAGGCCAAGGATTATT
J04162	134	T C ---	---	CATGGGAGTAATAAGAGCAGTGGCAGCATCTCTGAACATTTCTCTGGATTGGCAACCCCATCAT CCTCAGGCCCTCTCTACAAGCAGCAGGAACATAGAACTCAGAGCCAGATCCTTTATCCAACTCTCGA T/CJTTCCTTGGTCTCCAGTGAAGGGAAAGCCCATGATCTTCAAGCAGGGAAGCCCCAGTGAGT AGCTG
K01506	63	T C ---	---	CTGAACTCCAGCTGCCCTACAACTCCATCTCAGCTTTTCTTCTCATTCTCATGTGAAAACTAGT[C/C] CAGTGGCTGACTGAATTGCTGACCCCTTCAAGCTCTGTCTCTTATCCATTACCTCAAAGCAGTCATTCCT TAGTAAAGTTTCCAAACAATAAGAAATTAATGACACCTTTGGTAGCACAATAATGGAGATTATCCTTTTC ATTGAGCCTTTTATCCT
L18877	69	T C ---	---	TGAGTCTGAGCACGAGTTGCAGCCAGGCCAGTGGGAGGAGTCTGGGCCAGTGCACCTTCCAAGGCC CTT/CJATCCATTAGTTCCACTGCTGTGTGACATGAGGCCCATTTCTTCACTCTTTGAAGAGAGCAG TCAGTATTGTTAGTAGTGAGTTTCTGTCTATTGGATGACTTTGAGATTTATCTTTGTTTCTGTTGGA ATTGTTCAAATGTT
L31848	36	T C ---	---	GCTATTTTACATATCCCAAGCCCTTTAGGGCTACAGT[C/C]TCTTGTCTGGACCCTGTAGGGTGCCA TTTGAGTTTACAGCCTAGAGAAGAAAGGCTTTGGCCTGGTGTGGCATAGGCCCTGTAATCGT AGCGCTTTGAGAGGCTGAGGCAGGAAGATAGCTTGAGCTCAGGAAGTTCGAGACAAACCTGGGCAAT GT
L38517	137	G C ---	---	GGTCCAGAAAGCTCTCAGCCAGGAGGAGCTGGCCCTGGAAAGGAACTGAGCTGGGGGACACTGGC TCCTGCCATCTCCTCTGCCATGAAGATACACCATTTGAGACTGGCAACACCAGCGTCCCCAC CC[G/C]CGTCGTGTGTAGTCATAGAGCTGCAAGCTGAGCTGGCGAGGGGATGGTTGTTGACCCCTCT CTCCTAGAGACCTTGAG
L39059	123	T G ---	---	ACTTGAGAAGCAGAGCTGCCACCTTCTGGAGGCCACTGTGATGATGAGCCAAGCAATTTGGAGCCA AGTTGAAGGGACAGGGCAACAAATACAGTAGTATTCTTTTGTATTTTGTATATTTGJCGCCTGA AGATCATCCCGCAAGGCAGGCTGGAGGTGCCGGTGGCTGTGTGCTGGGATTTTAGTCTGTCTGG GAG
L41268d	173	G A ---	---	CAAAGTTGTCTCCTGCCATGAGCACCAAGTCAGGCCCTTGAGGGATCTTCTAGGGAGACAACAGC CCTGTCTCAAACTGGTTGCCAGCTCCAATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTGCAT CTTAGGGCATCGCTCTTCTCACCACCAACAATCTGAAC[G/A]TGCCTCTCCCTTGCCTTACAAATGTCT AAGGT





U06641d	166 C T ---	---	CTCCTCCTTTATTTCAGCATGGAGGGTTAAATGGAGGATCTCCCTTTCTGTGACAAACATCTTTC ACAACTTACCTTGTTAAGACAATTTTAAAAAGATCTTTTACAACTTACCTTGTTAAGACAATA TATTTCCAGGCTATTTAATACGTACTTTAGTC/TJTGGAATTAATCTATGTCAATGATTTTAAAGCTA TGAAATACATGGGGA
U09607	39 T C ---	---	GAGGCCTTATGAGGGTCTCTACTTCAGGAACACCCCA/TG]GACATTGCAATTTGGGGGGCTCCCG TGCCCTGTAGAATAGCCTGTGGCCTTTGCAATTTGTTAAGGTTCAAGACAGATGGCATATGTGTCAG TGGGGCTCTCTGAGTCTGCGCCCAAGAAAGCAAGGAACCAAAATTAAGACTCTCGCATCTTCCCAAC CCCTTA
U09608	82 T C ---	---	GAGCAGAAGGCAAGAGCGGGAAGATGAGTTTGGCGTTGTATTCAAAGGCCCTCATCTGGAGCCTC GGGAAAGTCTGGTCC/T]ACATCTGCCCGCCCTTCCAGCCCTTCCCGAGCCCTCTCTGTTTCTTC ATTCATTCAACAAATTTGGC
U10694	20 C G ---	---	GTGACATGAGGCCCATCTTTC/G]GCTCTGTGTTGAAGAGAGCAATCAGTGTCTCAGTGGCAGTGG GTGGAAGTGAGCACACTGTATGTCTCTCTGGGTTCCCTGTCTATTTGGGTGATTTGGAGATTATCCTT GCTCCCTTTTGGAAATGTTCAATGTTCTTTTAAATGTCAGTTTAAATGAACCTCACCATCGAAGTTAA TGAATGACAGTA
U13877b	162 T C ---	---	AAAAGGACTCTGGTTCAAAATCCAGGTTCCATT]TGCTATCTTTGTGACCTTGACAAAGTTGTTAAC CTCTTTGTTCAGAAATTTCTCCATGGAGTAACAATATCTAGGTTGGGAGGATTAAGTGAAGTTACATGT AAAGCACAGAGGAACAGCCAAGAGAT]T/C]TTACCGTGGTCTTACTAAAGTACATATCCTAACTTGG GGTTACCTTCAGCA
U15555	187 T C ---	---	TTTCTGTCCACTTTCACCTGGTTTAAATAGCCAGCCAGTCATAATAGTAGAGGAATCAGTCAAGCAA AAATGCTTTGGAAGAAATTAATAGCAATGCTGAACATCAGGAATGTAGATATCCGTACAGAGAGT TCCAGTAAATTTTATGAGTCCAGGACCCCTTTTCTAAGCAGTCTGGTCCATGT]T/C]TGGTCTCATAC CTCATATGCAGGATTCATICA
U17077	122 T C ---	---	TCCAATTATTGGTCCCAAAAGCAGCTTCCAAAGTTTGCCATCTGGATGACAAACGGAAGATCCACT AAAGGTCCACGGGATTAAACAGAACGTCCTTGAGAGACTGAGCGATGACACCACAC/T]G]TTGTTGG ACATTTAAATTCACCTCTGCTGAATAGGAGGAAGCTTTTCTTTTCTGGGAAACAACTGTCTCTTGG AATTA
U18543	58 T C ---	---	GCACATGCAGAAATAGACTCAGCCTATGTCCCTGATTCAGCTGGGTAGTTCTAGAATTT/C]AGAAG CTCCATCTTTTAAATGTTTATTGTTATGTCCCTCCCGCTTCCACCTAAATTTAGAGCTTTAA AGATGCACTGCCCAATAGGACACACGATGGTGTAGCTGAAGTTTGATTAGCAATTAGGCACTTCC AAGGCTTTAGTAGAGAGGCC

U25975b	164	C A ---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGCAATGACTATTCTCTG AAGACAACCAAGAGAAAATTGCAAAAAGA[C/A]AAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25975a	143	C G ---	---	TCAC TGTGTGGCCTCATACTCTTTTCCATTTTCTACAAGAAGCCCTTTTAGTATATGAAAATTATT ACTCTTTTGGGGTTTAAAGAAATGGTCTGCATAACCTGAATGAAGCAATGACTATTCTCTG AAGACAAC[C/G]AAGAGAAAATTGCAAAAAGACAAAGTATGACTTTTATATGAACCCCTTCTTTAGG GTCCAGAAGGAATTGTGGACTGA
U25997	61	A G ---	---	CAGGAGAGGTTATTACAAACCTCACCAACTAGTATCATTTTAGGGGTGTGACACACCA[A/G]TT TTGAGTGTACTGTGCCTGGTTGATTTTAAAGTAGTTCCTATTTTCTATCCCCCTTAAAGAAAATT GCATGAAACTAGGCTTCTGTATCAATATCCCAACATTCTGCAATGGCAGCATTCACCACCAACAAA TOC
U28413	29	C T ---	---	ATTCTGACAGCTAAATTAGCCCTAAATG[C/T]GGGTAATATTTTCCCTCATGTTTTAAATGAGGTT AATATTTGCATAAAATCCTAAACAGACTTCTGTATAGTTTATTTAGTCAAAATGTGTTCCCTGATCC CAGATGTTGTGGCCTGGGAAAGCCCTCATTGCTACAGTACAAGTAACACAAAGTCGTTGTACCTCAGTT G
U30884c	89	A G ---	---	TAGGGTAGCATTTAAGATTAGGAGTCATTAGCAGTGATGATTTTGGGACCTGCCGTATAATCTGTT CTTCTATTCCACGTTAGCCA[A/G]TTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCCACAGTTGAACACAAAGT GCTGTCA
U30884a	34	A G ---	---	TAGGGTAGCATTTAAGATTAGGAGTCATTAGC[A/G]GTGATGATTTTGGGACCTGCCGTATAATCT GTTCTTCTATTCCACGTTAGCCAATTGTTCTTGATGAATCTATATGAGTCATAGAACACAAATCTAT TGACGGAAGTCATTAGAATGGCTTGTGATATCTGATGGCTTGAACCTTGCCCACAGTTGAACACAAAGT GCTGTCA
U31216b	78	A G ---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCCGTCAATCA[A/G]CCCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCAACCAAGACCCCTTTACAACGTAGAGGAGGAGGATGCCAGCGGATTGCGCTTTAGCCCGCC TGGTAGCCCTTCCAT
U31216a	70	G A ---	---	GGGACAGCATATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAACA GCC[G/A]TCATCAACCCCTCACTAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA CCAGCAACCAAGACCCCTTTACAACGTAGAGGAGGAGGATGCCAGCGGATTGCGCTTTAGCCCGCC TGGTAGCCCTTCCAT



U31416c	76 G A ---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC CTCCTCAC[G]CCACAAATCTGGTGCTCTCTCTCTGCTTACAAATGTCTAGGTCCCACTGCCTGCT GGAAGAAACACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACCTTGACCCCTGCCACCTCTCC AACCTAACTGGCTTACTTCCT
U31416b	68 C T ---	---	AGTTGCCAGCTCCCATGTACCAGCAGCTGGAATCTGAAGGCGTGAGTCTTCATCTTAGGGCATCGCTC [C]TTCTCACGCCACAAATCTGGTGCTCTCTCTCTGCTTACAAATGTCTAGGTCCCACTGCCTGCTG GAAAGAAACACACTCCTTTGCTTAGCCACAGTTCTCCATTCACCTTGACCCCTGCCACCTCTCTCCA ACCTAACTGGCTTACTTCCT
U37519a	78 C T ---	---	ACGGTCCACACAGAGAAACCTGAGTCTAGCCATGAGGGCTTATGCTCCCAACTCACATTGTTCTCC AGACCGCAGG[C]TTCCCCAGCCTCAGGTTGCTGGAGCTGTCACATGACTGCATCCTGCCTGCCAGG GCTGCAAAGCAAGGTCTTCTTCTATCTGGGGACGCTGCTGAGAGAGGCCGAGAGGCCGCCAGAAC ATGCCAGGTGTCC
U37690	54 A G ---	---	GACCAGCTGAACCCACCCCGCTGTGCTGACCATGGCCCTGAGCGTCTT[AG]CCCCGGAATTC ACGAGGCTGAGGCATCCGGGAGCTGGCGTAATGCCTGGCCGAGTGTGTGTATCCCATACCCCACT CTGGAAGGAACCATCCAGTAAAGTCTTT
V00540	39 T C ---	---	TGAAACCGTTTCAACATGGAATGATCTGTATTGACTAAT[C]ACACCAAGTCCACACTTCTATGACT TCTGCCATTTCAAAGACTCATTTCTCTATAACCAACCGCATGAGTTGAATCAAAATTTTCAGATCTTT TCAGGAGTGTAAAGGAACATCATGTTTACCTGTGCAGGCACCTAGTCTTTACAGATGACCATGTGAT A
X15943	106 A T ---	---	TCAAGAAGTGACTGCCCTTGATGATGGGATGGGAAGATGAATGACTGGTTTTTACTGGGGTGTA AACCACTCTGAGCCTCTCTGAGACCATGTGGTTTTAAATATATCCATAAGGGAAGGTACCCACAC CAGTATCTGAGTTCCAGTAGCTAAGACCCCTAGAATTTGGATTTCATCTCTGTTTTTTCATGCTCTCCTT GTAACCCCTGAGATCATCAG
X52011b	148 C T ---	---	AGGAAGATCCCAACCGACCCCTTCTGGCCTAATCCTTAGATTAGGTCACATTACATTAACTTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAAAGTTGCGAAAATTGCG AAATCTGTTGTGCA[C]TTGCTCAAATGAAACGCCCTTCGGCTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT
X52011a	118 A C ---	---	AGGAAGATCCCAACCGACCCCTTCTGGCCTAATCCTTTAGATTAGGTCACATTACATTAACTTAGGA ACCCAGACCGAAAGTTGCTGAAAGGGAAGGAGACACATTACAAAGAAA[C]GTTGCGAAAATT GCGAAATCTGTTGTGCACGCTCAAATGAAACGCCCTTCGGCTTTGGGCTTTTATTTTTTGGAACTG CGAGTGGCTTAGGCTAGCCT

X54741	24 A G ---	---	CAGGCCACCTGTCTTCTCTCCACAG/GITGACAGCTTCTGAGTCACCCCTCTGTCCAGCCAGCTCCT GGACAAATGGAATCCCGAGGCTCCAGGACTGGGCTTGCCAGGCTTGTCAAATAGCAAGGCCAG GGCACAGCTGGAGACGATCTTGTGCTGGCAGGCTGGCTTGTCOCAGCCCACTGGCCCTTCTCC AGCAAGCAGTGC
X54869	99 A G ---	---	AAGCATTTGCGTTACAGTGCATCAGATACATTTTATATTTCTTAAATAGAAATATTATGATTGCAT AAATCTGAAATGAATTATGTTATTTGCTCTA/GJATACAAAATTTCTAAATCAATATTGAAATAG GATGCACACAATTAAGTACAGACATCCTAGCATTGTGTGCGGCTCATTTTGCTCAACATGGTA GCCGTGCTGACACCTCCAGAACGAGGTGCTGGGCCCCGTTCTGCTGGACCCCGGGAACCTCTC CTGCCGGAAGCCGACGCGAGGATGGCCCCAACTTCGCCCTGCCACTTGACTTCACCAATCCCT TCCTGGAGACTTG/AIAACCTGGTGTCTCAGGAGCGAAGGACTGTGAACCTTGTGGCTGAAGAGCCAGA GAAATGTGAAGAATGTGACAAAGCCCTTTAAGCGGTTGTACACACTTGATTGTATATAAGATAA/T/GJT CATACTGGAGAAACTCCAGAAAGTGTGACAAATGTGACAAACATTTAATTAATCTCATACCTTA TTGCACAGGAAAGCATTATACCTTGAGAAATTTGTATAAGAAATGGAAAGTCATTAATATCTGCT CATATCTTAACATCAGCGAGTT
X66924	147 G A ---	---	CTCAACCCATAACCTGAACACATCT/GJATCCTCCACCCAGACATCCACACATCCACCTCCATCC CCAAACCATCTCATCCCACTACAGCCCAACCCAGCCCAAGACTAATCCACAGCCATCCCAA CTCATCCTCATCCCAACTGCAGCCCCAAACCCAAACCCAGGGCCATCCCCAAACCCATCCCCAAGCC AACTCAACACCATCC
X78932	62 T G ---	---	ACCCCAACTCAAGTCCAGGCCCCAGGCATCTTCTGCCCCTGCTTGGCCCCATCCAGTCCAGG CGCCTGGAGCAAGTGTCTAGCTACTTCTCTCTG/CJCACTTTGAAAGACCCCTCCACTCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG ACCCCAACTCAAGTCCAGGCCCCAGGC/GJCTTTCTGCCCCTGCTTGGCCCCATCCAGTCC AGGGCCTGGAGCAAGTGTCTAGCTACTTCTCTGCACTTTGAAAGACCCCTCCACTCTGGCCTCA CATTTCTGTGTGATCCCCACTTCTGGGCTCTGCCACCCACAGTGGGAAAGGCCACCCCTAGAAAG GGCACCCAGAGTGACCAAGTCCAGGAGGGCGGCCCTCGCCGTGTCGGTGTCTTTT CAGCCCCGGAGAGTCTGACCTGGGGCTTCTCAAGCCTCAGTGGCCACGCTCCCCCGCTCT CTTTCTCCCAAGC/G/AIAACCAATGGCCCCCTTCACTCGGCTGCCGTGCGAGGCCGGGGCTT CTTTCAGAGC
X80026	25 T C ---	---	ACCACAGCCATGGTCTAAGGACATGGATCGGGTGCCCCAGACGTGTGCACAGGGACCCCTCTGCC CACTCTGGGCTTTTCAGATACTCTGACCAAAAGCCTGTCTTTAAOCGCAAGATGGGGCTT/GJGGC ATGGCAGGAGGAGCCATCGGGTACTACGCAGCAACACTCACAACTGTCCAGGCTGAGATAAATCCC GGGA
X80197b	99 G C ---	---	
X80197a	28 A G ---	---	
X85106	150 G A ---	---	
X87160	128 T G ---	---	

[illegible]



1282	130 C T ---	---	GTGGATCACCACACTACAGTCTAATTTTCAGATGTTTTTCATTACCCCTAAAGAAATCTTGTACCCATTA GCAATTATTCCTCATTCCTGCCCTCACCCAGGCCCTACTCTTTATCGCTATAGATTTGCCIC/TJACT TGACATATCATACACATGGAGCCATACATATGTGTGCCCTTCATGATTGGCTTCTTTCACCTGAGAATA ATGTTTTCAAGGT
6810	68 C T ---	---	AGTATCACACATACCTTAATATATTAGATATACACATAATAAATCACTCCCTACCTTGAAACCTTT A/C/TJAGAAGCATTTTTAATTTTACAACACAAAGCTCAACGACCTACAATAAGTCTAGTAGTCTG TTACGTGCCAAGGATAAGGCTGAACAAATAAATTAACCCCTTTAAATGTCTATGAACAAGTACAA TTTTCTTTTGAGTTCTGCAGAGCAATGACCCTAAGAAATATTTTTAAAGGC
6817	118 A C ---	---	CCAAGTACATTGGGTGAACGATGAGCTAGTGTCTAGTATTGCTTTTTGTATCCAGTTAAGACCA TCAGCATATACAACATCATCACTAACTCAACAATGTAGCTGCAGGGTAAC/A/CJTGTGGATACCCCTG TGTGCTCTACTGGCCTCCAAAGGCATTCAAGGGATCATCAAGATGTTGGACACACCTTGTGTTCAAATC TTGGTTCAGGTGGCCTGTGCAGATCGGCTTTTGGTTGGTGTCTTAG
6819b	212 C ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCCCTTCAACAGTTTTTGCTATACAAAATTTTCTGCTATTTTGTCTTAGCAAA CAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
6819a	166 G T ---	---	CCATTTTATTTTCTCTAAATTTTAAATAGAAGACTTTAATGGAAACATTTAGTACCATCATGTCA CCCTGAATGCCAGCAATACCTCGACTTTTACACACGCGAGGAGCCTAGTAAAGCCCCGTCAGTAGT ACACATTTCTCTATGGTCCCTTCAACAGTTTTTGTJCATATACAAAATTTTCTGCTATTTTGTCTTAGC AAACAGCAATAACTTTTGTGTTTCTCTATATGACACCTAATATCCA
681xx	39 A G ---	---	CTGGTATGTCATAAGCAATCCATAATTGTTATAGCTATTJAGJTTATACTATGGCACCATTTGGGACA CAGATTATATATGTCAGACACCAACGAAATGTCCTTTAAGATATGCAGCAAGCACAAATCTGTCTATGGT TTAACAAAGAAATGAACGTCTAGG
6972b	149 G T ---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTTGTAACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAACTATTGATTATTGC CACAAATTCAGAG/GTJCCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGTTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT
6972a	122 A G ---	---	AGGATTCCTCTTTTCTATTGATTGGAATAGTTTCAGAAGGAATGGTACCAGTTCCTCCTTGTAACCT CTGGTAGAATTCGGCTGTGAATCCATCTGGTCTGGACTCTTTTGGTTGGTAA/GJCTATTGATTA TTGCCACAATTCAGAGCCCTGTTATTGGTCTATTTCAGAGATTCAACTTCTCCTGTTTAGTCTTGGGA GAGTGTATGTGTCGAGGAAT

7598k	210	A C ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTTCCCT CAATGCAG[A/C]
7598j	208	A T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTTCCCT CAATGC[A/T]GA
7598i	192	G T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTT CCTCAATGCAGA
7598h	144	C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGATCC[C/T]ATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTT CCTCAATGCAGA
7598g	142	C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTTTTA ATATTTGAT[C/T]CCATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTT CCTCAATGCAGA
7598f	120	A G ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCAAGGAACTCA ATGAAATAAGCCGCTAACCGATTTACCTTGGAGAAATGAAATTAATTTCTTG[A/G]GGATGCCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTT CCTCAATGCAGA
7598e	83	C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCAAGGAACTCA ATGAAATAAGCCGCTA[C/T]CAGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTT CCTCAATGCAGA
7598d	77	C T ---	---	AAAGGTAATCAAAGTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGCAAGGAACTCA ATGAAATAAGC[C/T]GCTAACCGATTTTACCTTGGAGAAATGAAATTAATTTCTTGAGGATGCCCTT TTAATATTTGATCCCAATTATGTGAGAGATTTCCCTGATATGTTATCTTATATATTTTCCCGTATTTT CCTCAATGCAGA

7598c	56 A G ---	---	AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGCCAA/GJAGGAAC TCAATGAAATAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAATATTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598b	47 C G ---	---	AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAAC TCAATGAAATAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAATATTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7598a	30 A G ---	---	AAAGGTAATCAAAGTTCCCTCTATAAATTATGATTTACAAAAGACACCCAAAGGAAC TCAATGAAATAAGCCGCTAACCGATTTTACCTTGGAGAAATGAAATATTCTTGAGGATGCCTT TTAATATTTGATCCCATTTATGTGAGAGATTTTCTGATATGTTATCTTATTATATTTTCCCGTATTTT CCTCAATGCAGA
7998c	116 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGAGCTGTTCTATTACAGACATCTTGCCAGCTCTCCTGTA ATACCTTAAATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATAATCTTCTGAGGTTCTCT
7998b	94 A C ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGAGCTGTTCTATTACAGACATCTTGCCAGCTCTCCTGTA ATACCTTAAATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATAATCTTCTGAGGTTCTCT
7998a	75 A T ---	---	GTGTTGATCTCACTGGGTGCTGCAGGCCGAGCTGTTCTATTACAGACATCTTGCCAGCTCTCCTGTA ATACCTTAAATGAATGGGTAGTCTATCTTCTCAAGGTCCCAATAATCTTCTGAGGTTCTCT
8071	119 A G ---	---	AAATACAGAAATTTATTTAGAAACTGTTTAAAGTAGAAAAAACCCCTGTCAAGAAAGACCAGGTGG AAAATGGTTCCCAATAAATGGAATTTTAGGGCAACAAAAGTCTAAAAGGCCA/GJCAAAAAGAGA AATAGCACCACTGTCTATTGAACAAATGGCTAGTTACTTGTGATTTTGGCATTGTTAATCACTGAATC TGGGTTTCTCTGAAATTCACACACAGAGCATGCCTACACACATTTTATCAT
8467b	93 C T ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAACTGGGAAATCTCTGGATATTTGGCTTATCACTT TGACGCAAAATCCACTTTGCTGTAACTGTCATCCGAACTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
8467a	70 A G ---	---	AAGGCTTTCCTCTAAACATCAGTCTACGGAGAACTGGGAAATCTCTGGATATTTGGCTTATCACTT TG/A/GJCGCAAAATCCACTTTGCTGTAACTGTCATCCGAACTCCCTTCAGAGAGCAAGCAAAA TTAAGTGTGATACTGGAGCTTATGCATGCAAAAGCTTGCAAAAAGTATTAAGGAAAAATTACTG
8498	84 C T ---	---	AGGGTTCAGGGTTGGTTTAAATCAGGCTGCACACCTTTCAATCAATCTGACATCTCTCTATGTCA AACTGGCTTCAGCTAGC/TJAAATACCTTCAATTAATCGAAAAAGAAAAATTTGCTTTAAGGAAAAAA AATCCAGTTTAAAGAACAAATTAACATTAGTCTTTAAATAAAGGAGGGCTAATGTTTCATGTTGCT TTATACATCCTTCTCCTCAATACAGAACCGAATGTAATTTTCTCTAACTCAG



WI-18562	29	G A ---			CTAAGGAAAATTTAATGATGGAATATC[G/A]ACAAATATTCAACATCATTTAAAAACAAAGTAG CTTCTCTATTTCACATAGCTTAGTTGGGATAGAAATAGAACTAATGTTTACAATGATTCTTACATT TAGCATTAAATCAGAAACGA
WI-18618	51	A C ---			ATAGCAGACTTTTAAATCAATGCCAGAGACAAAGTGAGGCCGAGCTAAGAAC[A/C]CGCTCAGCTTCG TTACAATGAAGAAATGGTTTCCTTCGATGCAAGTATAATTGTAAACCCACAGTGTCTCGCACAGTTC AC
WI-18683	22	C T ---			TAGCTGTTTCAGGACTGGACTC[C/T]GGTCCCTTTATTGAGACTGACAGGCCAGTGGTCCACCCAAA CAAAATAAATTTCTCTCCCAAAGCCTGCCTGCAGT
WI-18520	75	G A ---			GACTTTGGTGATTTAATTGCTTTTCCCTTAAATATGAGAAATAGGTGTAATTTCTCCTTTTGTCTTT ACTACA[G/A]CCGGAGTGTGTAATACTACTACTGCCAAACACACGGGCATCCACTCTGTCTTCAA TGCCTCTTCCGTGAGAC
WI-18563	94	A G ---			AAATAAGTTTTATTGGCACACAGCCAAGCCACTGGATGACACATTTGTCACGGCTCATCTTGCAA TACAATAGCAGGGTTCACTAATGTGAC[A/G]ACATGGTGTGCTCACAAAGCCAAAGATATT
WI-18582b	69	T A ---			GTCCTATTCAATTTAGCTAGACCCATTTCATTCTGTTTAAATGGCTACATTTGTTTTTCATTGTGAGAC TT[A/G]TGCCATAATTTAATTAATCAGTGCCATATTGAAAGACATTTGGATCGTTTCCCAG
WI-18723f	94	G A ---			AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAA[G/A]TATATAGCTTATTGGTGAATCTTCATCCT
WI-18723e	71	T C ---			AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGT[C/A]ACAGGTACATAGGTAACCAAAGTATATAGCTTATTGGTGAATCTTCATCCT
WI-18723c	96	A G ---			AACTTTATTGATCTGACGATCAGCGATTAGTTCTCATCCACATTGACTGTCTGTAGATTTTGAAG TGGTAACAGGTACATAGGTAACCAAAGT[A/G]TATAGCTTATTGGTGAATCTTCATCCT
WI-18619	44	G A ---			TTTATTACAATATTAGGTGGCACAAATAACTAACAAAGCTTCTGA[G/A]ACAGGAGGTAAACATTCTCA TAGACTTTGCAACTCAGCCAGAAGTAAACTCGAAATA
WI-18715	76	G A ---			TTATTCACAAAAGTGATATTGCAGAGGGTCTGGGGCTGTACATGGCAGGGGCTTGGTGAGCTTGG TACATGGG[G/A]CTGGGAGACAAGGGAGCCTCCAGGTGGAAGGTATTTTTTAATAAAAAAATAA TGGAGCTACAACCAACCCCG
WI-18535	107	G A ---			GTAATAAAGTTTTATTGGCACAGCCAGCTCGTTTCATTATGCCATTGACATCTGCTGTTGOCCT ACACAGCAGGTGGGACCTGCTCTTCACGGGAGAGCTA[G/A]TTGTTTAAAGCAGTGGTCCCAAC CTTCTGTGGTCCCGGTG
D17525	107	C T ---			AGAGTGTGACACACAGGCCGAATCCAGGCTCTATCACTTACTAGTTTTCAGTTCTGGGCAGGTGAC TTTCTCTCTTCGAACTTCAGTTTCTTCATAAGATGGAA[A/C]TGCTATACCTTACCTACCTCGTAA GTCTGATGAGGAAAGATTAACTAATAGATGCATAGCACTTAACAGAGTGCATAGCATACACTGTTT TCAATAATGCACCTTAGCAGAAGTGTGCTCTACCAGGCAGACGAAG

DWU-133c	313	A G ---	---	TAATTGGCCACTGCCCTTATTATACAAACAGAAATGTCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGTTAAATGAATATGTTTCAAGTTTGAATTTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTACCCCTTTTAAAGATATGATTAGACT
DWU-133b	236	T C ---	---	TAATTGGCCACTGCCCTTATTATACAAACAGAAATGTCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGTTAAATGAATATGTTTCAAGTTTGAATTTTAATAGTAACCTCC AATTCAGTAAATGGTATCACTCGTTACCCCTTTTAAAGATATGATTAGACT
DWU-133a	199	C T ---	---	TAATTGGCCACTGCCCTTATTATACAAACAGAAATGTCTCATGACTTTTTTATGTGTACCATCCT TTAATAGATCTCATACACCAGAAATTCAGATCATGAATGACTGACAGAAATATTTTGTGGCAGTCCT GATTTAAACTAAGACTGGCTTGTGTTAAATGAATATGTTTCAAGTTTGAATTTTAATAGTAACCTCC TTCCAAATTCAGTAAATGGTATCACTCGTTACCCCTTTTAAAGATATGATTAGACT
DWU-36	102	C T ---	---	ATGAGATCCTTTAAATCCTTCCATGAACGTTTTGTGTGGTGGCACCTCCTACGTCAACATGAAGTG TGTTTCCCTCAGTGCATCTGGGAAGATTTCTACCTCTTGACCAACAGTTCTCAGCTTCCATTTCGCC CCTCATTATCCCTCAACCCCGAGCCACAGGTGTTTATACAGCTCAGCTTTTGTCTTTCTGAGGAG AACAATAAGACCATAAAGGGAAGGATTCATGTGGAATATATAAGAT
DWU-387	169	G T ---	---	GTGTATAAAATGCAACTGTTGATTTCTCAACATGGCTCACAAATTTCTATCCCAATCTTTTCTGAA GATGAAGAGTTTAGTTTAAACTGCACTGCCAACAAGTTCACTTCATATATAAAGCATTTATTTTA CTCTTTGAGGTGAATATAATTTATATTACAATG[G]TAAAGCTTCTTTAATACTAAGTATTTTCA GGTCTTCACCAAGTATCAAAGTATAACACAAATGAAGTGTCATTATTCAA
DWU-447b	172	-- -- ---	---	ATTTAGTGTCTTTGCGTTAAAAATCATTTGCAAAAGTATTTCTGAAGCTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAATCACTGTAAATTAATTAGTTTGAATTAGAGCACAAGCTTAGCTAATCAA CCATTATTTTCAATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGTCTTTCTGTAG GCCTTCTTTCTTACAATGAAGAGATGATTTCTTCTAGTTTATGGTTA
DWU-447	85	A G ---	---	ATTTAGTGTCTTTGCGTTAAAAATCATTTGCAAAAGTATTTCTGAAGCTGTCAAGCTGCCAGTCAGAT GGGCTGTTGCCATTTAAAGTACTGTAAATTAATTAGTTTGAATTAGAGCACAAGCTTAGCTAAT CAACCATTATTTTCAATTTGTTGTTCTAAGAGGATTGANAATCAGTTTAGTTTAAATGTCTTTCTG TTAGGCCCTTTCTTCTTACAATGAAGAGATGATTTCTTCTAGTTTATGGTTA
DWU-476	63	C G ---	---	GTAAATTCAGTTTTTTTCCAGTTCTCTTTTGTGCTGCTCTCAATTAGCGTTTAAGGTGAGTCGAT AAATCAACTGTCCATCAGGTGAGGTGTGCTCCATACCCAGCGGTTCTTCATGAGTAGTGGGCTATGCA GGAGCTTCTGGGAGATTTTTT

DWU-505	67 A T ---	---	TCATAAGGGCAGTATCTCTAGCTAGTGGCCATACAGAAAATTTCTATCACCATACAAAATTTA A/TJTGCAATTTATGTTTAAAGCACAGGTGTACCGAAAAGTGTGAAGTCTGAATTTATGGGT CTATGCATGCATTTTGCCTAACCTAGAGAAAGAGTTTGATAAATTTTACCAGCTTTGAAGATGGAT TAACTTTGACTTTGAGCTTTAACTTTTAA
DWU-512	131 A G ---	---	AAATCCAGGCATTTTCGAATCTGTTTTCATGATTTATAGAGGGTTTACACAAAAGTGCCACTTATTAA AGAGCTTCCACAGTGAAGATGGAGAAAGGTGAACCTTGTCTTGAATATTCAGATGTGTTTGGTCIAGI TGCGTATGGCAGTGAGCAGGTATGTGTTTGTCTTGTCTTGTGCTTGTGCTGAAATTAATTGCTATCAAGAGC AACTATGAACGGTTTTTATTCAAGATGCTCCAGAGTGAAGATGCCGAG
DWU-525	97 A C ---	---	AACTGCATATAGATAATTATCCAGGATGTGTGGCTCATTTCTTTCAGCTTGTCTTCTATCTGTTTGT ATATACAGTTTGTGAACCATATGATTGA/CJAAGAAGAAAAGTCTATGCTTAGGCCAGTCAGTACA CCCAATTTTAAAAAATAACATAATCTTGTCTTTCACAAATATAGTTGAACAAGATTTCCCTAAAAAT CCACCAGGATTAATCTCTAAAATTTAGTCTCTGATTTC
DWU-59	94 C T ---	---	CATTTCTTTGTGAAGGTAAATGGAATCACAAGGGGAAGAAACATGCTGAGAAAGTGTACCCGG CCCTTTCTTTGTGAAGTCAATTTGGC/C/TJGAGCCGTTCAGTTCCAGGTGGCAGACTCGTTTTTG GTAGTTTGTCTTAACTTCCAAGGTGTTTACTTCTGATAGCCGGTATTTCCCTCCTAGCAGACATG CCACACCGGGTAAGAGCTCTGAGTCTTAGTGTGTTAAGC
EST11	68 C ---	---	CTTGATCATGGGGTGAATTTTGTGTATCTGGGCTTCATGGGATGCATAAAATTTCCAGTTGGTAAG CAGCAGGTGCCGAGGGTCTGGATCAGAAAAGGCA
WI-19856b	63 C T ---	---	CACACTGGCATCTAGGCCCTTCGCTGCATTGCAGAAGGAGAGCCAGGTCCCTCCTGGAGAA/C/TJG CTGCGTTCCCGAGCCACACCGGCTTTGCACACACAGGCTGTGAGCAGGAGGTGGTAAGACGT AGCTGTAGACCCAAAGCAACCAAGCCCTGGACCCCTGCGGGAGAGGAGCACTTTAGAACATGGAA AAGTGTGTCATCCCATCATTTAGACAAGACACATCCTACATAATAAAAGT
WI-18014	40 A G ---	---	TCCATTTACATTTGGTGGCATTTGTTGAATAGCTACAGAAI/GJGAATGAAAGTGCACCATCAGAGT GTAATTAGGTCTGTGTGACCCAGGAAGTGTCTGTGTTAAACAGAGATTTCTCAAGGGCAAGTGGCTCT A
WI-18036b	97 T A ---	---	TTCCAATGTAAAGAGTCAAGTACCAAGTTAACTTCTAGAAATACAAAGAGAACATGATAAAATCTG ATCACAGTGGAAAATTTTAACTTCTTTCATAA/T/AJCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18036a	27 T C ---	---	TTCCAATGTAAAGAGTCAAGTACCAAGTT/CJAACTTCTAGAAATACAAAGAGAACATGATAAAAT GTGATCACAGTGGAAAATTTTAACTTCTTTCATAATCTGACAGGTCAAGTAAGCTAAAGGAAACATAT TAGGGATCTGAAGG
WI-18046	72 C T ---	---	TGTAAGGTGACTTCTATAAGCTTCTTAACTGTCAAACTTTTCACTTACTGAGATTATTCAGGCCAAT GTGT/C/TJGTTGGGTCTGAGATTGATTATCAGCTGGGTAAAGTTAACCTGTCTCTGTTTCA



WI-18063	105	G A ---			AGGCTTTAACTGATAACAAATTTGCCCTTTAATCACATACAAAACCTCTGCACCTTTCATTCCTCCTCCTC CCATGTTTCTGATTTGATGTAAACTTAAATTTGTG/A/TCCCTTTAACAAATATATACTGTAGCTGCA
WI-18078	86	A T ---			AGTTGAAAGATCAGAGAGGTTATGGTTGGTAGTAGCTGAAGTCAAGTTCAGATTCAAACCTGGTCCAGTGTG TTGTTTTTTTCAGCATCAG/AT/GTCCACTAGCCAAGTTGATCTCTGCAGTATCTACATGTGGT
WI-18091	90	T C ---			CCAAAGCTCACTCAGTATTTAATCATCTGCTAATTTTCATCCCTTTGTTAAATTCATCAGACACTGTGGT TTTCATCTCTAGAAAGTTTGACTT/CJ/GGGCCCTTTTATACCTTCCATATCTCAACTTGTTAAGC
WI-18119	38	T C ---			GCAATCTGTAAACAGTTTGGTAGTGGTATTACAGAGGAT/CJ/TGTAAATGGATTGGAGTACTTAC CACTATTTTCATCTGCTCTGAAATAGTTCACTAACCAAACTACTGACAACAGITTTAATTTGGTTCTT
WI-18142	66	T G ---			TTCAAGATAATTACAATTGGAAGGGGACCAATAATTCACCTTTTAAATCGAAAATAATCTATATACJ T/GJCCCAATAAACTCACAGTAAATAAGCTTCAAAAGCCTTAAGACACCAAAAGAGGAAAA
WI-18178	68	T C ---			GCATAGGTTGAGGGGTGTACAAGAGGAGAACAGATTCAAGTCCATGCTGGAGGTTAGTCTGGGG GT/CJCGGCGGGATGGACACACAGACACATAGATCTGGCATCTGATAGCAGGGCATACAG
WI-18244	35	G T ---			TCAATCTGAAAACCTTGCTGTAGCCAGCATGGGGT/GTJGGGGAGGTGATTATGGCTGGGGAAGATG GGCACTCACCCGACAGCAGCATCTAGCACCAAGTACAGAGGACGTTGAGGTGGCAGAGGGCTTT
WI-18245	115	G A ---			ACAGATGTCAGTTGTTGAAATTGGCCCATTAAGTATGGGGCTTTCTTGTAAAGTCAATTCCAA AGGCTTGCAAGAGTTTGCTATACAACGGAGGACAGAGAAACATGA/G/AJCTGGGAGTAGGCTCT GACAGAAGGTGGCTGTC
WI-18261	26	G A ---			GATTTGAAGGGATTGCTTTATTTAAC/G/AJTGAAAAGCGTGATAGAGGAACCTGTTTAAGATAAACAA CTTATAAATACTCCCAATTGTAGAGTGAAAGATTG
WI-18268	88	C T ---			TAGAGGGGAAAAGGAGGTGGCTGCTGGCCCTCAAGACATGAGAAACGGGTGGTGGCTTCCAAGC TTCCTTACTTCCCCCATAGAT/CJCTGACAATGTGCTGCAGAAAGCCTCCAACCTGGAAC
WI-18299f	107	C A ---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGGCCAATTTTT ATCTATTTGGGCTGAGAAATTCACAAATTTTGA/G/AJGGAATTCCTTTGGCCAATTTGACATATTCTG CAG
WI-18299e	101	A G ---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGGCCAATTTTT ATCTATTTG/G/AJGTCTGAGAAATTCACAAATTTTGAAGAAATTCCTTTGGCCAATTTGACATATTCTG CAG
WI-18299d	77	G A ---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGGCCAATTTTT ATCTATTTGGTCTGAGAAATTCACAAATTTTGAAGAAATTCCTTTGGCCAATTTGACATATTCTG CAG
WI-18299c	67	T G ---			TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACTTGGTTGGCCAATTTTT T/GJATCTATTTGGTCTGAGAAATTCACAAATTTTGAAGAAATTCCTTTGGCCAATTTGACATATTCTG CAG

WI-18298b	52 G A ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTTG[G/A]TTTGCCAATTTT TTTATCTATTTGGGTCTGAGAAATTCACAAATTTTGAAGAAATCTTTTGCCAATTTATTGACATATTCTG CAG
WI-18299a	48 C T ---	---	TCACAAGTCAATCTCCCATCCAAATGACAGTTTGTCTAAGATCATTAACCTTTGGTTTGCCAATTTT TTTATCTATTTGGGTCTGAGAAATTCACAAATTTTGAAGAAATCTTTTGCCAATTTATTGACATATTCTG CAG
WI-18307	76 G A ---	---	TCAACTTGTAACCAAGTTTAGCAGCAAGAGGATACCTTCTTAGAGACTTTTCAGTGGACTTAAACTCAG TTTCCGCTG[G/A]TGCTATGTAAAGCATCCACGATGGTTTTATTGTACTCTGCAATCTGCTTGGTCTAC TTTGGTATGAAATCTTTCTCTGACATTTACCAATCATCACTTAACTCCGGGGGTGGGTACTGATT TATC[C/T]TAGATCCAAATAAAGCATGCAGAAGTG
WI-18324	72 C T ---	---	ATGAAAGTCACTTCAATCATAAGGGTCAAGAGAAAGAAATGTTTTCAGAT[C/T]AAATCTATGAAAA GGTGTATCTGCTTGCAATTTAAGAAACAACACAAGTCA
WI-18350	48 T C ---	---	TCTTGACATGATCTGTGAAATAACGTGATTGTGGTTGAATTTCTGGAATAATTGAAGAATAAATTG ATTATTCAAG[G/C]GTGTCATTGGTTTATACATATCTCTCTCTCTCTTAATGCAAAAGCTATG
WI-18395	77 G C ---	---	TGCAGTGGCAAGACACTCTCTCGAGGAAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG GATAACATTGCCAGTATAACCATTAATTCAAACAGCAGCAGAAATTTGGAGGATAATTTGTT
WI-18398	62 G T ---	---	CTCGTTGGTATTCTCTCATCC[C/A]TTCTCTTTTCGCTCTTTCTAAATTAAGAAAGCAATGGAATT TTAAAGATCATCTAAGAAATAAGAACTTACATATGTAAACATTTAACTTATCAACTTGTACAAAGTC AATGAAAA
WI-18398	21 C A ---	---	AAGATGGGAAAGAGGAAATC[C/A]TTTCTTACTAGAGATTTTTCCTTTAATCCTTTTCAAAT TCAAAGGATCATCAAGGAGCAGGTGCAGAACTCTGGGGCCAGAGGCCCAAGTGCTA
WI-18409a	20 C A ---	---	AAAAGGAAAGAAAGGATGGAGTAAG JTTGGCTGATCTGGGTGATCAGGTGGACACTATTATCCAGAGGGGAAACACAGAGAGAGAGAGAGAGAGAG TTTATAGGTGGAGAGAGGA
WI-18442	62 C T ---	---	TTGATGTTAATACTGTCTCTGGAGATCGGCTAAAT[G/A]AAAGCATAGTTATTATTAGCTTTGG TATATTCTGCGACAGATTTAACAAGTAAGACATATATCAACCTCATATTTTCCAACCA
WI-18452	38 G A ---	---	ATATAAGCTGGAGACTGTGGAGGTGAGAGGCGAGTGGGACTAGCTGTTGAAAGAGAGAGATGTAGC AGTAGTAAAGATGAAAGACTGCAAGGATTCAACA[C/A]C]GGTTATGGCAATAGAGGTGAAAGAGAA AGGCCATATAA
WI-18489	102 A C ---	---	CTGGTGGGAGGAAACAAATTGTGGTATATTCATACAATGGAAACTCTTCAGAAATAAGAAAGGAA CAACCACTGAATCACACAACATGGACAAATCTCAATCATATTATGCTGATGGAGAGAAACCAATTCA TAAGAATACACAGTACAT
EST5b	93 A ---	---	

EST5	93 A	---	---	CTGGTGGGAGGAAACAAATTGTGGTATATTCATACTGGAACACTCTTCAGAAATAAGAAGGAA CAAACCACTGAATCACACAACATGGACAAATCTCAATCATATTATGCTGATGGAAGAAACCAATTCA TAAGAATACACAGTACAT
EST6	48 C	---	---	TTAGCTACTTTTCAGAAATTGAAGGAGAAATGCAATATGTGGACTGAACCGACTTTTCTAAAGCTCT GAACAAAGCTTTTCTTCTCTTTGCAACAAGACAAAGCAAGCCACATTTTGCAATTAGACAGAT
EST8	158 A	---	---	GGACAGGACCTCTATTCCCGCTGGTGACGAGCGGCTGATGGACTGAGGCCCCAGGGGATACTGGGOC CTCTTCTCAGGGCGCTCCAGGACCCAGAGCTGTCTCTGCTTTGAGTTTCCCTAGAGCTGTGCGGCCA GATAGCTGTTCTGAGTTGCAAGCAGGATGGAGATTGGACACTGTGTGCTTTTGGTGGGT
WI-18740c	104 GT	---	---	TCCTCAATTGTTGGGATGATGAGAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAACTCTCAATTAACCATCATGTATCCAGTAGTG[GT]ATAATTCAATTTTGATGGCTTCTATTTT TGGCCA
WI-18740b	96 CG	---	---	TCCTCAATTGTTGGGATGATGAGAGAAATGATTTGGGAAATTAAGTAACAACGACCTAGAAAAGT GAGAACAACTCTCAATTAACCATCATGTATC[GT]AGTAGTGGATAATTCATTTTGATGGCTTCTATTTT TGGCCA
WI-18985a	105 CT	---	---	CCAAAGTCTCCTGTTCGCTCATAAAGAGTTTGGGATGGGAGAGAAATCCAGACCATCTTGGGGCA GCCAGGCCCTTGCTTCATTTTACAGAGGTAGCACAA[CT]TGATTCCAACACAAAACCCCTTCCOC TTTTTAAATGATTTCTGTTCTAATGCCATAGATCAAGGCCCTCAGAAACCATTTGTGTGTTTCTCTT TGAAGCAATGACAAGCACITTTACTTTTACGGTGGTTTGTGTTTCTTAT
WI-18746	114 GA	---	---	GCCAGCAGCTGAAGTCTCTTTTCTCTCTCGGCTGGAAGAACATCAAGATACCTTTGCGTGGATCA AGCTTGTTGTAAGTGGCTTTTATATTACTTTTGTAAATATTCTT[GT]AJCCACATTTCTACTTCAAGCT TTGGAATGTTGTTACCG
WI-19112	212 GA	---	---	CCGTGTTACACACACACAATGGCAAGCATAGTCGCTGTTACGGCCAGGGGAATATGCCAAGG GACCCCTTAATGGAACACACAGATCAGTAGTGTCTATCTCATGACAACCAAGAAACCGACGACAAA TCTTTTGGGAGATTTTCTTCTAGTGCTTAGAAACATGGCTTTAAGAAACACGGTGATATCTTTGAG GGTGACAAGGC[GT]ATCTCTTCAACAGTTCCATACCAACTGCTTGTCTAG
WI-19092	232 AC	---	---	TGGTGGCTGGCTAGCTAGTTTCTACAGAACATAATTTGCCTCTATAGAAGGCTATTCTTAGATCATGT CTCAATGGAACACTCTTCTTCTTAGCCTTACTTGAATCTTGCTATAATAAGTAGAGCAACACAC ATTGAAAGCTTCTGATCAACGGTCTGAAATTTTCATCTTGAATGCTTTGTATTAAACTGAATTTTC TTTTAAGCTAACAAAGATCATAATTTTC[AT]ATGATTAGCCGTGTAAC
WI-19057i	175 GA	---	---	CCCATTATTATAGGCCAGTGATGTCTCAAGAGTAGAGGAGCGTCTACTGGTCTTCAACTCCTTCA GTCTTCTGACGGGGACTTTACCGTGACAGCGGAAGTGGTATTGTACGTCCAGGCACCGCAGCAGCTG TCTTCATGCAGGAACACACAGTGCCAGATCCCCACAGCTC[GT]ATCTCTTCACTTGTGTTTGGCCACA



WI-20103	168	C T ---			TGGGACTTCCAACCTCAGAGGATGTGGGATCCAGCTCAATGATACAGGATAAAGTGGGATGGGCT AGGATGGACAGGCTGTGGATATGGAGTCATGGGTCAAAGTCTTATCCAGATGGCTCCAGGTACAG TGGGCTTCCCTGGGCTGGAAGCTGGTCTCTCCCA[C/T]TTCATCTGCTCAAAGCTTCTTGAAGGAGC TGGTTGACTTCAACTTGCTAGAGCTAGCCTCATCTTTCAGTCAACTGGGA
WI-20441	111	G A ---			GCCTTACCCATTGTCACATATACATATGCACCACCTTTGCAGTGGCAACATATATATCCACACTA TAAACATACCACATTTATAATCTTGTAAGGACAAGAAATGGA[G/A]TTGAATAAGTACCCCCCAA CATATACAAGAAAGTTAGCATACTTACCCCGTTTTCTACTACATCAGAGGCAAAATAAGAAATCTTT TAAGAAATCTCAAGACTGGCTCATGGCAAAATGAATATGCTAAATTTGGGG
WI-19911b	116	A G ---			TGTTACAAAACCTAAGCCCATATACAAAATTAGGAACACATTTAGATGCCTCTTTTGAAGAACGT TTAGTCTTTTAACTGAGTTTAAAAAAAATAACAATGCAATTTTAA/GJACACTGTTTTTGA ACTTAAAGTGCAGCAATA
WI-20613c	165	A G ---			GTCCTCAAGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGAGGAGTTAGAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAGTTGGA[A/G]AAAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-20613b	156	A C ---			GTCCTCAAGGGGAGAAAACCTGGTCTTTTATGTACAAAGCACAGATGTAGGTACAGTATATAAACA GATACGTAGTACATCTGTAGTATTAAATGGCATGGGAGGAGGAGGAGTTAGAAAACATCTAAAC AGCTCCTTAGAAGGCCAATAATAAAGTTGGA[A/G]AAAGGGAGTTTCCACGCAGCCAGTGGTGAGC TGC
WI-19984	47	A G ---			CAGTAAAGAGTGATTCAAGTTGCAGTAATACACTGACAGGTAATA[A/G]TATAACATTAGAAAA GCAAAATTTCTTTAACTTAAGGACAGACTGAACCATCAGGTATGGTCTGAGATCAAGTAATACAGG TAGGCAAGAGTTTTTCCACACTGGAAAATGAAGGCAGTTTTTCCAATACTGTGAATTTACAAACAT TGGGGGAAGG
WI-20122	135	T C ---			GCCAGTTGGAATATGGCCTATACGAACCAAGAGTGTATACAAAATGGAAGTGGTCATCAGGCAATA ATTGTTTCCCTTGGAACCTGTCACCGACTGTCCATGCTCTGTGGGACTTACACATTCAAGTTTGACAG T/C]TGAAAAACCAACTGGAGCTGCTTTTCCAAGAAATGTTCTGTTGTCCTTCAAATAGGAATCCATG TTATTTCTTTCTTGCCCTTAAGCTCTTATATCTTTCAAAATGACCTAAGCTGA
WI-18846a	49	G A ---			GAGTGCCATACCTTCTCCAGGCTCTGCCCAAGAGCAGGAGGTGCTT[G/A]AAAGCTGGGAGCGT GGGCTCAGCAGGGCTGTCCCTCCATCCCGTAAGACCTCTTCCCTCCTCAGCAGGCCAAACATG GCCAGACTCCTT
WI-18959	123	G A ---			AGCAGTGGCCTTATTGCATCCCAACACCGCTCTTGACAGGCTGCCCTTGTGGCAGCAACGGC ACAGCTAATTCTACTCAGAGTGCTTTTAAAGTGAAAAATGGTCGAGAAAGAGGCCAC[C/G/A]GGAAGCGG TCCTGGGCGCTGGCAGTCGCGTGAGCGGATGGTCTGGCTGTTGAGATTCTCAAGGAGCGAGCAT GTCGTGGACACACAGACTATTTTAGATTCTTTTGCCCTTTTGCAACC





WI-19067d	202 T G ---	---	TATTGCTGCTTGTCACCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGCACATTCCCTGCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTCTTGGGCTCTAGGTCCTGGAGAAATGTTGTAGGGGTTTATTTTTTTTAAATAGTGTTCATAAAGAAAT/GIACATAGTATTCTTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19067c	153 G C ---	---	TATTGCTGCTTGTCACCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGCACATTCCCTGCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTCTTGGGCTCTAGGTCCTG/GC/JAGAAATGTTGTAGGGGTTTATTTTTTTTAAATAGTGTTCATAAAGAAATACATAGTATTCTTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19067b	151 T C ---	---	TATTGCTGCTTGTCACCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCCCTGGCTGTGCACATTCCCTGCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTCTTGGGCTCTAGGTCCT/GC/JGAGAAATGTTGTAGGGGTTTATTTTTTTTAAATAGTGTTCATAAAGAAATACATAGTATTCTTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19067a	57 C G ---	---	TATTGCTGCTTGTCACCTGACATTACGGCAGAGGCAAGGCTGCTGCAGCCTCC/GC/JCTGGCTGTGCACATTCCCTGCTGCTCCAGAGACTGCTCCGCCATCCACAGATGATGGATCTTCAGTGGGTTCTCTTGGGCTCTAGGTCCTGGAGAAATGTTGTAGGGGTTTATTTTTTTTAAATAGTGTTCATAAAGAAATACATAGTATTCTTCTCAAGACGTGGGGGAAATTATCTCATTATC
WI-19106	247 T C ---	---	TTAATCCAGCCCTACCTTGTTAGTTATTTAGGAGACAGTCTCAAGCACTAAAGTGCTAATTCGAATTTATGGGTATAGTGGCCAAATAGCACATCTCCACGTTAAAGACAGTGGATCATGAAAAGTGCTGTTTGTCTTTGAGAAAGAAATAATTGTTGAGCGCAGAGTAAATAAGGCTCCTTCATGTGGCGTATTGGGCCATAGCCTATAATTGGTTAGAACCTCCTATTTTAA/TCTJGG
WI-18944	147 A G ---	---	CAAGGCAAAATATCAGGAGCTTTTACACACCTACTAAAGTTATTATGTAGCTGAAACAAAATGCCAGAAAGATAATATTGATTCCTCACATCTTTAACTTAGTATTTACCTAGCATTTCAAACCCAAATGGCTAGAAC/JG/JTGTTTAAATTAATTTCACAATATAAAGTTCTACAGTTAATTATGTGCATATTAAACAATGGCCGTGTTCAATTCTTCTTCTTCTTAATAAATTAAAGTTTT
WI-18952	232 G A ---	---	CCCATCCCTGTGAAGGAGTAGGCCACTCTTTAAGTGAAGGATTGGATGTTGTTCAATACATAAAGTTCTCTGTAAATTACAACATAATTATTATGCCCTCTTCTCACAGTCAAAAGGAACTGGGTGTTGGTTTTTGTGCTTTTTAGATTTATTGTCCCATGTGGGATGAGTTTTTAAATGCCACAAGACATAATTAAATAATAAACCTTTGGGAAAGGTGTAA/G/AJACAGTAGCCCCCATCACAT
WI-18932d	177 C T ---	---	CACACCTCATGCTAGCCTCACGAAACTGGAATAAGCCTTCGAAAGAAATTTGCTCTGAAGCTTGTA TCTGATATCAGCACTGGATTGTAGAACTTTGTGCTGATTTTGACCTTGTATTCAAGTTAACTGTCCCTTGATTTGTTTAAATACCCCTGTACATATCTTTGAGTTCAA/C/TJCTTAGTACGTGTGGCTTGCTCACTTCGTGGCTGAGGTAAGAACGTGCTTGTGGGAAGACAAGTCTGTGGCTTG



WI-19042	193 A C ---		TTTGTGAGTTGGCTCTCGCAATGCCTCAGTAGCATCTCAGTGGTGTGTAAGTTTGGAGATAGATG GATAAGGGAATAATAGCCACAGAGGTGAACCTTTGTGCTTCAAGGACATTGGTGAGAGTCCAAACAG ACACAAATTTATAGTGCAGACAACTTCAGCAATTGTAAATATGTAAATAACTCTAACC[A/C]GGCTG TGTTAGATTGTATTAACTATCTTCTTGGACTTCTGAAGAGACCACCTCAAT
WI-18984	208 A C ---		ATTGGCCCTGTACAGTTTGCTTATTATAAATTCATTAAACACACTACAGGTGTTGAATGGTTAAAA TGTAAGCCCTCCAGTTTCATTTCAGTTATTCTGAGTGTGCAGACAGCTATTTGCGCACTGTATTAAAT GTAACCTTATTAAATGAATCAGAAAGCAGTAGACAGATGTTGGTGCAATACAAATATTGTGATGCATT TATCTT[A/C]ATAAAATGCTAAATGTCAATTTATCACTGCGCATGTTTGACT
WI-18851	90 T A ---		GCTTCAATTGGCGATTGATTCAGTGCACCAATGTAAACAGGGTTGGTAGTTGTTACTCATTTTGAAT ATACCTTTTCCCTATTGTATTCT[A/G]TAATATAGGATCCTGGAAATGAGACCTGGTGGAA
WI-18821b	76 T C ---		TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAACTGTCTAGGAGCCCTCTCTCGGAGGCC ACAGAGGCT[C/G]GGGGGTAGCCATTGTGCAGTCAATGCCCGGGGAAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-18821a	69 C T ---		TCAACTGCAGTGTGCTTCCCTCCCTATAGGGCTGGAACTGTCTAGGAGCCCTCTCTCGGAGGCC A/C[T]AGAGGCTGGGGTAGCCATTGTGCAGTCAATGCCCGGGGAAACTTGCCAACTTCGTGTCAG GTGCTGTGT
WI-19021a	20 C G ---		ACTCCTCTGCTGTCCAT[C/G]ACTGTCTCTTTGAACAGGAAAGTCACAGAGTTTAAAGAGAA GCAAAATTAACATCCTGAATCGGGAACAAAGGGTTTATCTAATAAGTGTCTCTTCCATCACGTTG CTACCTTACCCACACTTCCCTCTGATTGCGTGAGGACGTGTCATCTACTTACGTACGTGGCATAAC ACATCGTGTGAGCCCATGTATGCTGGGGTAGAGCAAGTAGCCCTCCCTGTG
WI-18908	70 G C ---		TGGAAATTCCTTCATCTGGAACCATCAGAAACACCCCTCACACTGGGACTTGCAAAAAGGGTCAGTA TGG[G/C]TTAGGGAAACATTCCATCCTTGAGTCAAAAATCTCAATTCCTCCTATCTTTGCCACCC TCATGCTGTGTGACT
WI-19037b	155 A G ---		CACGGTTCTCTGCATCGTTACCAGAGCGCTTCTGTCTAGCCACGCCCTGTATGACCCGCAATA TCCCCAAAGCTTTGGGTCTCAAGTCAATGCCGAATTTAGATGCTGGTCATTTCTGGAGAGGGTC CCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGOCAGGCACCTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19037a	47 C A ---		CACGGTTCTCTGCATCGTTACCAGAGCGCTTCTGTCTAGCCACGC[C/A]CCTGTATGACCCGCAA ATATCCCCAAAGCTTTGGGTCTCAAGTCAATGCCGAATTTAGATGCTGGTCATTTCTGGAGAGGG GTCCCTCCCTTACGAACACA[A/G]AAACCCAGCCACATGACTAGCACGCTGAGCTCTGCAGGGACCA GTGCCAGGCACCTGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAGGTGG
WI-19064	66 T C ---		TTGAGGAGGTGGGTGAAGTGTCTCTGGCAGGGATTGTGACACTGCATTGCTGGGCTGTGTTCTT C/CGGGCTCTCTGGACCTTGACCGTGGATACAGGCCATGTGOCATGTTGGTCTCTGGAGGG TGGGTGAATAAAGGC

WI-18972a	112 A G ---	---	AGCCTGTGGCTTATGTACCCACAGAGGGTCTGAGAACTGCTGGCTGGATGCCCGCTGCC CCCTCCTGGAAGCCTCTGCAGAGATGACTGGCTGGGGAAGCAGAGTCTGCTGGCCATGGAGCC TCATTGCAAGTTGTTCTTGAACACCTGAGGCCCTTCTGTGGCCACAGGCACTACGGCTTCTCTCC AGATGTGCTTTGCCTGAGCACAGACAGTCAGCATGGAATGCTCTTGGCCA
WI-19016b	184 C A ---	---	GTTTGCAAAACCAACATGTGCTCTTTTCAGTCATTCAGTGTTTTAAATATGACATGGTAGAGAGATAAG GTTATGGCAGGTAATTTTGTATGTATTAACGAAGTTCAAGATTAGAAATACATCTGTGTGTC CTGAAACCTTAGATACATAGCCGACTGTATACAGAGGTTCACTCAAC/AJCTCAACACTATTGAC TTTTGGGCTGGATAGTTCTCTGTGTGGGGTTTGTCTTGTGCACTGTAG
WI-19016a	161 C T ---	---	GTTTGCAAAACCAACATGTGCTCTTTTCAGTCATTCAGTGTTTTAAATATGACATGGTAGAGAGATAAG GTTATGGCAGGTAATTTTGTATGTATTAACGAAGTTCAAGATTAGAAATACATCTGTGTGTC CTGAAACCTTAGATACATAGCCGAG/AJCTGTATACAGAGGTTCACTCAACCTCAACACTATTGAC TTTTGGGCTGGATAGTTCTCTGTGTGGGGTTTGTCTTGTGCACTGTAG
WI-20096	21 T C ---	---	GGTTTTGGGGCATTTATTTCTC/GATAGAGACTGGCACAAAGCTTTGGGCTAAGGACACCCGCCCCCC ACCTCATCTAGAAACAATCTCTCGCCAGACTTG
WI-19591b	156 C A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAATATAAGTTAACTCCAAGCCATG AGTATAAGATTAAAGGCAGTTACTTTATTTTGAACAAGGAAGTGCCATAAGCACTCAGTGTGCCCC CTTAGGGTGGGAGCTCTTCC/C/AJCTACCACTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-19591a	45 T A ---	---	TGGGGCAATTTTAAACAAACAGGCAAAATATCACATATACCTGAAT/AJATAAGTTAACTCCAAGC CATGAGTATAAGATTAAAGGCAGTTACTTTATTTTGAACAAGGAAGTGCCATAAGCACTCAGTGTGT GCCCTTAGGGTGGGAGCTCTTCCCTACCACTCCCAACCCCAAGGCATCATTTTGGGAGAAAAA GTGCTTCTATCTGGCTAGCTGTGTATCTAGGGATTGCACCTTCTTACACGG
WI-20310	125 G A ---	---	TCCTCCAGCTGTCTATCCTTGTCTTGAGGGTTCTGTGTTACGGCCCTCCAGGCATGTTTCTTCAT TTAGGTAGGAACAAAGGCCAAAGAACATACAGCCAGCTCTCTAGAGGCTCCA/GAJTCAGAA CTGGACCTTTAACTACAAAGGAATCTTGGATGAATATTTTAGCGGGGCTTCAGGAGCAGGTAGC AGAGCCAAAGTGCACACTCAGGCCATCTTCTCCCAATGTCTCCCGGGG
WI-20860	224 G A ---	---	CTCTCCCTAAGGAGCCTTGGCCTTGCAGCCCATTCAGCAGGATGGAAGTCACAAGACAATGAGT GGAGCCTCATGCCCTCCATGAGGAAGCCCTTAGTATTGCTGACATCTGCCCTTTATCTGTCTCTCT CCCCAGTGTGTACACTTGGGCAAGCAGAGTGGTGGCAGACCCAGCCCTTGAGAGCTCTTGTAGACC GGAAAGGAAGGGCGGTCTAT/GA/GGTGATGGCTTCTGGCTCTCTGGCTT
WI-19359a	39 T C ---	---	GACGTGGACAAAGGAGGTTTAAATGAATACCTTTGTTC/GCATGTTCAAAAAGAGATTATTAAT ATTTTGTGACTGCATCTGTGAATGAAGACACTCAAAAGCCATGTTTCCAACTTAGGTTAATAATAA GGCTATTTGTCCACCCACTCTTGGGCATTGCTGCAATATCTGGGCTCAAGTGGAGGCCACGTG GGAACAAGGCCTCAGAAACAAGGACATGCAGCCTCCCTGAGCCAGTTCT



WI-19766b	93 A G ---	---	TGGCCTCAATGACTGGTACATTGGAGAAAGCTGTGCAGCAGCATCCTTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTCIAGIGACAAACAGAAAGGACACCAAGCCTGAAACCCCTCCGGACAACAGCAGAGTTACAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTCACCCCTTCACCCCTCCTCCTACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-19766a	31 G A ---	---	TGGCCTCAATGACTGGTACATTGGAGAAAGCTGATGCAGCAGCATCCTTTTCTGTGGTGGCAGGGCAGGAGATGAACCATAGGAGCCAAAGTCAGACAAACAGAAAGGACACCAAGCCTGAAACCCCTCCGGACAACAGCAGAGTTACAGCTGAGGGATGTCCCTGGAGGTTTCTGACCCATGAGAGGCCCCCTCACCCCTTCACCCCTCCTCCTACCAAGCTCTCCGGCAGTCATGGACTTAT
WI-20512d	126 C G ---	---	CTTCCTCTGTTGGCTTTGCATTTGTGCGATTTGGAAAAACCACTTGGAAAGAGGACTTTTCCTGCAA AACCTTAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGAIC/GJAAAGC TTAGAAAGGAACTGAAATTGCTTTTGAATATGGATTTAGGGCGGGCGTGGTGGCTCACGCCT TATTATCCAGGCACGTTGGGGAGGGCCAAACGGGGTGGGATCACTGA
WI-20512c	59 T G ---	---	CTTCCTCTGTTGGCTTTGCATTTGTGCGATTTGGAAAAACCACTTGGAAAGAGGACTTT/GJTCCTG CAAAACCTTAAGACTGGTTAAATTACAGGGCCTAGGAAGTCAGTGGAGCCCTTGACTGACAAAGC TTAGAAAGGAACTGAAATTGCTTTTGAATATGGATTTAGGGCGGGCGTGGTGGCTCACGCCT TATTATCCAGGCACGTTGGGGAGGGCCAAACGGGGTGGGATCACTGA
WI-19599	230 C G ---	---	GGGCTTAAATTCOCCTCTGTTGGGACTGGTCTCTCCAGTTTACAGCAAGGATCGCACCCCTTTTCC ATACCCCTTCTACATTGGAAAGAGCACACCTTGTATACAGAAATGGCTCCGTGAAGTCTTTTAAACG GACAAAGGTAAATCACAGCTAACAAACGTGATGTTGGCTCACACGTAAACCAACACCTCTTTTTCAGAACAGAGAGCGTTAAAGTAAAGGGAIC/GJTTCCAAGAGTAACACTGCTA
WI-20679	82 T C ---	---	TGTTTGAAATAAAATTTCCATGGTCTTAAATTGAAGTGTATGTTACTTTCTTTTGAATATCCTTTT TTCAATAAAATAATTCJTTCTAAACCACTCTATGTGTTCAACCTTCTGTTTAACTAAGATATGGGT TTTGGAAAGGCCACAAAGTCACCACTCCATGAAGTGGCGAATTGGTCTTTTGGAAAGCTCTC CAGGTGTTTCTCCAGAA
WI-19909a	29 T C ---	---	CCAGAAATAAGCCTGAATAATCTCTTTCT/CJTTAAATAATAATTTTCTTCTTCTTCTCCAA GTAAATCTTAAATGAACCTGTTCTAGTCTATTTTAACTAGGCAATTATAACACTACCTAGCGGG TTTTCTCTTTATACCTGTTCTGTACTGTGGAATCAACTAA
WI-20341	221 G C ---	---	TTGAGAGGCTGAGAGAGGCTGTTGAGACATTGTAATAAGTGCTTAGGGCATGAGACATTAGGAAG GCCACAAATTATGAGTAATGAATGTGGAGGCTGATGAGAAAGTACTGCTCCCATTTGTTTAGCAGGA GGCAGGAAAGTGATCTGGGGTCTCTGGCAGCAAAAGCGTGTGGTAAATATTTGGGTGACGTATGC ATCCCCCATGCATTGGTTTTCJATGTCTCCAGTGAGCTGTGGGCAAGTCT



WI-20113	60	T C ---			TTCTGGTACATGGTAAGTGCTCAGTATTACTGAGTGAATGAGCAAGACCTGAAATACTGTT/CJGGA AACAGTAAAAGCAAAATTACCAACAATTAGGAGGAATTATTTTCAGACATAGGATATTTAAACAT CACTCAATACTGGAGCATGATTCAGCAATAAATTCTATTCATAAACACAGGTAGATAAATGTCACA GCTTTAAATATAGTTAAGTACAGTTGATCCTCGTTATTCATGGATTCCGTTATT
WI-20895	107	G C ---			TGATGGCAAAGTACAAGGCTCTGAAAGAACAGAGTAACAAGAGCAGCGCAGTGCAGCGTGTGGC CACTTCCACACGAGCAACTTGACTTCATTAAAGGCAA/G/CJCTTTACTCTGTTACTTTTTCTC CCACATAGTTTAAACCAAATAGAAAGGCATTCTATTCTCACACTACTGCTCTCTAAGGTCCTAGGAA TATAACTGTACTATAGGCAACAGATGCA
WI-20721	72	T C ---			CCTGCAATCACAAAAGTGGAACCTAGTTGATATTTTGAATCATACTTGAATTAACCACTTCAGAAA TTCTAT/CJAAAACACTAGCAACTTCCTTTATCAGA
WI-19415c	161	A G ---			CTGGATTTTAATATTTCTGGCCTAATAACCAATGTAAATCAATAAAATTTGGTCAATATCTCCACCTC ATTTCTGCTAACATGTTTTCGAAGATTCCTTAAGTAAGTATTGACGACTGAGACTAGTCCGGCAA GTCAATGAGACCCCTTAGCTGATCTCAT/GJAGTCCACCTCATGAAGGAGATGATTCAACATCTCAA GCTAAGGTATAAAGTGTGGACATACAAAGGCTTACAAGTTTACACTTCCTG
WI-19348c	103	C T ---			GCTGCTCACTGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCTG GCGGTCGATGAAGAGACTGTTGGTCATGCGGTGA/CJTGCTCTCTCCAGGCTCATATGGATGTCTCT CGAGGTTGCACAGGGAACCTGCTCTGTTGTAGAAGCTTCTCC
WI-19348b	98	G A ---			GCTGCTCACTGTAGCCAGCCAGCTGCAGGATGGTGGGTAGCAAGTACGATGGGCCATGCACCTTCTG GCGGTCGATGAAGAGACTGTTGGTCATGGC/GJAGTGACGCTCTCTCCAGGCTCATATGGATGTCTCT CGAGGTTGCACAGGGAACCTGCTCTGTTGTAGAAGCTTCTCC
WI-19635	98	A T ---			ATTAGTTCGTGTTGGGCCACATTCAAGCCATCCACACAAGCTTCTGTAGGCCATTGTAAACACAATG TTAAAAGGTACAGTAAAATACAGTATTATJATCTTTATGTGTAGCACGGCTGTGAGGCTCATTT GTTGAATGAAGCATCCTTAGGCAGCAGCTGACTGCATGCAGATATGTGTCTGAAAGAACTTTGCTTT T
WI-19641a	46	A G ---			TCCAATTTTCAGAAACATGTTCCATGTTJATTGTGATAAGCACTAG/GJATTATAGTCTCATGTTT TTAATTTATGAATAACGTCTGATTCATTTGATTTTGTATTTACAGAAAGATGTCAGGGCTATCTCATTC AGTTATTAATAATGGATCAGAGTAGTAAAGTCAAGAATAAGTGCATAATGTGGTTTAAATTTTAAAA AATACTCAGAAATGAGGTAGTATTTTAAATTTTAAATTCATCCACCCACCTTG
WI-19642b	52	C A ---			ATATAGAGTACCATCCATGTTTCAAGCATGGCTGGACACATTATCCCCCT/CJAGGGTAAACCAG GACTATTGCATGAGCATTCCTTAAATAGGTATTTTGATGGACACAAAGTTTTCATGCTATTA
WI-19673b	180	C T ---			TCTGCCATGATCACATTGTGATGAAGAACATGATGGTCACTAGTAGGTAACCTTCTGTGTCATTGCCT TACTCTCAGTGAGGTGCTAGTGGATTTACCTACCCCTGCTTTTGATCACCACCTGTAAATCTAATAGT GAAAAGGCAATGATGTCTCAGTATCACTGTGAAAACATTTTTCJCTTGGACCAGCTGAAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCCACACGTCAAAAACACAGCCC

WI-19673a	35	G A ---	---	TCTGCCATGATCACATTGTGATGAAGAACATGATG[A]JTCAC TAGTAGTAACTTTCTGTGTCATTG CCTTACTCTCAGTGAGTGCTAGTGATTACCTACCCCTGCTTTTGATCACCACCTGTAAATCTAAT AGTGAAAGGCAATGATGCTCAGTATCAGTGTGAAACATTTTTCCCTTGACACAGCTGAAGAA TCTTGAGGAGCCTGAAGGCTTCAAGGTCACACGTCACAAAACACAGCCC
WI-19724	35	A G ---	---	TTTATTTGGGAAACAAAGGATTGTAATTTGGGTA[A]VJCTGAGTCACGGTGGCCCTGAGTAGTGTC CTAGAAAGCAACACGAGAGTTTGGTTTTCTCTT
WI-19307	196	T C ---	---	TCCTCCTCCCCAACTAGATGGTATTGATCAGTCTGCCACAAATGGTACCCCTTCAGCAAGAACTG CAAGCCCTTCTTGATTGCTTCATGAGAAATGGTGGCTTGGGATGGAGTGACATTCCTTGCTGT GGTGAAGTCAAGAAAGGAAACAGGCAATGTATTCATAGAGGCCCTTTAAGAGACCCG[T/C]TGG AAATGGGCCATGTCTAATTTGGTGTGAATAAACTAACCTCTTTGGCTG
WI-19269	85	A T ---	---	CTTCCCTCATCCCTCTTCCACACACCATCCCGGAACAAGTGCTCCAGGATTCCTGCCACTGGC CATTTGGAGTGTCC[A]TJTGGGTAGCAATGTGGAACCAACAGGCCCTTTGTGAGAAATGG AGGGGTTGAGGGAGTCCAGGAGGGCTTATTGAGGCCCTTGCCACTTGCTCATAGGGAGCTCG ATCTCCTCATCTGGACAGGTGAAGCGAATTCCTCCGGCGTAGGCA
WI-19946	122	C T ---	---	CAATGGACTGAATGAGTGCCTGGTGGGGGGGCACACACACCTTCAATACACGTCAAGGTG CTTCCAGTTTTAGAAACAGAAATCTGCATCTCAGCCTGAGACGACAGAGGTC/TJCTTCCCTG ACCCAGACGCACTCAGAGCCAGTCTGGTTTCAAACTGCATTAACCTGCCGCCAGAGATTAC CGTAGGCATCTTTAATAAACTAACTCCAGCAAAATGTGGGTACGGTTACTAA
WI-19956	141	G A ---	---	CACAGCATGGTGAATAGCATCAGATTGAATGAAAGTTTGTAAATGCAACCATAAATAATTATA ATAATATACATCAAGTAACTTTACAGCACACATTTTTAGGCCCAAGGTTTGATCTGTCTGGACCT CAATGT[G/A]CTCTCGGAGAGCAGCCACGTTAGCAGCAGATACCTACAGCTTGTCTACTCAA GTGATGGCCAACAGAGCTTCTGAACTCCTCTGGGGAGGTAGCTGACAAG
WI-19076	40	G A ---	---	TTGGTTGGATACTTGCTGAAAAAAGCAGTTTAA[TG/A]GTATTCAAAATACCTTTTAAAAA GTATTCTAGCACAAGATTTTCTGTAACTAGATTATGTTGTAACTTTTTTCTAAATCTTGTAGGAG TGTCGGTTGTTAAGAACTAGAGCTTATTCCTATTCCAAATCTATCTTGGCTCCTGAAAACTGCAGA AAGGCACTTGAAAGCTGTTCTTTAAGATATGGGATTTCTTTTATTCTT
WI-20218	26	T C ---	---	CCACACACTCTGGTTTTATAAGCTA[T/C]JAGGACAGAGAGATGGAACTGAAAAACAGGGTAG AAAATAACATAAATTGGAGGGGACAGTGGGATGCAGAAAGAAATGACACAGCCACATGTGCCCCA GTCAAATACTTTAGTCCCTGCAGCAGAAAGATGCCAAAGTCTCTATACTGGCTGGGGATCCTGCC ATGGATGCAGGAGAAAA
WI-20295g	154	T G ---	---	CAACCTTTTGACAAGGGGACGTGAATTTCTGATGAAGTTATCTTACCAAGTTTAAATTCATAATTG GGAATTCCTCTTTTAAATATCTCCAGGCTTGATTGGGAGGGGCTGGCTCTACCCCTTCTTCTTCCA TCCAGTCTATTGCCAGAT[G/C]CCAGAGAAAGCGGGAAGCCAGCTCTCCAGCATAGCCACTGTGG GTCGGCTTCACTTCTGTGCACTCCTCATGCTGGGACTTGCTTCTTGGGG

WI-20361a	192	G A ---	---	CTGGAGTGTGACCTAAGTGACATTTTATGCGCAATACAGTAATCTCCAAGCTTTTAAATGGCTTATGCAAGATGACAGAAATATGTGAATCTGATTGTCCAGAGTTACACTCTGCACTCCAAAGCTACAACAGTCCACAGCTGAGAGGTTCCCTATACTTCTACTACTGTGACAAATTTAGC[G/A]ATCCTTC AATGGGAAATTCCTAACTACACGAGACAATGGGTCTACAGTAGGCCCG
WI-20572	75	A G ---	---	GAGCCAAACCCAAACAAATAAAGACAGAACTCTTTTGTAACTAAGTCATACCTACTTTCTTCTTCAGAAATTAAGTCAATAAACATCATCTTTTACAACATGGAGAGCGAGTAGGCCATAATTGTTCA AATTCATCTTTCTCAAAATTTAAATTTGTTTAAATCCCAAGGTGCCTATTGAATTCCTTCAAAATA AACTGCCTATCAGGTATCATACCTGCAATGCTTCTAATATCTCTTGATTAT
WI-20588	133	G A ---	---	CATGACAAAGACAAAGATCAAGGAGTAACATAAATTATAAGTTGAATAAATAGTATACAGCAATC TTCACCTTTTAAAGAAATGTGAGATCCTTTGTTGTTTTTATTTCTTAAGTACAAATGCTAAACI G[A]GAGCCGAGCTCTTCCGATTCCAGG
WI-20593	79	A G ---	---	TGACCTCATCTGGGTTCTGGTTAGAACACAGCCACTAGAACAACTCCAGTCTTTTTCAGTCTGTTG CTGTACTTCAG[A/G]TTTAAATCTGGGAATGAGCATGCAGCAATGCTCCACCAGATGAGGAAGAAA AGCTGTTAAAGGAACCTCAGGATGTTGTTAGGAAGGGGAGTGGATGCCAGGCCCTTCAACAGACTAT CCAGAAGCCATTCCATGGGTATTTGGTCTGCATACTGTGAGACACTGAGCT
WI-19765	57	T C ---	---	TTCTTTGCCAAGCCTGTTCTCAAGTTATTCAGAACTGGGTGTATACCTTGCTCCTCAT/CJATGTATCT TGTCCCTGCTGCTTTTAGGTTAGCAAGGTGTATGAATACTTTTAAAGTTTGTGTTCTTTTCCCTCGT GGATCAGTGAATACTGATCTATTCTCTGGCTAGGTGCAATTTACAAAATGGCCATGGAACCTGAGC AAAAGGCCACGTGGGATAAATCACTCACCATCGACGCCACAGTATT
WI-19066i	239	A G ---	---	TGACAAGGGAGAGAGGGAATTTCTACTCATTTGCAAGGAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACCTGG CATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTTCTCCATATTCGGATGCTCAATTACAGT ACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACT[A/G]GTTTCTTTTA
WI-19066g	184	C T ---	---	TGACAAGGGAGAGAGGGAATTTCTACTCATTTGCAAGGAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACCTGG CATATGTTCTTGCGTTGGTCAACCTGTAGCTGAATTAATCTTCTCCATATTC[C/T]GGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA
WI-19066f	148	T C ---	---	TGACAAGGGAGAGAGGGAATTTCTACTCATTTGCAAGGAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAACCTGG CATATGTTCTTGCGT/C]TGGTCAACCTGTAGCTGAATTAATCTTCTCCATATTCGGATGCTCAATTAC AGTACCATTCGAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTTCTTTTA



WI-19066e	147	GC	---			TGACAAGGAGAGAGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGAACTGG CATATGTTCTTGCG/CJTGGTCAACCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTIA
WI-19066c	100	GA	---			TGACAAGGAGAGAGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATC[G/A]TCTTAGCCAGTCCAATCTCTACGAGGAAC TGCCATATGTTCTTGCGTTGGTCAACCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTIA
WI-19066b	87	CT	---			TGACAAGGAGAGAGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGCCATATGTTCTTGCGTTGGTCAACCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTIA
WI-19066a	72	CT	---			TGACAAGGAGAGAGGAAATTCTACTCATTGCAAGGAAATCCTCACTTAAGCTTCAGTGAGCCAC AAGCACTTAAACCCATGAACCTTCAGCTGATCGTCTTAGCCAGTCCAATCTCTACGAGGAAC TGCCATATGTTCTTGCGTTGGTCAACCCTGTAGCTGAATTACTTCTCCATATTCGGGATGCTCAATTAC AGTACCATTGCAGGCAAACTTTTCTTAAACGCCCTTCACTAGTTCTTTTIA
WI-20660	105	GC	---			TTTACAGCGAGTTTTCCTGCTCAATAAGTATGAATCTAAATAGATTAGGGTGAAAGAAATGTG TGCTAAATAAATCTCCCTTTTGAATGTATATTGT[G/C]TTAATAAGGGAAGCATTAAATATTA CAGACATAATTTACAAGGTTCTGAACATGAGTGATTCCTACTGTTTCTGTACAAGATAGAACAAA AAGCTATCCACCCGCCCCAAAATACTGTTTAAACAACACTATGTTTAAAGA CTGCTGCCAGCTTCTCTTGCCCTGCTCCAGATGGGGTCTCTGCGAGCTCCCTCAGTCTTCC TCCACCCGCCCTCTCTTCCAGCCCTGCTGCTGATGCTGCACTTGGTTC/TJTTCCGCTCCATCGCC TTGAAAGCTCTGAA
WI-18768	120	CT	---			TTCCCCAGGGTTCTGTATTGCAGCTAAGGTCAAATGTJAGTATTTAACTTCTAGTTGCTCTTGTG GTCTTCTTCCAATGATGCTTACTACAGAAAGCAATCAGACACAAATTAGAGAAGCCTTTTCCATAAA GTGTAATTTTAAATGGCTGCAAAACCGGCAACCTGTAACTGCCCTTTTAAATGGCATGACAAGGTGTGC AGTGGCCCCATCCAGCAATGTGTGTCTCTATCTTGCATCTACCTGCTCC
WI-18790	49	AT	---			GAAAGCCAGAGATTAGCCCCGCAATTCGGCATCTGTCAACCAGGACAGAAJATJGCATGGACAAGGGA TGAGCTTTACAAAGATGATGCACCTTTGGAGATCAGAAATTCATATTTAAGCAAAGTGATACAACA CAGTGATTGGGAATGCT
WI-18987	35	GA	---			AGGAGGCTGTTCCAGGAGTCTGCCAGCAGCTG[G/A]GTGGCCAAAGCCAGACACTCACCCACCTT CCCCAGTGGCCCCGTGGATCTGTGGTCTAGGCTGGACACAGGATTCAGAAAGACACAGGCTGCACA GAAAGAGCCAGATGGACCTGAGTGTGCTGCTCACAGCCCCCTACACTCAAGGCTGAGAGGCTCAGGAA AGTCA

WI-18919	26 C T ---				TGGATGAAACCACAGGGATTCCGGA/C/TGCCAGACCCCATTTTATACTTCACCTTTCTCTACAGTG TTGTTTGTGTTGTTGTTTATTTTATACCTTGGCCATACCACAGAGCTAGATTGCCCAGGTCT GGGCTGAATAAA
WI-18741c	64 G A ---				CTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTC[G/A] CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741b	38 G C ---				CTTCTGGTCAAGGCTTTGGACATCTCTTCAGTCATCA/G/CJACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-18741a	23 T G ---				CTTCTGGTCAAGGCTTTGGACAT/G/GJCTCTTCAGTCATCAGACAGAGTATCTCTGCTCTAGACCTCG CTGGAGTTCAAGCTTGAATTATTATATGCAAGTTAATTTTACAAGCCTGGATGAGGCTACTGA
WI-19179a	170 G A ---				TCAGAAAGCAGACATGGCATCTGTTCCCTGCTTGGTGTGTACCTTTCAGAGACCTGAATT TTAGAAATTGCCAGTCTGCCAGAGTGAGTGAGTAACTCTCTCTTCAGGTAAGATAGGCTATCTC AACACTGCTGAGTGATTCAAAACATATCAACCA/G/AJTAGCATTAAACCATTTTATTTCTGTCCTT AGTGCTGAAGATGCTCACCAGTTTCTGTGTACAGTAAGGCAGCATGCT
WI-19212	46 T A ---				CCAAGTTGCATCCATGTTGATTTTCTGATGAGACTAGAGTGACAGT/AJGTTTCAGAACCCAAATGII CCTCAGGTAGTTTGGAGCATCTCTATGAGATGGGATTATGCAGATGGCCTATGGAAATGCAGCTGC ATAATTAAACACATTATCAAGTCTCTTACAA/TTATTTCCGACGATGTCAGCTAAGTAGACCCCA ATGGGAGAGAAATGCCTGCTTCTTCCCTCTTTCTGCACTGCCATAT
WI-19183	210 G C ---				CTGTTGAAGGCTTCTCAGGCAAACTCCAGCTTAAAGCCCTAGACAGGTAAAGCACACATTGGATG GCAGCATGGGTTTCTCCCATTTTATGGGCATGAAATATGTGTTTGAATAAGGAACAAGCATTATT CCTTTGCCAACAGCCTCACTTAAGAGGCTTTTGTGCTGAGTCAAGCAACACTTGCTGCTCTGCC CTTGGAG[G/C]TGCAATTGACCTGCTCTCACTGGTAAGGTGACTTGGTGGC
WI-20014b	214 T C ---				TTGAAATCCAGTCTCCTGGCCCCCAGGAGGCTGTGTACCATAGATGTCTCTCTACTGGGGTC GTTCTGGCTTTTGTAGAAACTTGGTCTGAGATGTTCTCCCTGTCCATTACCATTCGATGTTCTTT TGTTACAGAGCAATGTTCTTGTATTCTGAAACTGGAACTGAACCAAGTTTGCCTTCTCCTAGTCACC AAGCATACTT/CJTCCTGGCTCCCCAAGTACTTAAATGTTCTCATCTGT
WI-19041	198 T C ---				GTCTCCCAGAGTGCTTCTGCACCCAGCCCTGTCTGCTGTAAAGGGATACAGAGAGCTCCCCG TCTCTGCATCCCTTCCAGGGGGTGCCCTTAGTTTGGACATGCTGGTAGCAGGACTCCAGGGCGTG CACGGTGAGCAGATGAGGCCCCAAGCTCATCACACAGGGGCCATCCTTCTCAATACAGCCJ/CJG CCCTTGCAGTCCCTATTCAAAATAAAATTAGTGTCTGCTTGCCTGTCTGT
WI-19135	20 G A ---				CAGTTACCTGCTTTCCTC[G/A]AAAGTGTCAATTTGTAAATTTAGTATTAACCTGTAAAGT GTCTGTAGGTACGTTTATATTATATAAGGACAGACCAAAATCAACCTATCAAGCTTCAAAACT TTGGGAAAGGGTGGATTAAAGTACAAGCACATTTGGCTTACAGTAAATGAAGTATTTTATTAACT GCTTTGCCCATATAAAATGCTGATATTACTGGAAACCTAGCCAGCTTCAC







WI-19134c	263	CT ---	---	CTCCTGTTGTAACCTGACAGGGTGACACAGCCCTTTTCACACTCTGTCTCTCTATCTTCTGCGGTAGA TGCCCTGGTGTAGGGCTAGTACTGATGATGCTTCCATCCAGCAAGGGGTGAGCCAGGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGACGGTGGCTAGAGCCAGCTGCACATCTCTTTTCAGAGCAC TTTCATCCACTTGCTCTCTCTACCTCGCACCTGGGTGGGAAAGGG
WI-19134a	162	TC ---	---	CTCCTGTTGTAACCTGACAGGGTGACACAGCCCTTTTCACACTCTGTCTCTCTATCTTCTGCGGTAGA TGCCCTGGTGTAGGGCTAGTACTGATGATGCTTCCATCCAGCAAGGGGTGAGCCAGGGGTCTCAG GCCCTTCAGAGCCAGGGCTAGAGGATGACGGTGGCTAGAGCCAGCTGCACATCTCTTTTCAGAGCAC CACTTCATCCACTTGCTCTCTCTACCTCGCACCTGGGTGGGAA
WI-19224	112	CT ---	---	GGTTTACCAGTCTTTCCAGGGAACCTCGATGAAGTGTCCAAACAAATGAGCGAGTGAACCAAGA AGAGGATGACATTAGATCCAGGAGATACAAACAGAGAGATAATCTCTTCAGGATGCTGTGAAGA AAGATCCCTGGATCCAGGATGATTATAGGACAAGTTGTTTCATAATCCAGCAGGCCAGAGACTTCC AGGGAACCTCATTCAGGAGGTGAAATGATGGATGACTCTCTCCAAAGATGAAAA
WI-19201	179	TC ---	---	GCAGTCTTAAGGACCACCTGGCCATTAGCTCTTGCTTTGATGGCATCTCTTTCCACCTTGCTCTC CTTGCTCTCTGTTAGTGTGGCAGGTATGACACTCATCTCAGTGGAACACAGCCCTCACACTGCC CTTCCGCCCCACACTTTGCCCTGCAGGTGCACCGAAAGGACITCTJGGGGGATAAAATTCAAAAA GTGTGATGTGCTGCTCAGAAAGTCAAGCTCCTCATGTCTGCTTGGCTCAA
WI-19034	45	TC ---	---	GAAATGGCTCCACTCAGAGCTACCCCGGTGATGAGGATAGGGGAAT/CJACTTCTATTACATTAAAG GCAACAGCAGTTAGTAAAGGTTTACAGTGTCTGCTGTTTGAAGTGCAATATAATTTTGTG CTAGCCCATGATCAATCGACTTCTATTGTTGATATACACTTCAGCATTTAAGTTCTGTGCAATTGAC ATTGCTACTTATAAACTTAGTCCCTAAGTCTTCTGCTGTGCTATATA
WI-19102	25	CG ---	---	TGTTCTGAGTCACGCTGAGGAGAGIC/GICTTCACTCAGGAGTTCACTGATGATCATGAGTTCA TGCGACGTATATTTTCTTTGGAAACAGAAATGAAGCAGAGGAACTCTTAATACTTAAATCGTTCT TGATTAGTATCGTGAGTTTGAAAGTCTAGAACTCTGTAAAGTTTGAACCTCAAGGGAGAGGTAT AGTGAATGAGTGTGAGCATCGGGCTTTCAGTCCCATAGAACAGAAATGGG
WI-18548b	65	AG ---	---	AAAGGAGGGAGAATCTTTTACATAAATGCCCTTGATCATCTCTCAGTCCCTCACTGGGGAAJA GJAAAAGCATCTNTCAAGTCTTGTCCAACTTTGGCTGC
WI-18548a	62	GA ---	---	AAAGGAGGGAGAATCTTTTACATAAATGCCCTTGATCATCTCTCAGTCCCTCACTGGGGGJAJA AAAAAAGCATCTNTCAAGTCTTGTCCAACTTTGGCTGC
WI-18700	97	TC ---	---	GGCAGCAGCTTTTAAATTTGAACACTTTCTTCTTGAGGACACACCTTCAGTACAGTTAACAAATGGT TACACCTGAAATCTGCTGAGAGCAGAGCTT/CJAGATCCACAATTGCAAGGCCACTGCTGGCTCA CTTCTCACA
WI-18501	121	CT ---	---	CAGAGGGAAAGTTTATTGAGTCAGCCACAGAGGAACAGAGAAACAGACAGAGGAGTTCTGTGT GCATGGAGGAAATCAGGGCGCCGNACAGCTGAACCTGCGCAGGACAGAGGGGCGCTJGGACAGCA GCGCATGCCACAAACATTCA

WI-18017	87 C A ---			ACAAAGAAATGGAAATAGGTTGGCGAAACTTATCTGCATGTACAAAGTAATCCCGTAGATAA GGAGAGGCAACCCNGGAACA/C/AJACTGCTGGATAAATGTTTCAATTAATTATATCTCTTTGTCAT CAGAGCTGGTGGAAATCAT
WI-18148b	101 A G ---			TTATTGCGTTCCCTTCGATAACCTCTCTTTGGGACTATGAGATCATCACCAGATGTGAAACGAAAGCA GTGATTTTCAGAAACCNCTGATTCTGAATATCCCA/GITGGCGGCATATGCAAGGAAGATGA
WI-18254	64 T C ---			TATACGGATCATGTATTGTGTGACCACCAGTACCACAGTCAATTTGTAGAGCAGTTAATCAGT/C JGCCAAAATCCCTCTTGCTTCTGTGTAGTCAGTCTCTTCCCAACCCAGGNACTTGGCAACCTGTTT TCCGTTCTAGACATTT
WI-18265b	117 C A ---			CAATGGGTGGACTGAGTGATAAAACGCATATTGAGAACAGAGCGCCTTCTGGCCNCTCTGCGTCC AAGGCTGTAAAGGTCTCAGGATTGCTGCTAAGTGAGCCATGAACCTGGCTG/C/AJGTTTTCAACCTTTC CTTGGGTGTTTCTTCAG
WI-18295	40 C T ---			ACCACACATTTGTTGAGAGCCTATTGTGGAGAACAAACAG/C/TJTTGGGAAGTAAAGGTTGATTACT TCCTCTCCAAGGATGATATGTTTAATGAATCCCTTNCCTTAGCTTCATTCATAATGCCAAA
WI-18459b	64 T C ---			GGCAAGAGACAGAGATTAAATTGAATAAACTCCAGGCTGTGACACGGGTGGGAGACACAAAT/ CJGAGTAATTAAACAACATAATTTTANATGACAGTGCAATTAATTACGTCCTGGGTAAGCCAGAG GGGAGGAGGGGCTTTTCA
WI-22585	56 A G ---			TTTATTTTAAATTTGCATCCTGAGATAATAAAATTTTATCTGACAAGTGAACAATG/A/GJGAGAAGC AGCAGTGAAGTTTCGGAGAGGCGAGGTATCCTTTCATTTTGGCACAGCTGTATATAGATTGA
WI-21155	36 A G ---			GGGCTGTGGAGTAACAGAACTTGATGGAAAATTTGGC/A/GJCTGTGTAGAATGATTCTAAAGCTTTC AGACAAATGGCAGA
STS-F02766b	88 G A ---			GCCTTTGCTCTTTGCTGCTCAGAGGCTCAGATGGATACGACAGCACTTCTTTTGAACCTTTTAT TTTCTGGCAGGAAGAAG/AJGGATCCAGCAGTGAGATCAGGAGGTTCTGTGTGTCACAGACAG GGAACAGGC
WI-19888a	98 C T ---			GGCAGATTCAACCCATAACAGAGAAATAACTCCTTATTGGAAACAAGGTTTTATTGATATGATG AAAATATTTGGAACTAGAAAGTAGCAGTGA/C/TJTGACAACGTTGTAAAGATATTAAATGCCACT GAACTGTTCATTTAAATGGTAATTTTCATGTATGTATTTTACCTCAATTAAGAATGGAACATGT CTTATAATTGTAAATTACATGAGANCATATTATGTTGGAAGTGAACACAAG
WI-21485	82 C T ---			TGAGACCATCCTCCTCAACAAAGAAATCAGTCAGTTCAGCACCTAATTTCCACACTGAAAGTCTACG CAATTTTCATGCAGA/C/TJTGTCACACAGTACAGTGCACAAATCCAGAGGGCAACACATTGTAATT CATATCATCCGTTTCCAAA
WI-20601a	125 T C ---			TCAGAAATTGCTTTCCTGCTCCCAACCAAAAGAAATTAATGAATGCNCTTACAATTGAGATGACTT GAAGTTAAAGAAAGGTACCTTCTGAGGTTGTCATGACAGGATTAGTCTTCTGTTT/CJCTTGGT GCAAGTTGAACCAAGTATTATGTACCATTTGTCATCAGAGCATCTGTTTCCCTGTGATGCCACTAG



WI- 20561b	94 T C ---	---	CGTTGCTTATTAAAGATGGCTGTTTATAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTATTG TACTTCAGATGAAAAATCCTTACATGTC[C]GGAATCAATGTCTTTTAAATTTACAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20561a	25 A G ---	---	CGTTGCTTATTAAAGATGGCTGTTT[A/G]TAAGTATAAAGCAGTTTGAGCAACACTGATTGTGCATTAA TTGTACTTCAGATGAAAAATCCTTACATGTGGAATCAATGTCTTTTAAATTTACAGATAAAGAATTT NCATTTGAGGAGACATACAATTGTAA
WI- 20116e	69 T A ---	---	GCTTTCATTTTCTGTCAACCCCTGTCCACAGTTATGTTGGCCTTCAATATATGCGTTAGAACAT A[T/A]ATAAATCTATATATATTTATACACACAACACACATTCTACCAGCAGTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCTCTCCCATGCCACTTAAATGNGCAGAGTTTGGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116c	59 T A ---	---	GCTTTCATTTTCTGTCAACCCCTGTCCACAGTTATGTTGGCCTTCAATATATGCGTTAGA CATATATAAATCTATATATATTTATACACACAACACACATTCTACCAGCAGTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCTCTCCCATGCCACTTAAATGNGCAGAGTTTGGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20116a	22 C G ---	---	GCTTTCATTTTCTGTCAACCCCTGTCCACAGTTATGTTGGCCTTCAATATATGCGTTAGA CATATATAAATCTATATATATTTATACACACAACACACATTCTACCAGCAGTGTGAAGACACAGA CTAGGCTTTACTAGGCTTGGGCTCTCCCATGCCACTTAAATGNGCAGAGTTTGGCTCTATGCAA GAATTTCAACAGAGTTGGTCTGGCCATCAGTCTGCAATTTCCCGAGATAA
WI- 20466b	133 G A ---	---	AAAGATTTCAGTCCTGGGACACAGTTTGGAAAACACTATTTATAAGTTGCACATATTACAACACAG NTCCCAAATGGTGAACTGGTATTCTAAGATGAAAGCTTAATGAACATAATGAAGTGAATAAACGC G/AJTGTAACATAATGTTTAAAGTTAAGAGCTTGCTCAAGTCAGTACAGCTCTTAAGATAATAAAT ACAGTAACACTACTTTTATTCTTGTCTCTTTATCCCTTTTCAGGTTTCGATT
WI-21444	39 A G ---	---	CTGGGCAGCAAGTAACCATTTTAAAGAAATACTCTCAAC[A/G]AGTTCTTTTATTATGGGTATTTCA GTTGTTAAACAAAGTTAAATACTTATTGGAACTAATCTTTGTATTTTATTCGAGGAAGAAGATCT ATAAGATTGACTTACTCATTGTTGACTGGTTTTTTGAAGCCTTACTGGGG
WI- 21034b	148 T C ---	---	AGAATGGACAATGATGCAGATGATTGTGAGCATTTTGATGAGAAAGTGTGATTAGAAGGATACAG CATAAATTTAATTGTAAACATGCTTATCTAGCTAACCTAATCTGTTTCTGTAGAAATTACTGGTCATGG GAGATTGGATAGA[T/C]GCTAACCTATCTCAATTTTAAGTAATGTGAGCAA
WI- 22091c	205 G A ---	---	GGCGTGTAATTTGATGCAATGTCCAAACAGTCAAGCTATCATTTGAATCCAAATATTTCCAGTAGAG ACATGCAGAGCAATGTCAATGTAAACATACAAGCATATTACCTCCCCCTTAAGTGACTCATATTTTC ATTACTTGTGTGTAGCTTTTAAAGGTTTAAATGTGTAGCATTAAGTGGTATTTACTTGAGGGCA ACA[G/A]AATTACGGCTTAAACAACACACTAATCATGAGGCTCAGGGATTG



WI- 21805a	45 A T ---	---	CAACTGCTCTGAGGCTCTTCACTAGCTGATTATAATCCTATATTATJAAAAAAATCTATAGTCTG CAGTCTTTTGACATACTCTCAAGGGTGATATGTGGTGGAATGCAGACTCCATCAATATGTGTGGTT TTGTTTGCTTTTGTAGCTTAACTGCTGTTAGNAATCCAGAGGAATATGATTGAGGCCAGAGTTA CATTGGTTCATAAAATTCGAACAGTTGAAGGCTGTTTTGTTAATTGCTG
WI- 21778b	155 T C ---	---	AAAAATCCATAATTATTGAACCCCAAGTTACAGAGAAAGTTCGTAACTTTTATTGAATTATTGAC TCTGCCCGGTGTCGTTCGTCTTCACTCCAGTCTGTCAATGCCCTGTGTAGGTGGGGTCCCCAG GTCTGGGCTTCTGAGGTCTCTGCTAGAAAGGAGGGCAGGTGGT
WI-20907	241 A C ---	---	TGAGTCAGTGGTCAGATGGGCGAGTTGCGCTCAGCTGCAGTCCCTGACTCCGGAAACACTGTGCCCT CAAATGATCTAGAGCTCATCTTGGCGGTACATGAGGGCGAGTTGTTTCTAGTACCCATTTAGCCG ATGGCTCTTCAAGCCCAATTCACACTGGGAAACACACCCCTCACAAGATGCCTATCCATTGAGTTG ATACAGGTTTTAGTAGCTAGAACTAAAAACATTTTTA/NCJAATTATCTA
WI- 21449b	222 C T ---	---	AACAGCAGCTCACTTCCAAATGCAAAATAAATTACAAATTTTAGAATAAAATTATAATGTTTA TAATGCGGGTCAGAAANTTGAAGGTACAACAGAAATCAATCACGCAGCACTGGAGCGGCTGGAG AAGCCAAAGCCCACTGGTCAGGGGTCCAAAGCTGACAAGAGTCCCAACCTGAGAGGTCTCCACACCC AAATCATACCCCTCAGCTTCCCA/CJTJGACAGAGCCAGTGTCTCTGGGTTAG
WI- 21558a	157 G A ---	---	GCTTACAAGGAAGCCTGTGGACAGGCGAGNTGGGTGGAACCGACTCCAGCTGGAAAACTGCCCTC CCATCCCCCTTAGCGCTTCTTGGCTTCCGGCTGATTTCTTCGACAGCAGTTCTGGCCAGGGCAAGG AGCTGTGTGGGGGCGAGTATG/AGCCAGGAGTCCCTTCCACAGATGAGGCCTAGGGCTGCAA AAGGCCCCGTGAAGAGAGATGTGGTCAAGGCTTTATGGGCTCTCCACC
WI- 22187b	178 G A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGCTGAGCAGCTCATGNGACCA GTCCTGGCCCTGACCAATGGGTGATTACATTTAAACCAACCAAAACAATAACCAAGA ACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTG/G/AAATTTTCATGAAAATTTCC CCTAAACCATAACAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI- 22187a	110 C A ---	---	TTTGCTGTGGAATCCATGAGAGCCGGAAGCATCGTTGGGCGCTGAGCAGCTCATGNGACCA GTCCTGGCCCTGACCAATGGGTGATTACATTTAAACCAAA/C/A/CAAAACAACAATAACCA AGAACAGATCACTTGCCATGGACATCAGTAATCTATTGGTAATGGTGGAATTTTCATGAAAATTTCC CCTAAACCATAACAAAACTGTCTCTCTTACCCCAAAAGTGTGGAGGAAAG
WI- 21609b	146 G A ---	---	TCATGAATATGCAGCCTCCATAATCTTCTCTCTTGTAAACAACGTGCAGTCCGTTCAAGCTGTAAA AACAGCCCAACCCCAAGACATCACAAGAGGCAAGAGCAGTGGCAGTGAGAGGGAGCCTGTAAAG GATGTTTCAAAG/G/AGGGTCCCGGCTATGTGGCCACTGGATGTAGGCAGTGAGTCCAGGCG TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG







WI-21609a	42 C T ---			TCATGAATATGCAGCCTCCATAATCTTCTCCCTTGTAAACAACGTTGTGCAGTCCGTTCAACAAGCTGTAAACAAGCCCAACCCAAAGACATCACAAAGAGGCAAGAGCAGTGGCAGTGAGAAAGGAGCCTGTAAAGGATGTTTCAAAGGAGGTCCTGGCTATGTGGCCACTGGATGTAGGCAGTGAGCTGAGTCCAGGC
WI-22512a	104 T G ---			TTTCGGTCTGGGAAGTGGCAGAGGCTGAGACANTGGCCAAAGAGGAGTTGGAG ACATTCCGAGCCAGTTTTTTCATATTGCTCCACTGCCCTAAATCCCTTGGTGCCCTCCCTAGGGCTTCA GGTAAGCCCTGACATCATGTGCTTTTGTGATCTGTGTGACCTCACCCATGTCTCCACCTNAGTTCC CACATTTCCCCACGCTAAGGCGAGGCTACACTTGACTGCA
WI-21028b	139 A G ---			ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGATTGATTGAGCAATCTAGGGGATATGTGACAGGGG TTTCAGTGCACCTGGTACAGAACACACAGGAGTTTTCACAATTTTTTATACAATGCTTGGGAAT CTACGG
WI-21028a	121 A C ---			ATCGGCAAGCTACAGCCTTAAATCTGAGCTCCTCAAGTGCACAATTTCTGTCCCTTTTAAGGGCTCA CAACACTAAAGATTTACATGAAGGGTCTGATTGATTGAGCAATCTAGGGGATATGTGACAG GGTTTCATGCACTGGTACAGAACACACAGGAGTTTTCACAATTTTTTATACAATGCTTGGGAATC TACGG
WI-18829d	58 A G ---			ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGNAATAACTTATGTGTACTTCTTGAGTTCATCA TCATACAAGACAAAGCACAAAGCACACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-18829b	35 T A ---			ACAACATGCCTGTTACAGGGGGAAAAATCCTAGGTTAAATAACTTATGTGTACTTCTTGATTTCATCA TCATACAAGACAAAGCACAAAGCACACCACCCATGCCTCTGAGGAACATTGGACCATGCACCCCTTGAAA AA
WI-20964	87 G A ---			AGCCAACTCAAGGCCAAAAAATTTCTTAATATAGTTATTATGCGAGGGGAGGGGAAGCAAGGA GCACAGGTAGTCCACAGAATAAGACACAGAAACCTCAAGCTGTGAGGTCAATTTGTAAATTA AAGAATACTAAGATTAGATGAACACACACTCAGAAATACTCTAGGAGAGCTGAAAAAAGAGGAAC AGATGTTAACAAACAAATTAAGGCTGCTGGGAACCTGAGTCCATGTTAAGCTTG
WI-20059a	59 T A ---			CTCTGAACCTAAGGGCCGTGAAGGCATGATTGGTTTTGGCACACAGAGTGGATAACCATTAJACAT TGGCTGGAATGAGGTGTCAGGAAAAATAANTGCACAAATCTAACACCATGTTGAAATCATGTCTGA GTTCTGGAGAAAGTTAAGTGTAAATAATTACAAAGACTGACATGCAACTCTTTACCTTACATTATT CATCTACAGACTATTTTCTCCCTTAGGAGATGAGGAGTATGGCCCTTAGGT
WI-22130b	165 C T ---			TGTTTTTGGGGCTGTAGCAGACTACATAATGAGCGGTGAAGCGGCTGCCCTTCCCTCTCTGACAC CAGCAAGGGGGAGGCACCATCACCGGCCCTGCCCATCATGCATCCATGATTACTAGCAGTAGGAA GCCAACGGGAANAGGACCCCGCGCTGCTGCTGTTGTTAATCCAGGTTAAGCTATACACGTTTAA ATACATGTCGGAGGTTACATGGTCTCATGTCAGTCCCTGTGATGGGAATGAC

WI-21861	117	G C ---				GCTTAGTCTCCACCCTTTAAATGTACTCTAGGTACAAAATAAACATTATACACATATAAGATCAGTCTTTCCAACTTTAGAAATGTATAAATAAGAAATGACATTTTAAATAAAATA[G/C]TTTAGTCACAGTCAACAAAACACTACCTTCTAAGGAAACTGTCCAGTGAAGCCGTTAAATTTGTGCTTTCAGCTATGAAGGA
WI-21980a	25	T C ---				TCAGTTTAAACACATTTCATCAAGGATTCAGATTAAATTAATGTCAAGTGAGCATAAAAGGAGATTATAACCCAGAAATGTGTTTTCTGGGAACCAAGTTTCAAGTGACTCAGGATAAGTTTTATTATTTCATGGGTGAAGCCCTGGGATAAAG
WI-21636	71	A G ---				TGCTTGTAATTAATGTGGTGTTTACATTATCCTATTTCACAGATGGAAACAGAAAATACCAGCTTTTTAA[A/G]TAGCAATATCTATTATTATAATAATATTGAAATAACACCATAATAATATCACTAAGGAAGTAATCTAATTGTGTTGATTTTGCAGAGGGAGAAAACATTACCTCTAGAGCTGAGGCTATTGTGCTCATGCAAACTCCAACTCTGAAGGTGGTAGAAACTAGGAAGGACAGGGATTTC
WI-22457a	112	G A ---				TTGCTATAATTTCTTAAATAATGAAAAGAGTACATCACAGCAGAGTATAGCCAAATCACTCATTAGACAAACAGTAACATACTGGACACGGTTTCAGGCATGAAGGATACA[G/A]CAGTTAATTAACATAAGGAACAGAGTCCCTGCATTCTCTGAAGCATAGGATGGGAAACAGTAATGCAGATTAAATACCTGGGGCCAAACCCACTGAACCTCACCCAGCTGAAACACTGAAGGATACCTGGGTAAGGA
WI-21524b	97	C T ---				GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAATAGCCTGATGTACGACCTTCGGGTCACTTATAATGGTTAATAACAGCATTCCTGTCTACCC[C/T]GATGATGCTTCTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTCTCCAAGTTACTTCTCTCCAGGGGATG
WI-21524a	35	A C ---				GCCGTGAGGGTTAGCGTATAATGAAAAGGTGTAAT[A/C]GCTGATGTACGACCTTCGGGTCACTATAATGGTTAATAACAGCATTCCTGTCTACCCCGATGATGCTTCTCTGCAATGGACTATTTGCCCAGTTGCAACAGGGCTAAGATTGTGCGCACTATGACAAATGAGTTGTTGATTGTTGGAGTTGCGGTGTCCTGTCAGAAAGATTCTTGACTTCTCCAAGTTACTTCTCTCCAGGGGATG
WI-22652a	32	G T ---				TTACCTTCCAAACCAGGCCACTTTGGAGAAAG[G/T]AAGAGAAATGCTATTATCAATAAGCCAAGACAATAGGGACTACCTGGGTAGAACCAAGATGGGCAGTCACCATACACCATCATCTGCGCACAGAACCTTTGACATGCTGCCCTCCCTACTCCGCACTCACCTGTCTAATTGGGACCTGAAGCTTCAGCATCCCTTCTTAGGG
WI-21703d	197	A G ---				CAACAGGCTCATGGAACAGAGCCTAGGGATCCAGAGCATAGGAGTGGTGGTGGCAGGGCTCTGTCATCCCTTCTCAGCACAGCACCATCTTCACCCCTCCTGGGAAAGCAGCATTTGGAGCCTACAOCACTTGTCCTTTCTCACCAGGGTAAGAAATGCAGGTATTTGCAGAGGGGAGTGAGTCTGGGAA[A/G]GTGGGCAGAGCACAGCTAGGGGCAAGGACTTAAGGGAACCTTGTTGGGGGAAGAG





WI-22724	117 A G ---				TGATATGATGCTGAGATTGCTTCCAAATATGCCTAGGAAGGAAGTGTATTAGAGATATAGGA CAATCAAGATTGTCAAAATGTATAGTAACTGTTAAAGCTTGCTAAGGGTAA/GTGTATTCTATTTT TGGGATATGTTGGGAAT
WI-22750	48 G A ---				TGTAACCTGTGTTTCTGAAAGTTGAGGGAAGCTGAGGCAGCTAATG/AJGGCTCATACAAGGT TTGGAAGACCCATTCTGACTACCTAAGGAGAGTCAGCATTCTGACCATCTGACTGTGCT
WI-22775a	60 A G ---				TGCTGTTTCTTTAGTTTCATGACGTTTATCACAATGTGCTACTGTTTCCATTGTTTACATC/A/GTTAGTA GGAAAGGGAATAAACTCCCTAAGGGCAGCAATAATTCTGTCTTTGAATCCTTTCATTGAGGCAAA TATTTGTTGAGCAACCAAGGGCCAGATGGGAACCTGAGGTATGTAGGTGTTGGGAGCCAGGAAGGAAG GGT
WI-22808	143 C T ---				CTTAGCTAATGAACCTGGCTATGTGACTATGATAGACCAAGAAAGCTACCCAGTCTGAGGGAG CCTAGTCCCTCCTAAATGCAGACAATGTACCCATGACAAAGGCTACAGCTTGCTTTAGCAACCAGGA GGATGAAGA/C/TAGCAAACTGATTAAAGAGAGTAGGTATAAGAAACCAGGGAGAGTGGGGTCCCAAT ATC
WI-21016	207 G A ---				TCTCTGCTGCTTGAGCCCTCATCCACCCCTCCAGCCCTCATGCCACACACCGTGTCCACAT/T CCCCATCCTCCCTGTCTGCTCCCATGTCAAGTCCAATTCAGGCCAGAGCCCTGGCAGCTTTTCTG GGAGACAGCATGAAAGGAGGGGAGTGAGATGGCAGAGATGGGGTGAGCCAGTGCGCTGTGGGTG CTG/A/TTGGCGTGTGATGTGGGGCCCAATCCTGAGGCCAGAGGTICA
WI-21031	31 C T ---				TTGAACACCTGACCTGACCTCTGACATGTGG/C/TCTCTGTTGCCCATTTGTCTCCAACGGTGGCACA TCTTCATCTTTGTTATATATCTGCAGGAACACTCAGTCTCTTCAGCAGCCGAGAAACACACACA
WI-21314	122 A T ---				CCATATCCAGTCTTCTTGAAGCTTCTATTGACTTTTAGGGTTCAGTTATTATATCCTTTATCACTAT GACTTTCATTTGATTTTATTGTTTCTTCCATTCTCTGTGCAAACTTTTGA/TJTTTTGTTTATAA ACTGTTTCTAAACTTCACTTAATCTCTATCTGTATTNCTTGTAGTTCCTGAACTTCTTTAGAGG
WI-21186	95 G A ---				AGCGAGCATCAGATCACCTAGAGGGTTGACTAAACAGACTTCTGGACCCCAACCCAGAGCTTCT GATTCAGTAGGCCTGAGGTGGGCTTAC/G/AJAATTAGTATTTCGAAGACCTTCCCTAAGTGTGCAG ATGCTGCTTGTCCCGGGAACACACTTTGAGAACTATTGTCTAAATGTCTCTCCTTCTTTTAA GGAGAGACAGGAATTCAGAGAACTGCTAATTTAAGCATAATGTATTGAAT
WI-21187a	94 A G ---				CCACGATAACTATAAAGCAGAAATAGCTTTGAAAATCAAAATACATATTTAGTAACACACATT CATTTTATAACACACATAAAGACACC/A/GJGNTCTCAGTAATGCTCTAGTCCAGGGTCTCAA AGTATGGCTTCAGACAAGCCCATTTGCATCACCTAGGGGAATTGCTAAATGCAGATTCTCAGGCC CTACCTACTGATCTACTGAATCAGAACTCTGAGGGTGAGACCAAGCAACCTGT

WI-21190	39 T C ---			TTTCCCACATACCAATGCACCTGTTGTATAACTATTCTGTGGGGTAAGCCCTTCTTTGGAGAC CAGTGACATAGACATGATCCCATTTATATTATAACAATAATTATTATAATCTGTACTATTACTGC TTTAGTTATCTAGTGTATTGAGAAAGGAGAGTCAGCATAGTTTATTTCCATGTATAATAAAGCTT AACACA
WI-19937d	186 G A ---			ACCATGTGCATTTATTGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAAACTTTGGAAGGAAA GAACTATTGCACAACCAACACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACACAGTGATGACATTGGTGTGTTCCCTCAGCAAGTC[G/A]TCCAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-19937c	185 C T ---			ACCATGTGCATTTATTGGCATAGGAATAGTGACCAAGAAATGCAGCANCTAAACTTTGGAAGGAAA GAACTATTGCACAACCAACACATTGTACATATCTGATTTAGACAAGCAAAAGCACTTCATGTTGTCT GTAAAGGTGTTCTATGGCAACACAGTGATGACATTGGTGTGTTCCCTCAGCAAGTC[G/T]GTCCAAACCTTC CAAAAGAAGCAGTCATTGAAAATGCTGACTTATGCATTGCCTCAGGAAGAA
WI-21117b	227 C T ---			GAAACGGGGTGCTAAACAAGAAAGTCTCAGATCCCACCTGAAATCTGTTTCAGTTTCACAGGCTC TCTCCAGAAAATGCATATGTACCAATTTGCATGTACAATTTAGAGCCTTCAATACATCTCTGGGG TCCAATCACATACTTCAGGTTTCAGACTCCTAGCTCCCAATATTCCTACAGTTCTGAAGANTTAGCAGT CCTCTCATTTCTACAGTCTGTATTTCCTACTGAATCTTGGGTGGGAG
WI-21122a	42 C T ---			TCACTTTGTATCAATCCCTGTAAAGCTAAAGTTATTCA[C/T]TTAACAGGAACCTGTGTTTTC TTATTCAAATGTACAAGCCTGACGGTTACTGTACATATTGCTAGCAGGAGACAACTGGAAATACT AAACAAATACTGGAATTCACATTACAGACAGACGAACCAACATGGGATGCCACACATAACTTCCT TTGTAGGTTTCACAGAGAGCCTATTGTGGGTGCT
WI-21254	53 A G ---			CAGTTTGTACAGGAAGGGCCCATGAATGTGGCGGAACTATTCACAGGAG[G/G]CAAGGAGAAG CTGTTCTCTGG
WI-21054	23 G T ---			AAGGAACTGCATGGGTACAAAT[G/T]TCCAATTCATACTTAACAAGGTGGGAAACGGGTCACTCT TGGCCTGCTCCAGAACAAAGGGGCGAGTCTATGCACCTCTG
WI-21059b	181 T C ---			GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCAGCTGAGCCTGGCTGAA CTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTCACATCTTAATTTCAAGCTGAAA AATCCTGGGGAAGAGACATACTTCACCTGAAGTCATTTCTCTATTCT[C/T]ATTGTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTACTATCCTTGCCTAAT
WI-21059a	63 C T ---			GGGACCAGGGTAACACCATTAGCAATATCCGTTATCAGCCTTATCTTCCCAGCTGAGCCTGG[C/T] GAACTACAGCTGCCAGCATTTCTGGGCTTGCAATTTCCAGCTTCGTCACATCTTAATTTCAAGCTG AAAATCCTGGGGAAGAGACATACTTCACCTGAAGTCATTTCTCTATTCTATTGTAGCCAGGGCAAAA TGAGATTAGGATTAGCTCAGCCAGAGTTAGGGTACTATCCTTGCCTAAT

WI-20442	37 T C ---	---	TCCACGTGAAGGAAGAAAAAANGGGGGGGCTT/CJTAAGGTGGCACAATTTTAAAGAAAT ACCATCCATTTTCTCAGTCTAATCTGAATCCATACATTAAACAAAGTGCAAGTGATGAGAGGAA CA
WI-21235	43 T C ---	---	GTGACAAGAGGTGAAGCAAGGGACAAAGGGCAGCAGGGCAGTCT/CJCTCGGGCCGATGTTCCAGGG CAAGCTACGTA
WI-22012a	57 T C ---	---	ATCAGAACTGCAATCTGCACATGAAAAGACCTGGGGGAATGCCTACATCTGGAATTT/CJCATTAG ATCAACGTTAAATTTTGTCCGACCAGTTCTTCATTGCTGATCACTTTTGATAATGACAGATCCAACAT GAAACTCCTGAAGCAATGAATATTTACCTTGTGCTTTTCATGCAAAATTTAGGGACCAAACTCAAAGG TTTCATCCATGCTGGGACACCAGATCTAAGGAATTTGTGACAGGGATCTTCT
WI-21149a	167 G A ---	---	AGGACCTGCTCACACGTTCCCTCACCCACCAGCTTTTGGCAAAGATAGTTGACTAAATAOCCACT AAATAGTGGCTTTTAAACAAATGACCTTATTTTATCTTTAACTTTAACTGAGTCTTATATA CAGACCTGCCCAACTGGAAGCTTTTACAG/GATGCTTCAGAAATGCGGCAGTATTGCACAATGGTT TGGGCAGGTTCTGTGGTTAAACATGGGATGGAAACCCAGGCTCTAOCCTG
WI-21376b	188 A G ---	---	GGTGCAACTTGGAAATAATGGTTTAAACAGGATAAGCATTAAGGAAACACTTTCAATGTGTG TTCCATTTGATGAATTTGTTTCTCTCTTTATCCCGCAAGTGGAGTTTCATGTCTCGGTGAACCA GACAGTGTGAATCTGTCCAGCCCAATCTGCAGCATTAGGGATGAGTTCTC/A/GJGAAGTGATTCT GAACTGAGCACGCACTCATGTCTGCATGGGGAAGTCTGTGGGAGAAGAGCCT
WI-21382d	125 C G ---	---	CCATTGCAGTCCAGAGATGAGAACTGGACAGAGGCAATCATGAACAGAGGGAGTCAAGAGA AGGGTTTCTAAGATGGAGAGTGGGGGGGTTTGGATCCAGTGGGATNTGGCTTCC/CJGAGGTT GCAACCCCAAGGAAGTCTCTGGAAGCAGCAGTCTGATGGGGAGCAGAGAGCTGCCATCCTC AGTCAGGGTCCGAGTCAGGGTCCGAGGAGAGTCTGTCTCATAGTCTGCCAC
WI-21437a	201 G A ---	---	TCCCTGAGTTGGAGTCTAGCATAGTCCCTCCCTCAAGAGGGGACAGGGTCCAGGGCAGAGC AAAATCCAGTCTGCTTCAACCAGGAGACTGCTTTGGGATGGAAAGTTTCTGGAGTCCCTCCATT CTATTCCTGTGGGGCAGGAACATGCCAGGGCTGCTGTAATGGCAGGGTCACTTTACCAGGGC/G /A/CAGGCATAGTGTGGCCCTGCTGCTGGGGCCACCTGGGAACAGT
WI-21202b	156 A C ---	---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATCT GTTTTATGAACATGTATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATTGAGGG AGGAGGAGAGAGTTGACCA/A/CJGTCTACATGCATAGACAGTCTAAAGCGTATCTCAACATG A
WI-21202a	61 T C ---	---	CAAAATAGAAATCTTTGTGAGTGGATTGACTTAATTTTATTTCTGTATAAGCTAAATATGTTGATG TCTGTTTTATGAACATGTATTTTATAAAATGGTCACAATATATTTTAAAGTTAACTGATTTATTGA GGGAGGAGGAGAGAGTTGACCAAGTCTACATGCATAGACAGTCTAAAGCGTATCTCAACATG A



WI-21627b	153	A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTCATTATGGATAATTTATGCTAGGAATGACAA CAGTAAGGGCATTGCAAAG/JTCCAAAGTCATCTAATAATAACCATAATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAAGGGTTTAAATGTGTGCTTA
WI-21627a	106	A G ---	---	GCATGAAAGAACTCCAATCAGACTTTATTCAATAAAGCAGCTTTTCATGAATGCTTCAGGTCAGTG TATGATCAGCTCAGCTTCCAGTATCAACTTGAGTACCTCAG/JTTATGGATAATTTATGCTAGGAATGA CAACAGTAAGGGCATTGCAAATCCAAAGTCATCTAATAATAACCATAATTTACATAATTTGTAGG GACAGTATACTAATACTCTACAATAAAGGGTTTAAATGTGTGCTTA
WI-21399a	75	C T ---	---	GGATTTGAGTCCCAACTTGATCTCAAAATTCACCTTCTTGTCATGTAAACAAGCTCATTCCTCTAAAGTT TCAGTTTC/JTTCACCAGTAAGGAAAGGTTGGACCAGACATGTTGGACCGTAATTTGCTTGGTAA CTGCCCTCTGCATTTGTCTGAGGTTGTGTGCTGCTAGGACTAGGAGGATCTCTCTGCTTCTGCTGCC TTACCTAGGCATAGTGCTGATAGCAGGCTGAAGCCCAATTCATACTGT
WI-20323a	68	G A ---	---	CGATGTCTGCTAAGATAGGAGGTTAAATCTTTACATGTGAGTGGTCCACAGACAGACATCAAT CIG/JTCTGTAGCAGGAGAGAGACACTTTAAGTTGCCCAAGAGTACAAATCCCATCTATGAGAC AGCAGTGTGCTGCTTCTTAAACAGTAACCAATCAAAAGAAAGATTTAGAGGTTTCAGACATT AGGAACAANTGTGGCCAGAGATACCACAGAGCCCTTGAAGGAAAGCCCTCACT
WI-21249	155	T C ---	---	TTCTGGCATTCAAATGTACATGTAAATCCAAATTTACAGATCAAAATTTGTTACACTAAGTTTCACT TAGTATCTAAGTATCCAATCACAATTGTATCTAAGTTTCACCTTTAAGAAACATTATAAAGGTAATT AAACTCTAGGTGTATCTTAIT/CJATGGAACTAGTTTATTTCCNATTTAACTACTGTTTCATTGCGTA AAGTATGTTGTCCCAATTTTCAGCTGTTTAAAGGAATTATAAACATTGAGA
WI-21504	147	C T ---	---	TGACACAGCATCAATTTTCATGAATCTTTGAAAGGGCCATTAGAAAAAATAAGAGCCAATTTGGGTC ATTTGAGAAACATTTTCAGCACAATTACAGTGGGGCAGCGGCGTTCCGGCTCCAGCTGGGTTTCCOC AGATGCAACAAT/C/JGCGGTTCTGGCTTCTCCACTGGTGGGATGGGATCGCGCTTCGGAGCTCT CAGGG
WI-21242	115	G A ---	---	CTGCACCGGAGGACAGCTGCTGGCAGGACTAATAACCCCTCCACCTGGCCATGTTGGTGGTGT CTCTATGGACCGAGGCCCTGAACCGGGCAGGGAGGGGCAGAGAACIG/JCACTAGCTTGGGGGTG GGCACCAGCTTCAGACCCCTT
WI-21475c	181	A G ---	---	TAGCCCTTCTGCCAACATCTGGCAATNGAGGCTGGGGTGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTCACTTGTACTAAGCACAG CAGTCTGAAGCTTGGGACCTGGGAGTGGCTTTTGGAGAAAGGCA/JGJAAAGCCACAGCAGCAAC ACTTAGGAGCAAGACCCCTTCCGTTCTCCACCCCTATTCTCCCTGAAG

WI-21475b	117	A T ---	---	TAGCCCTTCTGCCAACATCTGGCAATNTGAGGCTGGGTGGGACGTTGGCCTGATGTTGCCAGGAGTAG GATGCTGATGCTGCCAGAGAGTAGGTGGGCTCCAAACCCAGGCTTCTGATCTTCTGCTTACTAAGCA CAGCAGTCTGAAGCTTGGACCTGGGACGTGGTCTTTGGAGAAAGGCAAAAAGCCACAGCAGCAAG ACTTAGGAGCAAGACCCCTCCCGTTCTCCACCCCTATTCTCTCCCTGAAG
WI-20893d	207	A G ---	---	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGCTGCAGGG CTGTCTTCGGCGTTTAAAGTGTCTACTGAGGAATACAATCATTTGTACGTAAGTTTCATCACCAGCACTOC AGCGTCAGGCCAAACCTTTCGGTGACCTGGGNAACCTGCCATTTCTTCTCTCTTTTACAATGCAGT TTCIA/GJACATAACATTGGTAGAGTAACAACAACCAAGCCTAAATG
WI-20893c	179	T C ---	---	TGTTTGTTCCAGCCACATCTTCTCCAAAGGAACCCACCCAGCCCGTGTGCAGGCTTGCTGCAGGG CTGTCTTCGGCGTTTAAAGTGTCTACTGAGGAATACAATCATTTGTACGTAAGTTTCATCACCAGCACTOC AGCGTCAGGCCAAACCTTTCGGTGACCTGGGNAACCTGCCATTTCTTCTCTCTTTTACAATGC AGTTTCAACATAACATTGGTAGAGTAACAACAACCAAGCCTAAATG
WI-19941c	71	C G ---	---	GAGCTAAGGGAAGACCCCTTACCAGATAGGACTAACTGGAGGGGTGGAAGGAACAAGGTGAAA GGTATTC/GJGGTCTGGTGAGACAAGCAGGGGGCTGAGAACACAGAGCAAGGTGGTTGGAG GGAGCACAGCAGGGTGCAGGAAGGAGATGGGGGACATTTCTTATTCAGTGCATGTCCCTTAAAT AACTGGGTACAGGAGCATTNTGGAAGGAGAACCAAGGACAGACAGCAAGCG
WI-21552b	166	C A ---	---	TGGGTACATGGACAGATGATATGTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG TAATAATTACTTCAGAGTAATGCGATCTCTTCACTCAAGCATTATCCATAGTGTACAAAGAA TCCAAGTATACCTTGTATTATTAATAATGTACAAATTAATTTATTGAATTTAGTTACCCCA ATTGTGCTATCAAAATATTCAATCTTATTCTTTGTAACTATTATTGTA
WI-21552a	66	G A ---	---	TGGGTACATGGACAGATGATATGTTATGGGTTATATGAGATATTTGATACAGATACACAATGTG /AATAAATTACTTCAGAGTAATGCGATCTCTTCACTCAAGCATTATCCATAGTGTACAAAG AATCCAAGTATACCTTGTATTATTAATAATGTACAAATTAATTTATTGAATTTAGTTACCCCA TTGTGCTATCAAAATATTCAATCTTATTCTTTGTAACTATTATTGTA
WI-21512	54	C G ---	---	TCCTGTAATTCATGCTCCCTCCCTGCCAGAACCTTACAAAATATTTCTGTTC/GJTAGAGAGGGA AAGAGCTGGTGCTGCTCTGGAGGCAACGTCAGGTCCGGGAAGGCACTGCTGTGTGATCTGTC TCAGTGATGGGAGGTCTCCACTCCGCCACAGGAGCCTCGGGCCAGAGATGAGATATGCTGTAA TCCAGTACAGGGGCTGCTGCTGGGTCCCAACAGCTCTCTTTGGGGG
WI-21513b	192	G A ---	---	CACATAGTTTCTCAAGAGAGGATGAACCTGAAACTCCTCTAAGGCAGGACAAAGCACTTCCATT ATTCTTAGTTAGACCAGAACTTTAATTTTATATTCTCTTTAATACTGTCAAAATACACCAATA CTTAGAGGAAATATTCACAGTATACCAAAACATTTTAAAGATAAAGAGGCAGTGAAG/AJAGTAG TATTCTACATACCACAGTATACAAATGATGCCTTCTGCAGGTTTAGGAAC



WI- 21514b	133 C T ---			TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAGGAGCACATTACCATGGAGCJC TJACAGGACTCCAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAATAAATGAGG ANTTTAAGGCTCAGATGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI- 21514a	100 A G ---			TTGAACCTCTGAAGGTGGCTTATGTCTCGACTCCTCTTCTAGGACTGGTCATGAGCTGACAAGCATAG AGGCAAAAGTATCTCAACATTACAAACCCCAATCTTCAAGGAAGGAGCACATTACCATGGGA GCCACAGGACTCCAAGGACCTCAGAAAGCATTTAGCCAAATCTCCTTATGCAGGAATAAATGAGG ANTTTAAGGCTCAGATGGGTTAAGGGTGATTGTCAAGGGTCATAAGGAACT
WI-22020	27 C G ---			ATGAACATGTTGCAGTGGGATGAATTCGTTATCATGATGCTAAGTGAATAAGCCAGACACAAA AATCCAAATGTATCATTTCTACCTGTATGAGGGTACTT
WI- 18576a	113 A G ---			TTTCATCGGTTCTTAATACAGTACATCCTTTTGTGTAACAAAAGTCACACTGGCAATGATTATTACA GATCCAAATAGACTCAGGCTTCAGACATAAAAATTTAACATTTCAGTCTAGTTCAGTGATTAGT CACAGAAATTAACATCTGCCAGATGTACACAATTTGGTAAAACTACAGCTTCTCTCCACGGGGA G
WI- 21695a	141 A C ---			ATACACAGGCCACAATTGCAGGATGGAAAGGCAGTGGGCACCTTGGAAGTGACTACACATGGCAATA AGCAGCCTATCTTCTTTACCAACCAGAAAGTTTCTTGGGCATGTGATGGTAGGCCAGACCTTTCCAA GGGAATAJVCJTACTACACTAAGCCTACACTGTACTGTGAGAGTCATGGTGAACAAGGCCACAGGC AGTGGAGGAAATGTGATGACTTCACTGTGTTCAGANTTCTAAGGCCAGCAT
WI- 21574a	235 C T ---			AAACCAGAAATTTAGGTACTTTTGTATTATGAGGAACCTCACTATACTAGGAAGCAACTTATGAGTG TGTAATATTTGATCTAGCAGCAACTTTCACCTGATCTGCGCAGGTGACAGCTCTCAGTGAACAGCGC TCATCACCTAAAGTGAGAGGCTGTCTATTCTCATTTGTGAATGTCCCTCAGAGTCACTAGGAGGCCATT GGCAGGCCAGGAACTTACTGCCTACTTCTCTCTGTGTCTGTCAGGTGGGA
WI- 21644c	151 T A ---			TGACTGCCAAGATTTAGGCCCAACTTAGGAGCAAGGTCACCTCTAACCTTTCAGGAAGTCTTGGGT GTGACCCACTGCATAAATGGATTTTCACCATANTATTTAACAGACTCAAAGTGTACATACAAGCTTG TTTCATAAATAAGGATTAJTTCAATCAAGATCCCATGGAATGATGCAGTTTAAACATGTGTCTCAGC TTGCCTACTGACCACCTTCTCTTCTAAATATGCAACAGCACAGCAAGTC
WI- 21614b	55 G A ---			TGTCTTTAACCTCAAAAGTCCAAATAAACATATAGACATTTTGANTATAGCTATC[G/A]JTAAACA AACCTCATTATGATCACTGTGGCAATTTTCAGTCACCTAAATACGGAACCATGACTATTAAATAACA TTTACTGTGTGGGTTTGTGGGACTGAACATTAAACATACGTGTATTCTAAGGTACTAGGGAGTT GGAACAGTACTACGGGTCAATGGTATTTTGGGCAGTTGGCTGTGTGGG
WI- 21615b	151 C T ---			GACCGAGAAAACTGCAAGGCATATGATGTTTGTGGAAGTATCACATGACTATTTCAAGCTTATAGA GAACTTGCAAAAAGTACAAAGATGGCTATTTTAAATTTTCATACATATAAGATAAGGATGGACT CTTCACTGAGTATTATC/TJAGGACACAATCGACGGATGTATCTATTTGANTTATACCATAGGCC TATTCTATTTGGCCAAAGGAAAGGTAGGATGGTACTGTGGAAACGGA



WI-21981	61 T A ---	---	TGTCATCTCATTCTGGAGATCATAGATGTGGCAGAAATACATATTCTTGAAGAAAAAAATTAJGTCTCCCTTATGGTACTGTGATTTCAATAGGTGTGGGATAAGTACATGACAACATGCATGGGATAGA CACTCTGTTCTACAGATCCGTGCTTTGGGAATTACAGGAACATAAAGGATATAATGGATGGGTTATTACTTTTACATGTGGACAATCTAGTTGTAGGCGTTTAAGGTTAAATTTGG
WI-21660	120 C T ---	---	TCCAACTAGCCTCTCAGTATTTAGATGAGGATAGAACAGATACGGTGTAAACACGCCCTCTCCACTGCTTACTGTGTGTACCAAGAGGAGGAGAAAGCAGCTCACCCAGCCTAACCTGGCC[C/T]TGTCCTTTTTCAGGCTTCTCAGGATGCCACAGCACATCTGGGGAACCTGGGATGCAGGGAGAGCCAGGGTCTGTCTTCAGGAGGGTCACAGC
WI-19105c	211 C T ---	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAATAATTGTGGTCCATGTGGTTTGAGTCTGTTAAGAAGGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTTTGTCTGAGTTTCCAGGCTGGGCACAGAGGTAGGGCAGAAATTTGGGGTCCAGTGATCTCCCGACAACCTTC/TTCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-19105a	33 T C ---	---	TGGAAAGTAGCCCTTCTGGACAGAAAGAATAATT/CJGTGGTCCATGTGGTTTGAGTCTGTTAAGAA GGACACTAAGGCACATGGCTGGTGATCTTTGCGTCATAGACACGGGTGAGCTCATGGTGAACCTCCTCCTTGCTGTAGTTTCCAGGCTGGGCACAGAGGTAGGGCAGAAATTTGGGGTCCAGTGATCTCCOCACACAACCTCCTCCAGGGGCAGGATTTCCACCCAGGGCCAGGGTGCCCG
WI-21760c	81 C A ---	---	CAACCTAGTCACTCTACTGATGCAATGATTTGGAGGTGTCTTCTAGCTTTACAATAAGNGGAGG GACCTCTGACTGCA[C/A]CCTCTGTCTCAGTTTCAGGGCA
WI-21760a	35 A G ---	---	CAACCTAGTCACTCTACTGATGCAATGATTTGG[AG]GGGTGTCTTCTAGCTTTACAATAAGNGG AGGGACCTCTGACTGCACCTCTGTCTCAGTTTCAGGGCA
WI-21569b	198 T C ---	---	CTGCCATATTGTTCCAGCACCACTATTACTGTTATTATTCTCTTTGAGGAAACCAGGNATTAAG AAATCTGGTTTGAATTTCCATGATGCCTAACTCTATGTTAAATCCTTTTCTTACCACAAAGGA ACTTCTTAATCACCAGAGAAACAGAGGGAAGACTGAGATATGTTGCAGAAATTTATCTCTACT[C] AGAGACAATTATAGTTTCATAATCTTTCAGGGTTGTGCTTACTTGGGGGC
WI-20934a	72 T G ---	---	CCAACATGCAACATAGTCTTCTTAAAGTACATAGTAAAGGTATGAAACACATTTGTATTCA GAGAA[T/G]TCTAAGACAAATGGTCAAAATATTCAATGGCTGGCACTAGTGGTAATTCAGCAGAC AACAGCATGAGAAAGGCCGGGAGACAGTAATAAATACGTGCCCATTTGCAATGAGTTACCCCAATC AAGCCCTTTTACCTCCTTAAGATGGCAGATTAGAAACCCCTNTTCCCGAGGAGA
WI-21561	55 T G ---	---	TTTCCATTTTATTCAGCCGGGCCATCAGAACATAGCATCTATACCTTCGAAACCTT/GJCCTCTTAAC CTCTCCAGGCAAGAGGAAAGTATGATCATATTGAATTCCTCAGAAATGGTGGGATCTCAAGACTT TTTAGAAAGTGCTTATTAAGTATAAGAGGCTTGAAATATAATGATGATAAATGGTAGCCTTTCTGGA AATAATTTTGTGTAATCTGTTTAAAGATTTTTGGATGCATTGTCCCCA



WI-22082b	67	CT	---	CAGGACTTGGTTTGCTGCCAACTGCACATAAATGTCCTTTTGTGTTGAGTTATTGGTTGTGTGTC /T]GTTTTCTTTTGCATAAGAAATATGTCCATTTAGTCCAGAGGCTCTTGCTTTATCCGGATGACGG AGGGTACACGGGGCTCGCTCAGTTCCCGCGAAGGACGTATTGCTGAACTGGGACGAGTCTACTC CTCCCCACAGGAGCCACGATTTCAAATCTCTTTGCTGCAACCTCT
WI-20993	139	AG	---	AACACAACTCCATGCTTTCAAGATTCCACACCCAGATACTAAGACATATTAAATTTACAGCAAT TAAACAGTGTAGTTTGGTACATAAACACATATAGCAATGATACAAATTAGGGGAAACCCCTGG GCTTCT]A/G]TAAACAAGTGAGTATACATTAAAGACAGTATTGCAGAAATGGCTTCAGGATTAAATTTGA TTAATTTAGAGAGAGCCTATTTTCAGGTCTTCCTAGCTCATCCACACATCAC
WI-21723b	125	AG	---	AAGCGATTTTATTAAATTGATTTGGACATACTGTAGTCAAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTCGACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCCCCA]A/G]CAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-21723a	82	GA	---	AAGCGATTTTATTAAATTGATTTGGACATACTGTAGTCAAAATAATTTTCTGAAGATAACAATTA TGGACTTTAAAGCTC]G/A]ACATAAAATTAGTAGCTTCAAAAGGGTTAGTCATATTCCCCAACAACA GCATGATAAAATAATTCAACTATGTAGAAATATAGAACTCTAGGACTAGCTGGAAACTCGGAAATC ATT
WI-22132	99	TG	---	CAACAGATGCTTGAGCCAAAAGCAACATAGGCAGAAATACAATTGAGAATATCTTCATGTTTC AACCTTTAATCTGACTTGCCCTTTTACTATCCTT]I/G]CCCCATTTCTTCTAATCTCTTTTGCTTACAA TATATTACCTTCTAGGTATCACCTCATCTCTATAGGAATGCTTCTAGTTTAAATGTCCTGCCCAACA ATACTAACCCATTGAAGGATAACTATGGAAACCTTAAATGGGACAGTGGG
WI-21008a	106	AG	---	TGACAGATCACACCACATTTTGTGTTGTAACCTTTTCTCTTCAAGAGTCACCTTAGCTTAAGCCAGAA GATTCTCTTAAAGAACACATACACATGTGCACACAC]A/G]AGAGGCAAGTACAAAATGTAAACC CCACCAAAGTGCAATGTGAATGAAGTGCAAAAAGGCTTCATTTGCAAACTCTGAGGATCATCTCT CTGCTTCAGGAAAATAACAGAAAGGTCCTAACTGCCCTAGGCCT
WI-21761b	138	CG	---	CTGAGGCTGCTCTAACTTCAINTGACGGAGCAGTTTCTGCTTGAAATAACTGAAAAGATTTCAT TTTCTCTTTGTGTACAAAGGATTCAAAATATTTTACATCTTCTCTGCTGAGTTAAACGTGCCGTGG CT]C/G]CAATACACACCAAGCCAAGCGTAACTTGGCTGCCTCAGGAAGGCTGGGAGGAAGTGCCAG ATGGTA
WI-21079c	166	GA	---	AATGAAAATGCCACCCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTGCGCAAAATCAAGTTGT TTTAATACCAGTGTGAGCTTTGATTCCTCCATGAAATTAAGAGCTGTGTGCTCACTTGTTTACATAA CTCAGGCCACCCTGAAATATCTGCTAGTGGG]G/A]AATTTACAACCCACTGACCATCTCAGCTCAA GCCAGATGACTATCACCTACACATCTGCCAGGTAATAGGCATGGGCAAT



WI-21079a	50	G A	---	---	AATGAAAATGCCACCAGAGGTTAACAGCTTGCCATGCATGCAACTGTGTG[A]CGCAAAATCAAGT TGTTTAAATACCAGTGTGCAGCTTTGATTCTCTCCATGAAATTAAGCTGTGTGCTCACTTGTTTACA TAACTCAGGCCACCCCTGAAATATCTGCTAGTGGGAAATTTACAACCCACTGACCATCTCAGCTCAAA GCCAGATGACTATCACCTACACATCTGCCAGGGTAATAGGCATGGGCAAT
WI-22129a	45	T G	---	---	TCTGTAGATTTAGCCATGCCATATATTTAACTTTTAAGGAAAAG[T/G]TTATATAACAGTCATTGCT TGGTAGAAATCCAGTCTGTCAATAAGTTAGCTCTAACAGTTAACATTGAAGTCTTATACCTTATATTTA AATGTTTAGCAATCTCTACTACATTTTCAAATATAAATAATTTGGTTGCAAAATTCAGNAAAGGGCA TTAACCAACATGGGACTGATCTCTGGGGCTTCCACTGACTAAGGTTTTA
WI-21941	79	A G	---	---	TGGAGTTAAGTGGGCTCTGCTATTTCCCCCAAGAAAGACTCGGAAGATGTGATTCAGGGCAGAGT GAGGGCAGAC[A/G]GGATGAGGCTCTTCTGTAAAGTCCAACAGACGCTCACAGATGCTGGGAGGCT GGGACTGCCAGGTTGGAGCCTCACCCAGAGAGCCTCAGCTGCAATTGACCCACACCCACCCTCACC CAGCACACAGGCACACGCAGGGCACACGCACACACGNTGCACTCACCCAGC
WI-18916b	42	C T	---	---	AATGGCATCCCTGTGATAOCAAACATCTTCAGCAGCTCAGC[C/T]GGCTTCCCACCTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-18916a	35	G C	---	---	AATGGCATCCCTGTGATACCAAACATCTTCAGCA[G/C]CTCAGCCGGCTTCCCACCTTCTTGGTACCC GGTTAACTGCCAGNGGGTGACAGTGATGCCAGGGCTCGCCACTACTGCACTGGACACAGCCTCACC AATGCCACCTTCATA
WI-19828c	200	A G	---	---	TTCCCTTCTCCCCAAGAAGTGGGCAGAAAAGCTTTGTTAACCTCCTTTTACAGATGAAGAAAACAA GATCAGAGGTGCTAAGTGTGTAGCCTAGTGCCAGGNCCTTCTGGCCCCAAATCTGGGTCTCCCCAAG CCCATGCTTCTCCACTTCTCACAACTTTACTTCTCTCTGACCCCTCACCACCCCAAAT[A/G ]CTTTTAACTCTGAAAAGAAACCCAGCTGCACACTGGGCACACTTGACCT
WI-21863b	47	C T	---	---	CACAAGAGTCTGTACAACCTTAGGGACACACGCCCTGGCCCTGCCC[T/C]TAGCTGCATGCCACCCTC ATATCCCACCCCATCCCAGCCTCTGCCCCGACACCCAGGCTCCCTGCTCTGTTGAAGTATTTT CTCCAAGGCAGGAATGAGTCCTTGATCCAAQCACAGCATCT
WI-198860	51	C G	---	---	TTGACCTAAAGCCTAGCATAAAATTAGCTAAGTAGAATGTTTCCAAGATG[C/G]CTGCATCAGTAT CTCCCATCCCACATAATTTCTGTTGATTTTGCCATTACCCATAAATGGTGGGATCTACCTCCCCT CCTTGCAAATTTGAGCTGNNCCTCTGATCCTGTCTAAGGATCTGAAGCC
WI-19889b	80	C T	---	---	ACCCAGCTCCTTACCCCTGGCTTTCAGTAGGCTTTGGCTAATGGCCANTGAACCTGCAGGGCAAG AGGAGTGAGGGG[C/T]TACAGCATTATTTCCCTGTTTCACTCCCTGTTAGCTTTGGTAGTGGCTGTAT TTCTCTACTGATAGTTCCCTTGCCACAGTCGTAACTATTGC

WI-19891c	172	C G ---			TGTTGGTCTGAGATTACAGCTTACTACAAGGAAGCTGAGAAATGCTTGGTGCCCCCTCCCCCGG ACTCCTCTGTCTGGGAAACGTGGCTTTGNCTCCAGACACGTGTGATGOCAGCTCTCCTCAGCGG AGTCCCGATCCCTCAATTTGCCATCTGTCTGACTCCTGCTTCCCGGGCGGTGGCGCTGCTTGT CAGGCAGCGGGGGGAGGAAGGAAGGAGATCCAGGGTCTGTCTG
WI-20155a	81	C T ---			GCACCTGTAGGGGTAGCTTCCATGGTTCTCAAGCACGGGCTGTACATTACCTTAGGCTGAACAT TCCCTTGGGGGGG[C/T]GCAAAACTGCTTTGAGGAAATNTCCOCAGGAGGAATAAACTAGAAGACGC ACCTGCTATTTCAACCATACTATGGAGAATACAGCTAATGAAGTGGTGGCAGAAAGCTTGGCCGCTGTGA GTGCCCCAGGGTAAAGTCTCTCTTCTGTCCAGTCCAGAGCAGAGACTTCTC
WI-20270b	91	T G ---			AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCGTCAAGTGTACAAT ACATTTCATGTCCAGGATAAGGAGCA/T/GIACAACAGGATTTATACCGTGGCAGCGGCTATAGGCA CGATGATACAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGAAGGATGCT GGGTGATCTTGTTTCCCGCAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20270a	53	G A ---			AGCCATACAATGCATTGCAAGAAACAAAGCAGCTGTACAGGAGTGGGACGCG/TATCAGTGTAC AATACATTTCATGTCCAGGATAAGGAGCATACACAGGATTTATACCGTGGCAGCGGCTATAGGCA CGATGATACAAATATAAAGTATATTTCCATCTATATAAATACACAGCTGGGGTGGGAAGGATGCT GGGTGATCTTGTTTCCCGCAGAGGGCTGGGAGGCGAGGNGGGTGGTGGAA
WI-20622	130	T C ---			CCACTTTCAATATTTACAAATGCTCAGCAGCAATATGAAAAGCTTCAACACTTTCCCTTTGTA ACTTGCTGCAATAAATGCAACTTTAACAAACATACAAATTTCTCTGTATCTTAAAGTTGAA[T/C] TACTAATTTTATGATGTTACTCATATTTTATTCATATACCTTTAATGACATCATTTGCCAATACATA CATTATTTCTNTAATTTTATTTTACAATAAGCCAACATCTGTATGCAG
WI-20768b	190	C T ---			TTCCCACTCAAACTCCACCCCAACCTTCTGGAAGGCGAGGCTAACAGGACCTCTGCTGCTGG TCACGACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTGTATATCACCACTTA CAGGAGAGGTCTATTTCTGGGCAACCCAGAGNTCAGCAGACATACCTGCTGGGA[C/T]CAGGGACTC GTAAATCGCCTTGGTCCAACTCTCTATGCGGTTTAGCTGCCCTCATTC
WI-20768a	71	C T ---			TTCCCACTCAAACTCCACCCCAACCTTCTGGAAGGCGAGGCTAACAGGACCTCTGCTGCTGG TCA[C/T]GACTGATTACTTTCAATCCAGCTGCAATGCAAACTGAAACTCATTTGTATATCACCACT CTACAGGAGAGGTCTATTTCTGGGCAACCCAGAGNTCAGCAGACATACCTGCTGGGACCAAGGACTC GTAAATCGCCTTGGTCCAACTCTCTATGCGGTTTAGCTGCCCTCATTC
WI-21909	153	A T ---			TGTTTGCTTTGTGCCAGGTACTCTACTGCTTTACATAAATTATCTATTCTGTGCATCTAACGGCAA CTAAGTATACGCTTACATCTGCTAGTGGCACCTAAATAAGGATATTGTTGGTCATCTTTAAAGAA TGTCTTAACATACCAAAAGI/TJAGTGGAAATCAATAGATAAAATATTAAAGTCTTACAAAGCGTAC GACACTAAAGTAATATAGGATACCCTAAATTTATATTCTATGTATGGAAG



WI-22202	128 A G ---			TGTTGCTTGGTTGCTTCTGGAACATATTGGACACACTTGTTTTCATAAGCTGTCTGACAGT GGCACAATCCCATCCATCTTCAGGCCCTTTAAATAGGTCAATTATGAATCTGAATTTCTT/AGJTTAAT ACTCTGGTGCAATTCATCTGCAAAAGCAACTGGCACAACCACTCTTGGCGGTGCACTCTCTCGG AGAACATCTAATATTGAGTCTAGTCTGTGCGGAACCTTCTCCAGCTCAC
WI-22189	70 C T ---			CCAAGGATGAAATTTCCACATTTATTTTNCITTTATGTGAATAGAAATGGCAGTGAAGTGTCTATG AACTTGAGGCGGAGGAATGGCATGGCGCTGGCTGCGGTACAGCCTGGACGTTGTGCTTCCAAAGTACAC TATGTGTGGTGAGACAAAGGGT
WI-22283	109 T C ---			GGGAGGCATCATAGAAACCCCTCAGCCAGAGTAGGACATTGTGATTCTCAGCCACTAACGA GCTGTATGACCTTGGTCACTAGGCCCTCTGCAGGCTCTGGTTGTTGTTTTCATTTGCAAAATAAACCCCA GACCGGGTCACTCTTCAGTTCCCTTCCAGCTCTATTTATTTATGATTTGCTCTTAGTCTTTATGAGCCA TGTATGATTTATCAGTCTCCCTGATGCACCTCACTCCAATGATGCAAAAG
WI-22290a	136 C T ---			GACGTCACTCTGAGGGCTCTGCCAGGTGGATTAGGTGAAGAGAGGTTTATGGCCTCTAAGCAOCCG GCCAGTAGTGGGAATGCCACATGCAATGGGTGAGTGGGATCTGGGGGGGTGAGCAOCTTGCTTTT [C/T]TTCCAATCTCTCTTCTTAGCCAGAACTTTGCGAGAGCCCTTINATTTCTCTTCCCTCTATTCC CCTCCTTTCCCAATGTGCTAAGGTCCCAATTCAGACCCCTCCAG
WI-22292	53 A G ---			CCAGTGGAAAGGTTTACAGCCATAGTGAGGTTCCCCATTGCTCAGTACCAGA[AG]GTTTGAGTAC GGTCGTTTAAAAATACTTATCTGACCACAGTGGAA
WI-22387	186 C T ---			ACCTTGACACCTGCCATCCGGTGCCATCTCCTGGCTGGCACATCTATACCACCTCTGGCTCTGAAAG GCTTGTCACCAAAATGGGCAGCTGGGCTAAGGCATATTTAAACAAAGGCTCCAAAGGACCCCTT TCACTTGGGTCTAGCATCCAGCCTCTCTCAGCAAGGCAAGGATTTGTTGTTCTTCTTCTTCTG AACAGGCCCCAGGCGAGCCAGGCATGCCATCCTGCACTGCACTCAACCT
WI-22395b	127 A G ---			GCCGTTCCAGTATTGATAATAATTTGTGTTTAAATTTCTATACAGAAATGGTTCTTCTTGAATATTT GTAGGATGGATGAATTGAAAGTGAATTAAGTCAAGATAAAGGGGGCACTCTTTAAT[AG]AAG GAAATGTTACCAATCCATAGTGAAGAGTAGAATATGTTCTTTTAGAGTAGNTAGAAAGTCCCCAGG CTCCT
WI-22405	90 A C ---			TTTATGGCTCCTGAGTGCTTCCACCAGCTACACTTTACCTTGTATCTATAAAGTGTAAATTAGAGT AAATACATTGGCTGTAAAGTGG[AG]GATCAGGTGCTCTCCACCACCAAAAGCAAACTGCTGA AATGTGGCAAGTTTCTCAGTG
WI-22419b	67 T C ---			CCCTTCTGGACAGTTTGCTTTATGTGTTTCAGACAATCAAGGNTGCCCTTCCAGGCACAGCCAGTGCTT /CCTGGATGGCATCAGCACAGGCTCCCTGCCCCGGCCTTGAAGCATGGCTGTGTGCACGAT
WI-21342d	59 T C ---			ATTTCCCTTCTGTGTTTCGTTTCCCTTTTGTGAGTAATNAGCAATACACTGAT[CT]TGAA ATCTGCATGATTAATAACATTAAAGTTTCATAACACACCCCATATCAGAGTATAAAGCAAGAG GTTGAAAAATATCCCCCTAACCGAATGCAAAATTAGGTATCCCTCAAAATTGCACATTTCTCCTCTAGTT T



WI-21763b	154 A G ---	---	CATACCCCTTTAGGTGCCACACATTGATCTTAGTTAACAGTCTTGTTAGTTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACCTTCCAAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT GCTCTCCACAGCTGATT[A/G]CAGACATTGCCTGTGCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-21763a	135 T C ---	---	CATACCCCTTTAGGTGCCACACATTGATCTTAGTTAACAGTCTTGTTAGTTCCCTCTTTAGGCTTCAAGA TAATTGTGATTTTCATCGCACCCAGATACCTTCCAAAGTGGAGCCAGGCTCAGACTGTTCTCAGTCACT T/C]GCTCTCCACAGCTGATTACAGACATTGCCTGTGCTTCTACCCAGCAGCTGTCTAGTGCACCTT GA
WI-22440	64 A C ---	---	CAGTCCATTTAGTCCCCAGTCGAGGGTGCACTTCTCTTATCTTGCTTAAGCCACTTGGGT[A/C] TCCATTCCAGCTCTGCACCTTCTCCAGTTTCTCATGTTCAGAAAGTCCCTGGAGGGAGGCTTTCTTGG AAAT
WI-22449	74 T C ---	---	CAATGAATGTTGTGGCATAATGATTNCCATTGTGTGACAAATTTATTAGCTGGCATCCGAATACAGTAC TTCTTTT/C]GAAATAATACACAAATGGGAACGTGACA
WI-21965a	112 A G ---	---	CAGGTTCCACCAGAGGCTTTATTTCAGCCACTCAGGAOCCTGGCTTCTGCTCCAAAGGCACTGAACA CAGTCAGGCTCTTTAAACACTGGCAGGGACCTCCCCACAGCC[A/G]CCCCACAGGGTCTCTGTT TOCCAAGTCTGATGGATTTCAGGCAAGACCTTCACACATTCACCCACTACCTGCTGGAGAGGGGTC ATGAGGCAGCCTGTGGTGCCAGCTCAGTGTGACACACTGCCAATGTGC
WI-21687c	115 C G ---	---	CACCTGGCAGTTGAGTCAGATTGTAGGAAATTAACCCAGATGGGTCTACATTTTNTTCAAGTTCA AACCACATGTTTCTAGTCAGAAAGTCTCATGACTTCTTCTCCTAAG[C/G]TGTCTATGATCAGAC CACCTCCTAAATGTGGCTTTACCCATTACAGGCTACAGTTGAATCAGGCAGGAGCAGCTGCTGGAG AG
WI-22374a	149 T C ---	---	AGCTTTTACAACAAAGCGAGGGTTTAAGGAGCCTGAGAAGAAATTCACAACACTATTGACTATACAGAG TCTTCAATTCCAAACAGTTAATAGTAACCTTGGTGGCACATACAACATGCATTGAATACTCTGTAT TATTCAGTAACTAAAT/C]AGGNTCCTGCATCATCTCTTTCACA
WI-22250b	132 C T ---	---	ACTTGCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCATCTAGTGGGTATTATGGGGTCTCTGCTCCTGCTGCTGTATG[C/T] GGANCCAGGAGTGGAGGAGCGGTGGAATAGACAGGGGAG
WI-22250a	89 G A ---	---	ACTTGCTTCAGGCAGGCATTTCTGGGATCTAAACTAGAAATCCTTGAAACAAATAGTACCAGCCA CTTTGAGGAATGTGCATTCATCTAGTGGGTATTATGGGGTCTCTGCTCCTGCTGCTGTGTTATGC GGANCCAGGAGTGGAGGAGCGGTGGAATAGACAGGGGAG
UTR-04932-2b	192 G C ---	---	GCAGCCATCCTCTCTCCAACAGCTCCAGGCCACCTGGGGCCAGAGCACTCATGCCAGCAGCAC CTACGTGGCCCGAGTACGGACCCGCTGGCCCGCAGGTTCTGGCTCTCAGGACGTCCAGCAAGTGGA GCCAGAGGTTTGTGGGACTCCAGCCAGGGGATGAGGCCAGCCAGCAACCTG[C/G]C]AGTGCCTTC TTTGACGGGGCCCGCTGCTCAGCTGCTGCTGGAGGTGAGGAAGGAGGT

UTR- 04932-2a	149	C T ---	---	GCAGCCATCCTCTCTCCAAACCTCCAGGCCACCCCTGGGGCCAGACCACTCATGCCAGGACAC CTACGTGGCCGAGTAGGACCCGCTGCCCCAGGTTCTCGGCTCTCAGGACGTCCAGCAAGTGGA GCCAGAGGTTTG[C]/TJGGGACTCCAGCCAGGGGATGAGGCCAGCCAGCAACCTGGAGTGCTTC TTTGACGGGGCCGCTGCTCAGCTGCTCGGAGGTGAGGAAGAGGT
stFIBBb	412	G C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGTTGCCA CGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCTGCTGCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCAGTCTGTTACGATGTCTGAGCTTCTTAGAACCTTCCATGGT
stFIBBa	341	T C ---	---	GTGAGGAAGATGGACCTGGACAGACAGTCAGCTCCACACCTTGGCTGAGCAGCTGTGTTGCCA CGGAGCATGAGCCCTTTCCACAGGCCCTTGCCACTGTCTCTGCTGCTGCTCTCTGATCATGCCAGG TTTGACACAGCCTCGAGTCTCCCATGTTGTAGTACATTCTCCAAAGATGCAGCCAGGAGCCTCTCTGA AGGACCAGTCTGTTACGATGTCTGAGCTTCTTAGAACCTTCCATGGT
stGLV2	61	T C ---	---	GTCACAAGAGGAGCGCTCTCGGACAGTCTCCACACCTGCGCTGGCTCTGCTGCTCTCACT/CJCTC CTCACTCAGGACACAGGTGACGCCCTCCAGGGAAGGGTCTTGGGACCTCTGGGCTGATCCTTGGTC TCTGCTCTCAGGCTCACCGGGGCCAGGACTGACTCACTGGCATGT
stSG1001 7c	70	T C ---	---	GTTCAGGCTCATCTTGAACTCCTGGTGTCAGCGATCCTCCACCTCCAGGCTGCCAGGGTCTGGGAT TA/T/CJAGGCATGAGCCCCACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1001 7a	33	G A ---	---	GTTCAGGCTCATCTTGAACTCCTGGTGTCAGCG/G/AJATCCTCCACCTCCAGCTCCAGGGTCTGG GATTATAGGCATGAGCCCCACACCTGGACACAAATACATTATATACTCTAAAGTATAGGATTACT TTAAGAGAAGGAACTAAAGTATGATGGCTTACTTTCTAATCC
stSG1002 3	63	A T ---	---	TAATGATAATTAGGGCATTCTTCCACACGAAGATGACACAATTGACCCAATATCAATTGAGGC[AT] AACAGTTTGGCTGTTTTCAGTAGTATGACAGTGA
stSG1009 6	36	G C ---	---	GTGGAGAAAGATCGTCTTCTCCCTCCCATGACCGCGCTTCCCGGGCACTGTGCGTTTCC ACCCGAGACGCCCTTGTAGGGACCCACTGCCACTCGCTGTGTGGCTGGGTTCCGCTCTAG GGCTCGAGTGTTAAG
stSG1011 8	107	C A ---	---	TAGGCTTAAACCTGGAATCTACAAGCCAAAGTCCCTCCCTGAGGGCAGTACCTCCATTGGGC ACAGTCCAGACCCAAAGTCAAAGATGCCCATTCCTTGGC[C]/AJCTCAGCCCTCAGTTCTTCATTCC ACGAGGCCGTGCTGTTGAGTTTCTCCAGTGAG
stSG1012 0	89	T C ---	---	TAGTAGTAAGAAAGCAAGGAGGATTGCTTATGCGATGACTGTTTACAGTGGTGTGACTATGC CGTGTTCACGAACACTTAAAT/CJGTTGTTGTAATCTGATTTTATCCTCGTCTTACAAATG
stSG1017 8	42	C T ---	---	TTGAAGCAATATTGTCTAGCACCTCTGCTGGACATTAAGTCCG[C]/TJGGGAGGAGAAAGTGAACAGGAA TCGATTCTTGTCTTTAACTGCCCTTAGTTAGGAGATGTTAAATACTTGGC



stSG1019 3	136 G A ---	---	GGAACAATACTACCTAAGGACAAATACTATTATTAATAAAAGTCTTCTAGTGTATATTGTGTAA CACATTTCTGGAGCTGTAGGAATAACCATTTTATTTTCTGTAGTGCCATCTATACAACTTTTAC TTG/AJTGGAAACTGAGATTAAAGTTGCAAACT
stSG1020 2c	143 G T ---	---	AAGCTAACTTAGGTGAATGGTGCACTCAAGGCTCTTCCGAGGGAAGCTCAGTCTGGCTTGCGAG AGTCAGCCTTGGTCACTCATAACGGGCTCCAGCTAAGCGTCAAGGAGCAGTCCCACTGCTTCT CGCTGTCA/GTCAAGACCAAGGAGATGCCACTGCTGCTCTTCTTCTGCTACTTTCT
stSG1020 9b	75 A G ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTCAATAAATAAATAAATCTCCTTAAGATCCCACCTTAT TTTTTA/GCTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1020 9a	34 C T ---	---	TCCTTTCTCTTTTCACTCTCAGTCACCATGATTTC/TAATAAATAAATAAATCTCCTTAAGATCCCACCT TTATTTTAACTCCAATAAATGTAATTATCAGCTGCTGAATT
stSG1021 8	29 T C ---	---	TACTAGACATGCAAAATGAGAAGATTACA/T/CJGTGAATATTTAAAGAAGTTATATTGTTTGACAT AATATGCATTGTACCCGGGCATAATAAAGTTAAAGCCAGTTATTCTGA
stSG1025 2	108 A C ---	---	ATAGGTTTCAGGAACAAATCATTAAATGGAATAATGAGAAGATTCTTTATTTTGGACCAATTTT AGGCACCTTAAGAGTTTCTTTCTTCTTCTTCCCTTGATCA/CJAGTGAAGATATGATAGGGAATTC AGAAATTTCTCTCTTG
EST10915 0	123 A C ---	---	CTGTATTAATTAAGAAGGCACTATTAATGAGGGACGGAAATACTACCTGTACACAAATTTCTGTAC TTTAACAGCATCTTCAATAAACCCTTTAAAGGATAATGGTTTACGATCATTTTAAAG/CJATTTTAA GAACTGAGTTATTGGAC
EST11023 1	166 T A ---	---	TTTTTTGTTAAACCAACCCTGAAAGTTTCCACATGTGAATATAGATACAACAGTGAACAAAT ATGTGGCCTCCCATGTACATTGGTTACCTATGTACAGTATCCTATACACAGTAAACAGCAGGGC AATTAGTCAATTAAATAAATAGTACATGTTA/T/AJGTGAATAAAATTAATTTACAAAGGCTTT TCCACTCGTGGATTGATTCCTTTTGGAGGGAGGAGTAATCCTGG
EST14096 8	71 G C ---	---	GGGATGTATATTACAGATAACACAACCTCACAATAATACCATCAGACATTGAAACTAAGGCCATTCT GTGA/GCJTATTTTAAACTTGGTGTGTTTGCACATAATGATCTTAAAAAATAATGAATTACCAAA ACCAAGATTCTCTTCTAAATGAAATTTAATGCAGGTACAGGATAACTTTAGGGCTATATCTAATC TGAAG
EST22113 6c	125 C A ---	---	TGCAATTGTGAGAAAGGAGGAGGGGCCAACCCCTGGGACCTCATCTCTGTCTAGAAATGTGAGGTGG CAGGGATGCTTAAGTCTTCTCTGCGCAGAGACCCGAGGTGCAGAGATGATTCTTCTCA/CJCCCTTC TCTCAGGGTCTGGAG
EST22555 7	60 G A ---	---	TCAAGCATGTGTAGGCACTGCCCGCCAGACCCCTTCTAATCTTGACACTGGAAGGTG/AJAA CCTGGGAGAGAGAGACACTCCCTCCCTAGCTTCTACCTGGGCACTCCCAAGATGAGCATTCTC TTGGAGACCAATAAATAAGGACAAAGACCAAGGGCTCAGAG



EST22917 6	74 C T ---			GTAAACCTTGCAACGCCATGCTAAATGGAAGCCTGACTGACAGGGGCTCTTGGGCTCTCAATGCA ATAGAAAC/TTTGACATGGGGCCAAAGACTTCCAGACAAAGCAGCGAAGGGTAGAGGATATAG GTTAGCATCATCTGGTTGTGA
EST38458 6	65 A G ---			CAAGTTAGAACCATGCATCAGCTTTTCATCCATGGTGTAACTTAACCTCAGGCTGTCCTACTCA/AV GTTGGTTTGTAGCTAGCTCAGCTCAGCACACAGGAAGCTTGGAAATTTGGAGGCTCCAAGTCACTCTCCA GAGGGGAACTTCAAAGAGGATTCCACAGTGAAGCAGAAATCATGGGGCAAAAGTC/AVGJCTATGG GGCCAGACTGAGGTTGGACCAACACAGCACTCCAAAGCTGGGCCAATCCCAACCGCTGGTGAAGCCGC ACAGCACGGAGTAGCCAT
EST36745 3	56 A G ---			TGTGACCATACCAACCTATGCAATAAAGAAAGAAATAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATAACAAATGTGTGATCTCCTGAGACACACATTTATAACATTTCTGTATG T/ATTTATGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410c	201 A T ---			TGTGACCATACCAACCTATGCAATAAAGAAAGAAATAATCCTCACTTAAAAAACAACAAAA AACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTTGGGA ATTTATGGTTTGAATAAATAACAAATGTGTGATCTCCTGAGACACACATTTATAACATTTCTGTGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410b	139 G T ---			TGTGACCATACCAACCTATGCAATAAAGAAAGAAATAATCCTCA[CTTTAAAAAACAACAA AAAAACCTTTGCAATGCTATCATTTTTCAGGCTCTTTTGAAGTGTGAATAAAGTTTCATAGCATTTT GGAAATTTATGGTTTGAATAAATAACAAATGTGTGATCTCCTGAGACACACATTTATAACATTTCTGT ATGTATATTGTGAGTGGTCTCTAGTGGCCAAT
STS- R37410a	48 C T ---			TATCGTGGGAAGTTCCAACCTCATACTTATGCTGCTTTTCTACTTGTCTAATATTGGATGCTTCTTGCCA GGCTC[CTTTTAAATTGTGCTGTAACTGGGAAGAAACCTTCTACTCTCCACAACCTGAA CAATCTGAAGAGATGCATAGCGGATTGGTGGCTTTTCAGCAGCTGTGGGAGGTGGGACTGAGGAGCG ACTGCTAATCAGTATGGGTTTCTCCCGGATGGTGAAATGTTCCGGACCTAGATA[CTGTTGACGA AGGTAGCACGACACTGTGAGTGCACTAA
UTR- 04350	125 C G ---			GAAATAAACTAAACTGCAAGCAATCACTGTTAATAAGAAATGTTCTTCTGTTT[CTGACAGTTG AAGTGGGTGTGAGATGGGCATAGCAATGAACAGTGGGAGCCCAATGAGGTCTCAGAAATGCGGGCAAA CTCCCTCTGTGAAAATGTAT
stSG1026 6	55 T C ---			GTATAATTCAGCATAAGCCAAAGCCTTTTAAATAACCAATACTATCATTTTATGAAATCTTTTACA AGA[T/G]AAGCACAGTAGTACAATAATTTAAGCATCTCAAGTCTCCATTTAAGAGTTGACTATC
stSG1028 2	70 T G ---			CACCTTAGATATGAGGAAAATGGTTTAAATGGACACAAAGGAGTCAGCCAGCTTGGAAACCAACATAG TTTCATACCACGTTGAAACCATGTGTTTGATATGCAATAACAGCAAAATAATTTTTCACT[CTC/A]TTG TCAATGCCAATGCATTGAAAGGCCCCAGAAAATGAGAAAAGGATAACAACTTTTGATAAAAAAGGTA AGAATTTCTGTGTG
stSG1031 0	128 C A ---			

stSG1033 1b	116 T C ---			TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCATTTCCGG GCTCCAACCTGTCTAGGAAGCCCTAGACCTCAACACCAACACCTCCATTCGCAATTTCTCTTTTGG CTACTATGTCTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
stSG1033 1a	107 A T ---			TTTAAAGCTACATGTCTGAAAGAATGATGCTGCTGATTGAATAAAGGAAGAAAGGATGCATTTCCGG GCTCCAACCTGTCTAGGAAGCCCTAGACCTCAACACCAATTCACCTCCATTCGCAATTTCTCTTTGG CTACTATGTCTTTCCCTGACTTCTGCTCTCCAGCTCTCTGGGCTGCTGCTTCCACCTGTTTCATCTGA CTTAGGACCCCTCC
stSG1243 b	225 G A ---			ATTGGCAATGGGAAATGACACCAATCATTGATTACAGAAATGGTTTATAATCCTCCTCTTG AAATTATGTTTCCAGCCAGCATGTAGCTTATGCTGCAATCCAGCACTTCGGAGGCCAAGGAGA AGGATCGCTTGAGCCAGGAGTTCCAGACACCGCTGGGCAACATAGTAAGACCCCATCTCTGTTTTT TTTAAAAAGAAATTCTGTTC[G/A]AAGTATTCAGACCAAAGGAGGT
stSG1345 b	60 G A ---			AACTGACGTATCACAGGGGCAAGTATCTCTGTCTATAAATTTGAACTAGTTTGCTTCTTAC[G/A]CGCT TCACATTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
stSG1345 a	54 T G ---			AACTGACGTATCACAGGGGCAAGTATCTCTGTCTATAAATTTGAACTAGTTTGCTTCTTACGGCGCT TCACATTTAGCATGGGCCAAATTCAGGAGATGCCATGCAATGTCCATAAATGGGGCAA
stSG1385 b	117 T G ---			TTAATGTATCCAGGAGGGGCCAGGGATGGAGGGGGTTGAGGAGCGAGAGCGAGTATTTT TGGTGGGATTACCACTTTTCCCATGAAGAGGGGAGACTTGGTATTTGT[G/T]CAATCATTAAAGAA GACAAAGGGTTTGTGAACCTTGACCTCGGGGGGATAGACATGGGTATGGCCTCTAAAACATGGCC CCAGCAGCTTCAGTCCCTTCTCTGTG
stSG139	69 T C ---			TCGTCTCCTTTCCAGTGTCTCTGCCAAGCATCCCATGATGTTGTACCCGCACAGCACTTTGTGTCT TTCGCTTTGAGCACTTGCCACTCTGGTGTGCTGCTGCCACTGATTTGTACTGTCTGTGCTGCC
stSG1427	103 T C ---			GATCTGGTTCCAGACAAGGCTGATTCAGAGACTCCACGTGGTCAAGGCTCTGTTGTTCATCCCT TGCTCTCCACTTCCAGTTTGGCTTCTGTCTCTCAATGAGTCTCTCTCCATGTGGCAACAAGATGGC TACTGGTGGTCCAGGTTCACTCTCTCAGCTTGGAAATCCAGCAGCAAGAAGATGTCTCACTCCCA AAGTCCATAACTCAATCCTTGGGAAG
stSG1471	50 A G ---			CCCTGGAGTTTCTGAACATAGGAAGAGAAATGCAAGTCATGTGTAGGTCC[G/CTCCCTTGCATGA AATGTGGGAGAGGGAATAAAGTTAGGCAACATTTAGCAATCAACAGAACCCCTTCCCTATCCTACC GCA
stSG1483	44 T C ---			CAAAACCAAAATCCTTCCACGATATATTACTATTAGTCTAAGT[C/TTT]AATTCAAAGTTGAGA ATGACGAATTCAGAATTCTTTCATACATAAATTGCTTCTTCTAGTCTGCAGATGGTA
stSG1696	67 C G ---			CACACCCACAAGTTTCATGCTAATGCCAAGTATCAAGTCTTGAGGACAAAGGCAAAACCCAGTGTGCA [C/G]AATGTGGAGGATGTCTGTGTCAGCTGTAGTTACTAATGCAGGAAACCCCAATGCAAGAGGAA AATGCCTGA

stSG1847 b	95 G A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAATGCTACCCCTAAATGAAGAATT AGAGGTTAAATAAAACAAGTGAGAGACC[G/A]TTTACTTACATCAGTTCGGTTTATAGACATTTGAA TCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATGATCACTGTGCT TCAACACAACCTG
stSG1847 a	49 C A ---	---	TTGCAGACAACAATGGAAGCTTTAAACCTCTTCAACACAATGCTACC[G/A]CTAAATGAAGA ATTTAGAGGTTAAATAAAACAAGTGAGAGACCGTTTACTTACATCAGTTCGGTTTATAGACATTTGA ATCATATCTGAATGACTGACTTGTTCCTCAATGTGAAACCAAAATTAATAAATGATCACTGTGCT TTCAACACAACCTG
stSG1897 a	83 A G ---	---	CTTAATGCCCTTCTCTCTCTGTCACAGGAGACAGATGGTAACATAGAGGCATGGGAAGTGG AGGAGGACACAGGACTT[G]GCCACACACCTTCTCTCCGGTCTCCCAAGATGACT
stSG2022 a	86 T C ---	---	TGCTTTGAGGTTTCAAACTCTGAGATATCTATGCGAAGTTTATAAAAGTACATTTGATCAAGGTACAA TTTTTAACATTAAATACAT[C/A]TTCCATAATCTCATCTATTTAACATTAACACAGGCCTTTGTTGT TGTTATTTTTTCTCCCTACAATATTTCTGACTCTGTAGGACAGTGGCCTCAGTTGGGGGTTGAC T
stSG2076	104 C G ---	---	AAACGTTGCCCAAAATTGTGTTTCAGTTTCACAAGTATAAAATAAGACTTCTGAAAAGTTTACA ATTAGTTATAAACACACTTAAGAATATATTTTGACATT[C/G]ACATCACAGTGGGCATTTT
stSG2108 c	71 A G ---	---	TTGAGCAACAATGATTGCGGAATTGGGCGAGCTCCAAACCAAAAATGATT[C/G]AGGGGCTCCACAG GAGC[A/G]TAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2108 a	49 T C ---	---	TTGAGCAACAATGATTGCGGAATTGGGCGAGCTCCAAACCAAAAATGATT[C/G]AGGGGCTCCACAG AGAGGCATAAGGGGAAGACTTTTATAGGACAACTGTAGAAGTAAGCAAGCAGACGTTTGATTG GTTACAGTTACACAGTTGTCTTATTTGGTCTATCTTATTGGGAAAGTCTGTAGTTATGTAATTGTAAG TTTGTGGGCTGTGCTGA
stSG2141 b	173 A G ---	---	TTATTCAGGGGACAAAGCTGCACAAAGGAATGTTCTTCTATTATTTAAACAATGACTGCGGTGAC TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCACTGGCATGGCGATGGTGAGGTGGGT GCAGTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAG[A/G]AAGTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATTCTTGTGCTCTG
stSG2141 a	113 C T ---	---	TTATTCAGGGGACAAAGCTGCACAAAGGAATGTTCTTCTATTATTTAAACAATGACTGCGGTGAC TGAATCTGACTGTGTGAATAATCTCAGAATGGCAGCACCACTGG[C/T]ATGGCGATGGTGAGGTG GGTGAGTTCCCTGTGGTCTCTATTGCTTGAAGAGAGAAAGTCCCTATTATTATTTAAGGC AGTTTTCAGAGCACTGGCATTCTTGTGCTCTG



stSG2148	50 A G ---	---	TGGGAACAACCGGCTAGTCTGAGTCATATTTTGTAGACCGTGATTTCIAGIAAGAAACAATAA ATGTGGATTAGAAAGGAACATCCATTACTGTATTTTCGATACTTGTGATGTTCCACAGACGAGCTC ATCAC
stSG2175	68 C T ---	---	CTCAATGAGGACTCCATCAGCCAAGCGTTTATATGGCAGATGAGCTGCTACAAATCTGTTGTGTGCT [C/T]GCCGCGTGACTCAGCTAATGCTACCGGGTTGGAGCGCACACGAGCCAGCCACCTTTTCCAT ACCTGGGCAGAGGGAAGGAGTGGAAGGACCA
stSG2189	41 C T ---	---	CAAGTGTGAAAGCTGGGATTGGAGCCTGATATTCACACTA[C/T]CTACATTCCTCCAGTATAATA GGAACCTCATCGCTAACTTTGAGCACCTTAGTGTCTGAGTACTTCGTATAGGTTATCTCAATCCTACTC CAGCTTTGCGAAC
stSG2200	49 T C ---	---	TGTTGATGAOCATAGAGGATGCAAGCTCCGGGCTGGTTCTGTATGATG[C/T]TTATATTATGTAT AATGTCTTACCTGATGATACCCAACATATTACTAGCCTTATAGATGAGGATGGCAGCTTGGCTG GTCAAT
stSG2243	85 G T ---	---	CATTTCTGCCTCCTGCTCCAGTACTACCCGTCAGCAACTGCCTCTCGTATAAATAAGTATCAA GATGTCAGTAGAAAG[G/T]AGAGCATCTCTCAGCCCTGGAAACAGAGTGTGGAGCTTCAGCT
stSG2257	65 A C ---	---	TCAGTGATTGTAGGAGCTGGCTAAGTCACTGTCTAACTCTGTGAGGCAGGCTATCAGAAGGCGCAG[A/ C]CTGTCAAGAACTCTCGCAAGCACTGGGCTGTCTCTCAGGCAGAAATTTCTTCT
stSG2306	67 A G ---	---	GTCATCAGCGTAGAGGTCACTGGTATAAACAACAGTAGCTATATGATATTTGGGAACATATTTTACA [A/G]TATGCTCCCATTTGGGTTTTCAAACTGATACAAACCATGAGGTGAACACTTTTCACTGTTTCACAG TTCTCCAGAGA
stSG2334	70 T G ---	---	GAAACTACCCACAGCATCATGTTAAAGAAGAGAGATGAAGAAATAATCCCGCAAAAACA AAAAT[G/T]GCAGTGGAGGGGCTGTGGGAGGGTGAATG
stSG2339	63 T C ---	---	AGAGCAGAAATGGTGAATCAACAAGACCTCAAATTGTCTTGACTGCAGAAGTAAGTGTGTAC[C/ G]TTCTCAGAGTCAOCATTACGGTGACTGTGTCTATTCTGGCTGTCTTCTTCAICA
stSG2465	76 C T ---	---	CAAGACTAAGAAGCCGACCCGAGTGGTCCACTCAAAAAGAGATTTCTGATTCTACCTCAAAATG CAGAAACCA[C/T]TACAGATTAAAGAGAAACACACACACACTTTGAGAAACTCGCCCTTCTC ATCTTCAAAGTGTGGGTATGCA
stSG2549	140 T C ---	---	TTGCAGGCTTGTATTCACAATAACAAGTCATGTATAGAGAAATGTAATGATACTTGAAACCAA GATATATAAATATTGAAGTCATTTATGCCTTTTGATGACTGGTTAAATATGCAAGCAGCTAAAG GAATAT[C/T]TACACCACCCACCCCTTTTAACT
stSG2577	123 T G ---	---	AATTGCCAAATGGAAATTCAGAGGATTTTAGACCAACTTTGCCCTGTTGCAATCCAGTTTGGT CCCAATATAGGCCCTTCTGCAAGAAGAGATCAATGCCGAACCGAACTGTGAAGCA[T/G]GAACAATC CCGGCCAGATTAAATT

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stSG2577 a	121	C T ---			AATTGCCAAATGGAAATTCAGAGGATTTTAGACCAACTTTGCCCTGTTCATTCGCCAGTTTGGT CCCAATATAGGCTTCTGCAAGAGAGATCAATGCCGAACCGAACTGTGAAG[C/T]ATGAACAATC CCGGCCAGATTAAATT
stSG2700	58	G A ---			ATCTCCTCGACTGCTTTAGTGGGAAAGGAATCAATTATTTATGAAGTGTCCGGCCCC[G/A]AGTCAG TCAGCGTTTGGCGGAAATAAACCACTGTGTCAGAGAGAGGAAAGGCTACTTGTAGCCGGACACCA
stSG2724 b	101	T G ---			AAACAAGCTTTGTCAATTTCCACTACATTTTGTGTCTTTTATTAATTTGCAATGTCTATAAT TTAATACTTATATCCAATTGCTTGCATAATCAAT/GTTTTTTTAAATCCTGGGTGTTGAAAGAAC
stSG2776 a	65	G A ---			GTGGCCGATCTTTACTTTCCAGAAAGCGGTAAATAAAACCTGTAGAAAGTCTCGAATATGC[G/ A]ATTGGCCCTTTGGAGTTAGGCCAGGAACCTTCAACAAGGACACTGCTGGCCAACCAAAA ATATCCACTAATCCGAATATAGTAACCCCTGTCTGTCCGAATG
stSG2791 b	109	G T ---			AAGGAAAGGTGGAGGGAAGGAAGGAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTACTTCTGAACGGTAAACTAGCAATTTTAATAATATT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2791 a	100	A G ---			AAGGAAAGGTGGAGGGAAGGAAGGAATTACAATGGTTAGAAAAGAGCAACTAAAGATTATTTC TATTACTTCTGAACGGTAAACTAGCAATTTTAATAATATT[G/T]GGGTCCACTTAAATCTATTA AAGCAGAAAGTGTAAGCTATCTCCATTAGTGAAGAGATGAAGTGACAAAACCAATCAG
stSG2826	85	C T ---			CCGCAATTTTCAACACACATTTCTATGAAACTAAGGGTGGATCATGTACAAACACAAAACAAGC TCCCTCCCTCCAAAACAAC[C/T]GAACAAAATAAAGAAAGAAACCCATGAATGCCCAGGTTTA ATTTTTTTCC
stSG2850	88	G A ---			ATGGGTGCATTGTAAAGGCAAAATTAATACTTTTCAGGCAGGGCTGGCAATTTAATGAGCTGA TGTGTCCCAAGGAGACGGCC[G/A]GGCTCACACATCCCATCAATACTCTCCCAT
stSG3031	71	T C ---			ATACTCAGGGGGCTGAAGGCAATGTGAAGAGTGAAGTCAAGTCTGGCAATTTCTGTGGTGTGAGC AAA[T/C]GCCCTTTATTTAATGATTCAGACATCTGGGCAGCATAGCT
stSG3058	81	G A ---			GTCCCAACTCTCTCTCTTAGAGAAAACCTGTGATTACCTCAACTTGAATATGAACTGTGATTG AAAAAGTCAAAAC[G/A]TGAAGAAGCATCAAGCCAAAAGGCAAAACTGGCTGAGGC
stSG3092	94	T G ---			CAGCATCTCCAGAACATTCCTAGAACTGAACCATTTCTGTCACTATTGAAAACAAAGCCAAAGTTC CAAATCCAAAATAATAATGAACGTGC[T/G]GATAAACATTCTTCTTATGGTTCCAGCCCCCTACTTT AGTT
stSG3230	95	A G ---			AAGAAAGTACTTTGGTAGCTATTTAATAAGAGGGGGTGGGAATGAATGTCGAGATACGAGCACCTG CATCTTTTAGTCAATTGTCAGTGGAGTC[G/G]GTGGGGTGTCTAAGTGTCTGAACTGAAGTAG
stSG3245	160	G C ---			ACATCTCATACCCAGTAAGATGCAAGAAAGGAATATCTGAGAGCAAGCAGCCCTGCTCCAGGGGCC CAGGTATGTAGAGGCCAGTGGGGTGGCCACTTGGTGTCTACACCCCCCTGCCATCCAGTCTG GCCCAGTACCTACCTGGGAGGT[G/C]GTACTTGGCTTAAGTACTTCAATGCTTTAT



siSG3265	42 T C ---			AGGTGAATGAGTTACTAAATGTAGCATTATTATTAAGGAAT/CJGCATTGTGAATAGTTTCTCAG TTTTCAATTAGGAAGATGATGATTTAGCCACATTCAGTGTATGTTTCTAAATAACACAATCGAC AGGACTGTCTGTTAGTACAAATGGAGGACAGCTTTTCAGGGCAATGGGATTTCTTGATAATGCTAA ATCTGTCTTGTGAGCTGAATTTCTTGGGCTTATGTGGCAGTGTGGTAAAA
siSG3269 b	141 C T ---			TGTACTTACTGTGTATCCTATCCATTCCTTCCCTGAGCCTGGACTGCTTCCAGGGAGACTAGG AGTGAAGGGAGGAGTCTCCCAAAGTTACCCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCTAAA GCATGA/C/TTGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAAACT
siSG3269 a	24 A G ---			TGTACTTACTGTGTATCCTATCC/CAGTTCCCTTCCCTGAGCCTGGACTGCTTCCAGGGAGACT AGGAGTGAAGGGAGGAGTCTCCCAAAGTTACCCCTTTAAGCTTGATAATTAGCTCCATAGCCATGCT AAAGCATGACTGTAGATCCCAAGTCCCTGACACATTTTCTTCTAAGAAACT
siSG3284	130 C T ---			TTAACTCAAGAACTTTCAGTTACAGGAAGATTATCTAATATTAATGACTAAATTACAAAAAGC ATAAAATGTTTGAAGCCATTTTAAAGTTGTTTGAATCCATATTAGCACTCAGACTTCCCCA/C/T TCCCTAACTTTTGTTAATTGCTGTAAATGGGACATTTGTTGTTTGTATCTACCC
siSG3292	99 A T ---			GTCTCAAGTGAATCTGTAAATACATTTTAAAGTCTGACTTCAATCGGTACATGAGGCTTAGACATA CACATCATTTGGACAAGTGACTTAAATATCTAA/C/TTACAAATCAATAGCATTTTCTAACTTCAA
siSG3323	26 C A ---			TAAATGTCATATCTTTAGCTCTCAGT/C/AJCCAGTGTATCCATTTTCCCCAGCCGTAGAGCTTTTCTG TTTCTGTAGATTTGCCGTGCTGGACATTTGATATAAATGGAGTTGCTGTATCATGTTGCACTTCTCTC ACCTAGCATGATGTTTTCAGACACATCCATGCTGTAGCATGCGTCAGTGTTCATTCCTTTTAA
siSG3369	69 C T ---			GATCCCCAGTATTATTTTCTAAATTGAACCTGTTGTGGAAATAAAATCTGAGGACCCTCAGAG GG/C/TATAAGGGAACCCCTCTTTGTCTTAGTTTATAAGGACTTTCT
siSG3398	125 G T ---			CAAGACTGTAAGAACGTAGGCTTGTGAGAGTGAAGGAAGGATGCTCGAACTTGCCAGGACTCAGG CTTCAGCTTCACAAATCCCGAGGAAGGAATGACATTTCCAACTGTACCTTTGTAGC/G/TCTGGGT CAAAGTCTAAGAGGAGACAAATAATAGAGACT
siSG3416 a	43 A G ---			TCCTTACTCTGTTAACTCAGTCTGGAGTAAAGGATGCAATCACG/C/GTCACTGTAGCCTGGACCTCC TGGGTTCAAGTGATCCTTCCACCTCAGCCAACTGAGTAGCTGGCTGCAGGACAAGTCAOCCATGCCCTA CCTAAGTTTGTAGAGACAG
siSG3424	173 T A ---			GTAAGACAAGGTTTGTCTATGTTGACAGGCTGGTCTTGAACTCCTTGCTTCAAGCGACCGTACCA CCTTGGCCTCCCAAAGTTGCTGATATACAGGTTGTGAGCCACTGCCCCCGCGACTTTTAAACTGAAT GTTGAAAATCATCTGCTCTTTGCTGGGTAACACTGA/C/AJCAAGTTGCTTAACTTTGTGAAACCAC TTTCCCTTATCTGTAAACAAATGGACAAACAGAACTTTTCCCTTCTCTC
siSG3436	88 T A ---			GTTTCATGTTAAAGATTAGGAAGCTGTGGATGTGAGGGGTCAGGTGATGTGAGGCTCAGACAGA ATGAGTGGCAGAGAGGGCCCTT/AJGAAATAGCTTACTGTGTTTCTCTATC



stSG3483	103 C T ---	---	GATACAGAAGATAGTGTGGTATGGATAGTATGAAGGACAAATAATACAAATATATTTATTG AAATAACAAATAATGCATACACAGCTCAATGGGTCAC[C/T]TGGAAACAAACTTGCTTGACTATATTA CTGA
stSG3491 b	71 G A ---	---	CAAGATACTTCATTGTCCTAAGTAGTGCAGTGGCAATAATTTCTCAGCAACAGGACGATTTG AAGA[G/A]GTGGAAATTACTGTGCAAGGAGTACTTTACCTCCAATAGCCTGCAATTTAGCAGTCTGA ACAATCTTCTAATCTTTTACTGGCACCTGTGGATTCTATTAACTCATTTATATACTATTTTCTGTGATG ACAGAAATAAGTTAAC
stSG3523	33 C T ---	---	TAGCCATCTTACTCTAGTTCTTTTGGGTTTTA[C/T]GCATATATGTGTACAAACACACACACACC CCTAATTCCTCAATGCTCTTGGCATAAGTTTTATCTCTTACTGGTCTC
stSG3536	213 A G ---	---	AGTACAAACACAGATTTAAAGAGCTCAGCAGTATTGACACGCTGGAAATTAATGGAGACATCCACTT ACTGGAAGTAAGGAGCTGGTAGCTACCTACACAGCTGTACAAACCAAAATACAGAAATGGCTTC TGTGATACTGGCCTTGTGAACGCATCTCAGTCTATTGTTTATATTGTTAAATGAGCTTG TGCACCATTAGIAGTTCCTGCTGGGTGTTCTCAGTCTTGCCATGAAGTATG
stSG3583	112 G A ---	---	GAAAAGCTTAACATACGATCCATGTGCAACCCCAACACAGGATCTACGAACTCTGGCATGATCCA CATCGCTACACATACCATGCTGGAAGTGCACATCCACACAGGCAC[G/A]TAACATACACAGTACTGT CTAGTTATCAACACCTAC
stSG3586 a	60 G C ---	---	CCTAGTAACATAGTGAGACCTCGTCTCTACTAAATTTAAAAATCAGGTGTGGTG[G/C]ACG CCTGTAGTCCCTACTTGGGAGGCTGAAGTAGGAGGACTGCTTGAACCCAGAGATGGAGGCTACAGT GAGTTATGATGGCGCCATTGCACCTCCAGCTTGAGACTGTTTCAAAA
stSG3589	101 T C ---	---	ATATAGTGTGTAGCATTATAAACTCCTTTAAAAGCAATCTGGCCATATCAAAAGGCAAAAAGT GTATATACCACCTGGCACAAAACCCCAATGA[T/C]CTATTTCGAAGAAATGTATCCAGATGAAA GTATCCAACAACAAAAGCTATATACAC
stSG3590 a	70 A T ---	---	GAGAGATGAGCTATTATTCTTTTACTTAATGAAGATGTAAGAAATGATCTTCTTCTTAAAAAAA AAA[A/T]TTTCTCTGATGTCCTTGACCCCTGTAGGAAACACATTCAGTTTCTACACT
stSG3619	78 A C ---	---	CAGTGAGACTTCTCATTTTATAGCAAATACATTTTTCAGCTTAAATTTTCTTGAATTCATATACGCT TCTGTCAATTT[A/C]AACAACTCCAGAGAAACTGGGCTCTATATATTTAAG
stSG3644	40 T C ---	---	ACATATGTAAGTCCCATTAGTAGCCATATTTAGGATGAGA[T/C]GGATTGAGAGGCATGAACCAAGG ATGCGTAATAATCATTATGAAATAATAAGTTATCTGGGAAACGGCCATTTGTCCAACATTTACTAA GTGCCCTACTA
stSG3646 c	70 G A ---	---	CTCATAATTAGATTGAGATTGTGCATTTTGGCAAGAATATATGATGATAACAATAATATGTCTTACT GGT[G/A]ATATAACTTTGATACTTGGTTAAGATGGTGCTGCTAATTTTCTCCATTGTAGAGTCATT CTTCCTTTGTA

stSG3646 b	55 A G ---			CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATGATGATAACAATAA/GJATGTCTT ACTGGTGATATTAACTTTGATACTTGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3646 a	43 A T ---			CTCATAATTAGATTGAGATTGTGCAATTTTGGCAAGAATATATG/AJTGATAACAATAATATGTCTT ACTGGTGATATTAACTTTGATACTTGTTAAGATGGTGTCTGCTAAATTTTCTCCATTGTAGAGTCATT CTTCTCTTTGTA
stSG3693 b	85 A C ---			ATTGTTCCCTGAACATTCCCGTGGTCTCCCTCTGAAGCCGATGACCATCCAAACCTGGACTCACCT GAAATATCCTACGAGGC/A/CJTCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAATAAGG
stSG3693 a	30 C T ---			ATTGTTCCCTGAACATTCCCGTGGTCTCC/CJTTCTGAAAGCCGATGACCATCCAAACCTGGACTCA CCTGAAATATCCTACGAGGCATCGCCCTCCGAGACTGACGATTATTAAACCCACACGGAATAAGG
stSG3698 b	145 G A ---			TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCAATCCCGAGGTTGCTCTCTGACTTCCACCAT TCACTGACTTTTATTGCCAGAGAGCTCCAGGAATCCACAGTTCTTGGAAGAGAGGGGCTCTAAGTCT TTATTGGG/G/AJAGAATACCCACCTTCCCTCACTGCAGA
stSG3698 a	51 C G ---			TCTTGCCCTTTGTGTACCCCTAGAGAGATGGCACCAATCCCGAGGTTG/C/GJTTCTGACTTCCA CCATTCACTGACTTTTATTGCCAGAGAGTCCAGGAATCCACAGTTCTTGGAAGAGAGGGGCTCTA AGTCTTTATTGGGGAGAATACCCACCCACTTCCCTCACTGCAGA
stSG3724	107 C T ---			ACCAGCCTCATGTGCAGAGGGTCTCTGCTGGATCCCACTGGAGCCATCCCTGGGCTAGACTTCT GTCTCCCTCACTTCTAAATGAGTGTCTCAGTGATGTGAAG/C/JTACACAGGAGTCCCTCAGGGCAAA GTGGCTATGCTGGTGT
stSG3725	104 G A ---			GCCAAACAAAAGATCTTTGGAGTTTACTGACGGCAGCAGTTAATAGCACAGTCAACAGCATTTAA ATCAAATATATTATACAGCCAACAGCAACAGCCC/G/AJAGCAGGAATCGGCACATAGTCATAA ATAACATCAGGGGTAATAACGGCACATTTA
stSG3751	128 G A ---			CGGAAGAAAGAAACACAAATCCACAGGAACAATCTATGGTTCATACCTTTTAGAAAGATGATTTTG AGGGCTTCAGTATTTAAAGGGGAAAGCAGGCTGGAGGGGAAAGAGAGAGGATATGTGCC/G/AJTT GCTGACTCCATGTGTGCAAGAG
stSG3787	49 T A ---			TTCTGTGCAAAAGAAATCCACATCATTGTTGGTAGCAGAGGATCTCTTAT/AJAAAGTTCCCTAAGA CACTGAGGGCATAAACCAACAAATAAATAAGGAGTGATAGGCTAAGCAGTATCTTCCCT
stSG3880 b	115 G C ---			GACAAGAGGAAGAGATGCGCCAGAGACAGGGCTGGGCAGCTGGGGTCCCTGAGTGCCAGGGCC CAACACACGTCTGTGGTCAAGGCCCTCTCTGGGAGCAGGTTCTA/G/CJGGCACGGAGGATGCAG GGCTGGAGGGGACCCCACTCGGGGACCCAAAGGAGTCCATTCTGCCCT

stSG3880 a	36 G C ---	---	GACAAGAGGGAAGAGATGCGCCAGAGACGAGGCTG[C]GCGCAGCTGGGGTCCCTGAGTGCCAGG CGCCACACACAGTCTGTGGGTCAAGGCCCTCTCTCTGGGAGCAGGTCTAGGGCAGGAGGATGCAG GGCTGGGAGGGACCCACCTCGGGGACCCAAAGGAGTCCATTCTGCCCT
stSG3895	44 A G ---	---	AATCAGCCATTGTACACATTGCAGCTATGTATTGTTAGTGTGTT[AVG]TTTTTTTCCATTAACTAA TACATGCCCTCATAGATATATTCAATTAGTGTATCACCATTGGGAACAAGATGCTGATTGCTCAACTG AAAT
stSG3902	104 T C ---	---	TCTGTTGAGACTGGAGAGACGAGTACCAAGCACCGACTCTGGTGGGAACCTGGCTTCCCTGATAACA TCATCTATTTACCTAAATGTGAACCTGCTTTCTTTTC[C]TCAGCTCAATAGCTTAACATCTAATTC ATGTTGCTCCCTTTGCTGGACAAT
stSG3935	50 G A ---	---	GGGTGCTGTACGGACAGGCACACCCAGCAGTTTCAACAAGCAATTTGTCC[G/A]CTAGTGTGCAGGC TCCTCCCCAGTTTCCACAGGCTGAGTACTATGGGTCAACAACCTTCTCTGGACGT
stSG40	25 A G ---	---	GAGGAAGAGGTTGAAGAAAGTGCTGA[G/A]AAATATATTTAAGATTTCTTGGGAGAAATCTCGTGC CCAAACCTGTGTATGGATCCCTTACTATTAGATAAGGAACAATAAACCCCTTGTGTATGTATCA CCCA
stSG4009	32 A G ---	---	GTGTGGGCTGTCTGATGATGAATGGCGGCTC[AG]TACTCTTTACGGTCTTACACTTTTATGCTCCT ATGAATTCCTGATGGCTTTAAGGGCTGAACCATATCTGAAGGTTTCCACACTGCTTACA
stSG4033	123 T C ---	---	AGAAGCCTTGGGACAATGGCAGTGCCCTTCTGAGTAAGACATGAATGCCATCTGGAGGATCCATT TGAAACTACAGTGCAGTAACCAAGAACCTAATGTTTCAAGCATAAAGGTACTTTT[C]TGTGAAC AGTGGGCAACAC
stSG4038 a	29 G A ---	---	GCTGAGAGCAGTGTACAGCCAGCCTGTG[AC]GCGAGGCCACTCTGTGCAATAAACATGTTCTGCC CATGTTCTCAGTCAGGAGGTTCCAGGCTCCCGGAGAGCACCTGAGGGTTCATCACT
stSG406	53 T C ---	---	ACTGTGTTCAACAGTATTGCGTTGTGTCAGACTAGGAAGCTAAACGAACAATA[C]GGTTTAGTT TTGCTGAAGACTGGCCTTATTAATGGACAGCTTTCCTAACAGAGATTATTAACCTTTATCAGGTGTT AACATCTGTTTCAGGAACATGGCA
stSG4095 b	55 G T ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTGAGTCACTATTGTCTGTAGATGTATTAG[G/T]ATAAAAA GTTTGCTTCTGTATACTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAAATCAAG CCTTGGACTAACCCAGGGCATTTGCCCTTCATCCTGG
stSG4095 a	27 A C ---	---	ATCTGGGCTGAATTAGTCAAGCAGGTG[AC]GATACTATTGTCTGTAGATGTATTAGGATAAAAA GTTTGCTTCTGTATACTTTAAAGCTTGCTTATCTCATCTGTAAACCTATGTGTCTTGAGAAATCAAG CCTTGGACTAACCCAGGGCATTTGCCCTTCATCCTGG
stSG4120	65 G A ---	---	TGCATGTTCCACATCTTTTCATACAGCAAAATGTATAATAAAGTACCTTATGGATAATCAC[G/ A]CTTTTCCCTCAGAGAGCCACAGTTAAACAGCTTCCAGCACACCATTATCCACCGAGCT



stSG4128	54 A G ---	---	CTTGGCAGATAAGGACTCGTTTGCAGATATGACTTTCCTTTGTGTACATTTCT/AGTTATATTATTT TACTTCTTCTGAAATGCCACATAATTTGCAATAATGATTCACTCCTTAGCTCCAAAGCAAGTCC TTTATCAAATGCAAATGTTCCAGAGGG
stSG4209 b	128 G A ---	---	CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAGC AGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTC/G/AJGC AGGGGACCCACGGAGGCGACAGGTGCTTTGATGCTCCGGAAGAGCTGAGCTCCATTCCA
stSG4209 a	65 G A ---	---	CACGAAACAGATGCAGCTACACAGTGTGTAGGACCGAGGCTCACAACATCCACATGGCACAAG /AJCAGGGCCGGCCACTCCAGGCAACGAAGCCACCCCGAACCTTGCAGAGGCCGCACTCCCTCGGC AGGGGACCCACGGAGGCGACAGGTGCTTTGATGCTCCGGAAGAGCTGAGCTCCATTCCA
stSG4254 b	31 G A ---	---	CATTACCCAGAACGCCATGGAGGACCCAGAGC/G/AJCCACGGCCGGGACTCCCGCGATGGCTGGGGGG GCTATGGCTCTGACAAGAGGATGAGCGAGGGCCGGGGTGCCTCCTCCAGGGGCGAGACGTGAC TGGGGGACCATGGCCGAAGAGAGGATGACCGGTCATG
stSG4301	81 T G ---	---	TGCAACAGCTCTGAGAGGAAATCCTTGGCAGATCAAAGAGAGGGTAGTGGTCCACACTTTCCAT TTAAGCAAATAAATTT/GJAGCTTCTGAGTAGTTGTTCCAGTTTCACCCAACATTTTG
stSG4331 b	71 T G ---	---	CTCACAAGGCCAACACAGAAAAGATACAAATACATTCACAGCTAATATTTAGTTTATGACAC AGAGT/GJTTTTCAAACAAGTTTAAGTGTACCTGAAGAGCATGTTAAAAGTTTAAGTTATCACTT GGAGAGCAGATTCTTGCCCTCGCCCTTGATGATTTCTTGAGGGGTGTGC
stSG4340	76 G A ---	---	TTTTGCAACAACATGGATGGACCTGGAGGCCATTAAAGTGAAGTAATGATACAGAAAGTCAAAAACC ACATGTTCTC/G/AJTAAGTGGGAGATAAACAAATGTGTACACCTGGACGTGGAGAGCAGAA
stSG4361 b	109 A C ---	---	TTCCCAACCAATTGAGTGACAGAGCTCAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGGCAC AAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGACCTTCACAACCTAGAAACGACTC AGCGACTTTTCTGTGAGCAAATGTCGAGG
stSG4361 a	24 T C ---	---	TTCCCAACCAATTGAGTGACAGAGCT/GJ/CAGTCATGCAGAACTCAGGTTTGCATGACTCAAAATTAGG CACAAAGTTCTTGGAATTTCCATAAGGGATAACTGCATCTTTTGACCTTCACAACCTAGAAACGACTC AGCGACTTTTCTGTGAGCAAATGTCGAGG
stSG4376	73 A G ---	---	TTTCACTGCTACTGGTTTCGGTGTCTGAGTCTCAAACTGCTGTTTGCAAGTGTCTTCCAAAGGGGAG AACAGI/GJCTGGAACTCGGGCTCTGCAAGAAGCCATTCTTCCAAAGCCATTCTTCTCAGCTGC
stSG4381	50 T C ---	---	GAAGGCCACAACACTCCATAGCCAGAGAAATGACAACATACGATTTTCTTT/CJTCAGTCTTGTAGT ATCCACAGTAGTGATGTCTGTCCATGTACAAGTGTCTGTCCAGAACACCCATTAAATTCATGCC
stSG4410	79 A G ---	---	ACCAATGGTTCTGCTATGTGCTATCCGATATTTTGGCCGATCTGAAATACTGCAAGGGCTTAACCAT TCAAACACCCGC/AJTGACAACGAACCCAGTGGACTGTGAAACTCAGGCTGCAGGAGGGTGGCTTGT CAGCTGGGT

[illegible]



stSG4850 8	38 C T ---	---	GGAATCTAACTGGGAATGCCGAGAGGAAGGGGCTCTCTGTGCACCTTGACAGGCCACGTCAGGAG AGCCAGCGGTGCTGTCGGGAGGTTTCCAAGGTGCTCCGTGAAGAGCATGGCAAGTTGTCTGACAC TTGGTGGATTCTTGGGTCC
stSG4879	86 A G ---	---	AACTCTGAAGGGGTGACCTCAACCCAGCCCTTGTTTCTGTGAGGTCTGCTTTTGACAGAAATGGCCTG CCCTGGGACTGGAGCAG[AG]CTTGGGTGAGCTCTAGGTGGAGGGTGGTGGAGGGGCATAGAAAT AAACCTTCC
stSG4885	104 G A ---	---	ACTGGACTGGCTGCTTGTGAGCCGGCTGAGCGGGCTGGGACTCGGCTGAACCACTCGCTCTTCAG AGACTCGCCCGGTGACCACTACGCTCTGCG[AG]GTGGGAAGCAGAAGCAGGACC
stSG4896	112 C T ---	---	AAACAATCAAAACCAATCCCGCAGTCTATGTACAGGGCCACTCCCTGCTCTCTGCCATAGAGA GGTTGGGGGCGAGCTGAGGAGTGGTGGGCTGGGCACTTTCTCTCAGCCACAGGCCCTGAGG AATTAATTGACTG
stSG4932	22 G A ---	---	ACAGTGCCGATGGTTACACAAT[AG]TTGTAATGTATTTAATCCACTTACGAATGATTAATAATGA TAAATCTTATGTTATTTCATCACTACCAAAAGGCTGTGGTGACGGGTGCTGGTTCTGGTCT
stSG4950	24 A G ---	---	TCATGACTCCAGGAAAAGGTCT[AG]TCTTAGCTTCTCTCTCCCTACTTTCTCTACATGGTCAGC ACTGTAATGTAGCTAAGATATAGTAAGGCATTGCTCCTACCCCTACACTTCAAGG
stSG4957	136 G A ---	---	AGATACGGGCAAAACACTGGGATGGCTTCTGACAACTTAAGAGGTCTCCGAGTTATATCTGGTT GGGAAACACTGACCCAGCCCTTATCTCTCAAGACTCTAGTCATTGGCAAGGAGGATTCTAGAGCC CC[GA]GTGACACAGATGGGGCCCTGCTCTATATTCAC
stSG4961	91 C T ---	---	GAAAGTGCTCTGAGGAGGTGACTCTCCCTGCTGACAGGGGAAGGCTTAGCAGAGCTTTGTCTTAG AGGAGTAGATGAAAAGGAAAAGTA[CT]AGAGAGGGCATTCAGGCCAAGTCAGCAACACAGACAA
stSG4967	72 A G ---	---	ACTGGTGCCTCTCAGCAGATTCAAGGGTCTGTCAGGGCTGTTACACAAACTCAGTAGGAGTGCAA GGGCT[AG]TACCCCGGAGCTAGACAGCCCTGGGTTTGAATCTCACTTCTCCCTTTTCTTGTGTGC AACCTTG
stSG4997	22 T C ---	---	CAAAGGAGTAGGAGCCCAA[TC]TTTAAATGGTTTCTCTCCCTCATGCTATTTGATCCAAAAA CTATATACAAATTTGTAGCAGTCTCTGTATAGTTATTACACATGTTTAGAAGGGAGGAGGCAAGAA GGGATAGGGAGATGGTGATCCAAAT
stSG6312	37 C T ---	---	ACAGGTTCTCACACTTTGAGCCCTTAGTGCAAAAACA[CT]TATGCCATGCGGGAATAAAATGCTT ATCCAGTGGAGCGCTCCCTGATGCATTGAAATATTAGGATACTCAAGCAGAAAGAC
stSG6345 8	107 G A ---	---	GCTCTGTCAGCAAAATCTCCAGGACAGAAGCAACAAGACAGTAACACACATGTATGACCCCTTA CAAGTGCTTTAAGATTTTAAAAATGTGATGTTTGTCCAC[GA]TAGTTTCAGGCAATTAAGAATAT GCAACCCAGAGAAATTTCTGTGAAAACATTTTGTCTCTTTGGCCTGGTGTGGACAGAAAGGGTGGCCAA ATGGATTGAGTGATGAGCAGACATG



stSG6362	88 G C	---	TGTGAATGTACACTCAGTCTAACAAATACCTATTATTCTCTGGTTAAGAAAGTTTAGCAGGAGC CTCCAATGAGCACTGTATGTA[G/C]AGAAAAGGGAAGGAGCAGGAGGAAACAGATCTGCACAGA AT
stSG8010	62 G T	---	CACATCTGTGTTCTGGAGCAAGGGAACACAGAAAGGCCAGGAGTTTGGGTGTGCACTGG[G/T]T GTCTTTCAACTGGGTGGAACCAAACTGAGTCCTTGAAGTCTCGCTCTGAGGCTGCAGAAAGATAGA TGGCTT
stSG8022	53 G A	---	AGCTCCTGACTCCCTGTTTCACTGACGTGTCATGTTGGTAGCCTGAAATGGAOCAC[G/A]GTGGGAGTTAT TTACACCATGGAACCTGGAATACTCTACAAATCAATGCGTTTATTCTTTATTTTTCAGAGGGCAGGTT TATCAGCACACGCTGTATCTCC
stSG8032	67 G C	---	TGATTGTTAGGGATAAGTGGGCATTGTGTTTACAAATTACTTCCAAAGAAATTCAGAAATTGTGTGT G/CTGGAGGCAGGTAGCAAGATAAAAGAGGGAGGACAGCTGGGTTGGTAAAA
stSG8064 b	46 C A	---	AGCTGGCTCTTCTTCTGTGCGTTCGGGAGGCTTCACGTCTCTG[C/A]CCGTGTCTGCTGGTGGCC TGCAGGACCAGGGGTGGAAACAATGCCAGGAGAAATTCCTGTACATCAACAGGGAACA
stSG8064 a	23 G C	---	AGCTGGCTCTTCTTCTGTGCGTTCGGGAGGCTTCACGTCTCTGCGCTGCTGCTGGTGGCC TGCAGGACCAGGGGTGGAAACAATGCCAGGAGAAATTCCTGTACATCAACAGGGAACA
stSG8072	59 A G	---	CACCATCATCATCGAGTAGGCTGAGGAGCAGGAGGGGTGGTCTTGCTGTCTTAGGG[AG]TGCC AGAGCAGAAAGGAAGTCCGAGTATTAGTGGCCGATGCAGTTCAAGCCTGTGCTGTTCAAAA
stSG8100	40 A G	---	ATACACCCACACACCCCACTCAACCTTGATCAAAATTC[A/G]AAGTGTAACATAAGTATAAGAAT ATCATGACTAGTTAAAGATAGCAAAATACCATAAGGTACAAGTTCAAGTATTAGTATAACAAGTAT CTGAGTAACAAATGTCTTGGAAATGGG
stSG8102	138 T C	---	AAGGCTCCTTTGAAGCATGGTTTATTGTTCCATTAACTGTCTCAGCTATACTGAAGTATGATT GACAAATAAACTTGCATATATTGAGATGTACAGTGTGATGATACATGTATGTATACAATGTGAAA TGAT/CTGTGATAATCATAATCAATAATGGTATATTGGTTTAGGAAATGTGATGTT
stSG8105	110 A G	---	CAGTGGTTCTCAAACTCCAGCGTACACGAGGATGGTCTTGCTGTGTTAATACACAGATGACTAGGCC CACCTGGGAGTTCCTGTTGGAGTCTAGGCCCTGAGAAATATC[AG/TT]CTAACAAAGTCCAGGTGA CCCTGAGGCTCTTGGACTGGGAACATGCTTGAG
stSG8130 b	96 T C	---	GTGTGTACATCATTGGGAATGGAGGAAATAAATGACTGGATGGTGGCTGCTTTTAAGTTCAAAATT GACATTCAGACAAGCGGTGCTGAGCC[TC/G]TGCCCTGTCTTCAGATCTTCACAGCAGATCC
stSG8130 a	36 C G	---	GTGTGTACATCATTGGGAATGGAGGAAATAAATGA[C/G]TGATGGTGGCTGCTTTTAAGTTTCA AATTGACATTCAGACAAGCGGTGCTGAGCCCTGCTTCAGATCTTCACAGCAGATCC
stSG8145 b	124 T A	---	TTGTGGACTTCAAAATCTTCTTCAGATTTAAATGACATTATGCATGTACATATTTTAAAAATT AGACACATTTTAGAGAACACAAATTGTGAACACAAAATCTAAGAAATGAATGAGATGTT[A/J]CTGAAA TCTGATTCAACACTTATCTTAACTGACTTCTGTCAATCCTCTGCTGTGAAGG





ESTD-AT3a	--	--	--	---	---	AGACCTCAGTTTCTCTGTAAAGGGAAGTTTGTCTTGATCTCCATGGGCCAGCCAGCACTG GTGCCCTGTGAGTCTGTATCAGGTAGAGGAGATGGACCCAGGTGGAGAGAAATTTGAAAGGGCATTTG GAATTCAGAGCAAGAGACAGATATTAAGAGCTGGGAAATGTGG
ESTD-B3AR	--	--	--	---	---	GGCTGCCAGGGTTCCGTGGGAGGCGCCCTAGCCGGGCGCCCTGCTGGCGCTGGCGTCTGGCCACOC GTGGGAGGCAACCTGCTGTGTCATCGTGGCCATCGCCCGGACTCCGAGACTCCAGACCATGACCAACGTT GTTCTGACTTGGCTGGCGCAGCCGACCTGTGTGATGGGACTCCTGTGTGGTGGCGCGCGGCCACCTT GGCGC
ESTD-BA511	--	--	--	---	---	GGGCAACATAGTGAAACCCCATCTCTACAAAAATACAAAAATTAGCCAGGTGTGTAGCAAGTGC CTGTAGTCCAGCTACTTGGAGGCTGAAGTGGAGGATCCCTTAAGCCTGGGAGGTGGAGGCTGCAG TGAGCCAAGATGTGCCACTGCA
ESTD-BCL2	--	--	--	---	---	AGCTGGATTATACTCCTCTTCTCTGGGCGCCGTGGGTGGGAGCTGGCGGAGAGGTGCCGTT GGCCCCCGTTGCTTTCTCTGGGAAGGATGGCGACGCTGGGAGAACAGGGTACGACAAOOGGAG ATAGTGATGAAGTACATCCATTATAAGCTGTGCGAGAGGGGCTACGAGTGGGATCGGGGAGATGTGG GGCGCGCGCCCCGGGGCGCGCCCGCACCGGGCATCTTCTCTCCCA
ESTD-BCR	--	--	--	---	---	CAGTGGCTGAGTGGACGATGACATTGAGAAACCCATAGAGCCCCGGAGACTCATCTGCGCAAGA GACCAAGAGGTCAGCTTCTGTGTCGCCGGGAAAGGGAGGCGAGTGACAAGCTAACTCTGCTTCAA ATCAACCATCGGTGGACACTGTGTGGCTGCCATCTGCTGCGACA
ESTD-BRCA1a	--	--	--	---	---	AAGAAGAGAACTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAAGATCTCATGTTAA GTGGAGAAAGGGTTTGCAACTGAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGTAC TGATTATGGCACTCAGGAAAGTATCTCGTTACTGGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAA CCAAATAAAT
ESTD-BRCA1b	--	--	--	---	---	ACTAAATGTAAGAAAAATCTGCTAGAGGAAACCTTTGAGGAACATTCAATGTCACCTGAAAGAGAA ATGGGAAATGAGAACATTCCAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAAAATGTT TTTAAAGAAGCCAGCTCAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTA TTAATGAAA
ESTD-BRCA1c	--	--	--	---	---	ATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGTTAAATAAGGAAGATAC TAGTTTTGCTGAAATGACATTAAAGGAAAGTTCTGCTGTTTTAGCAAAAGCGTCCAGAAAGGAGAG CTTAGCAGGAGTCTAGCCCTTTCACCCATACACATTGGCTCAGGGTTACCGAAGAGGGGCCAAGA AATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAGGATGAAGAGCTTCCC
ESTD-C1R	--	--	--	---	---	ACACAGGTGCTGGCACTGGGGCTGGGATCCCTCTCCCTAATTTGCTCCGGGAAGCACATTCATCAA CCCAGTCAGTTTGGGGGACAGCCATGCACCTGAGCCTCTGTAGCCTTTCAACCATGCATTCCATCTAA GCTCTGCAAAAT
ESTD-C6	--	--	--	---	---	



ESTD-C7	--	--	--	--	ATATCGTGGCCTTAGTTACCTAGAGCTGGACAATCCTGCTGGA	---
ESTD-CB22	--	--	--	---	GGCAAGTTTATTGATAGAGAGGAATCAATAATGGCAATGAGGAGACATCACCTGGAATGTTAG GCAGTGCCTAACTGGGGATGGACAGACAATGGCAGTGCCAAACCATAGGGGGATACAAAGAC AGGCAAGGAAGGGTAGAACCATCAAGAGGAATAGGCTGTGACCCCAAGCAAGGAGGACCTAG TAACATAATTGTGCTTCATTATGTGCTCTTCCCGGCTTCTCTCTCACACAC	---
ESTD-CB23	--	--	--	---	TAGAACCATCAAGAGGAATAGGCTGGTGACCCCAAGCAAGGAGGACCTAGTAACATAATTGTGC TTGATTATGGTCCCTTCCCGGCTTCTCTCTCACACATACAGAGGCCCTACAGGACAGACAGCT CTCAGAGCAACCCCTAGCCCATTAACCTCTTCCCTTCCAGAGGACCTGAAACGCTGTCCACCCGA GGTCCGTGTGTTGAGCCATCAGAAAGCAGAGATCTCCACACCCAAA	---
ESTD-CB24	--	--	--	---	ACCAGGACGAGAGCTCTCAGAGCAACCTAGCCCATTAACCTCTTCCCTTCCAGAGGACCTGAA AAACGTGTTCCACCCGAGGTGCTGTGTTTGAAGCCATCAGAAAGCAGAGATCTCCACACCCAAAG GCCACACTGGTATGCTGCTGCTGCTTCTACCCGACACGTGGAGCTGAGCTGGTGGTGAATGG GAAGAGGTGCACAGTGGGTGTCAGCACAGACCCGAGCCCTCAAGGAG	---
ESTD-CB25	--	--	--	---	GTCTTCTTTCAGACTGTGGCTTCACTCCGGTAAGTGAGTCTCTCTTCTCTCTATCTTCGCCGTG TCTGCTCTCGAACCCAGGCGATGGAGAAATCCAGGACACAGGGGCTGAGGAGGCCAGAGCCACTG TGCACAGGTACCTACATGCTCTGCTGCTGTGTCACAGAGTCTTACCAGCAAGGGTCTCTGTCTGCCACC ATCCTCTATGAGATCTTGTAGGGAAGGCCACCTTGTATGCCGTG	---
ESTD-CB27	--	--	--	---	TTTCTGTTTCCCTGAAGATTGAGCTCCCAACCCCAAGTACGAAATAGGCTAAACCAATAAAAAAT TGTGTGTTGGCCTGGTTGCATTTGAGGAGTGTCTGTGGAGTTCTGCTCACTGACCTATCTTCTGA TTTAGGGAAGCAGCATTCCTTGGACATCTGAAGTGACAGCCCTCTTCTCTCCACCCAATGCTGCT TTCTCCTGTTCATCCTGATGGAAGTCTCAACACCACTTCCATACC	---
ESTD-COL2A1c	--	--	--	---	AGAAATGTATATAGTCTCAAACTGGCCATCTCCATTTTCAGTCCAAAGTTATACAGCTAGACAAGA GTGTGACATACGTTGCTATTTATGCTCTCTTCTCTGTCACCTTTCAGGGTGTCAAGGTGGAAGGT GAACAGGGTCCCGTGGTCCCTCCAGGCTTCCAGGTAAGTCAACTCAAGCATATACAATACTGCCCTTG GTCAGCCTATTGAGCTGTAAATCACCATACCGTACCT	---
ESTD-COL2A1d	--	--	--	---	TGAGAGAACACCTAGTCTCCATCCTTCTCTCTCAATGGCAAGAAAGTTAAGTGACCTATCTAGGGC AATAGACTGAGTTTGTCTGGGAACCTGGAAACACTGGACTTCTTCTACTGCGAGCAGACAAGACTTAACC AAGAGAGATTAAATGGCAAGATATACAATAACAATTTTATTTGACCACCAACTATCATGGAACAGC ATT	---
ESTD-CPT2	--	--	--	---	GCCGCAATGCCCGGAGTTTCTCCAATGTGTGGAGAGGCCCTTAGAAGACATGTTTGTATGCCCTTAGAA GGCAATCCATCAAAAGTTAACTTCTGGGCAGATGAAGAGCTACCATCACTTCTCATCATGAAGAC TGGAGGCCCGGCATAGTGTCTCATGCTGTATATCCAGCATTTTGAGAGGCTGAGGGGTGATCAG TTGAGGTCAGGAGTTTGAGACCAACCTGGCCAACAT	---

ESTD- CTLA-4	--	--	--	---	---	ATGGCTTGCCCTGGATTTCAGGGCACAAAGGCTCAGCTGAACCTGGCTACAGGACCTGGCCCTGCAC TCTCCTGTTTTTCTTCTCTCATCCTGTCTTCTGCAAGCAATGCACGTGGCCAGCCTGCTGTGGT ACTGGCCAGCAGCCGAGGCATCGCCAGCTTTGTGTGTGATGATGATCTCCAGGCAAGCCAC
ESTD- CYP2D6	--	--	--	---	---	CAGGCCAGCGTGGTCGAGGTGGTCACCATCCGGCAGAGAACAGGTGACGCCACCTATGCACAGGT TCTCATCATTGAAGCTGCTCTCAGGGTTCCCTTGGCCTGAGCAGGCGGAGAGCATACTCGG
ESTD- D11S1873	--	--	--	---	---	AAAAACAATTTAACACCTTTCAATCATATACACCATAAATTTCCATTTTTCACATAAGTCAGTT TGAGCTGAGTTTCCAAATTACTTGCAATCTAAATGTCATAACTGATTAAATGCAAGTTCAACAGACA ACTTTCCCAAGCATCTACGATCAGAAAGGTCAAATATTACATATCTGGATTAAATATGCCCATAT CTGCATGTC
ESTD- D17S33	--	--	--	---	---	CATCCCAAGCCCATCCTCTTAGCCACTGGCAATTTTGGCGCCTCTGACAGATACACTCAGGGCCGT CATGCTGCACACATCCAGGGGGCCCTACCTTTGTAGTCCATGGAAGGCTCCTCTGCGGCGGTG GGTTGTGGCTATGTGGTGTCTTGTGTAGACGGGGCTTTGGTTTCAGTTGCACATATGCGTTATT GCAGATTGCTTTGCTTTCCACCTGAGCGGCTC
ESTD- D18S8	--	--	--	---	---	TTTGAGACCACCTGGCCACATGGCGAAATCACATCTCTACCAAATTACAAATTAGCTGGGTGT GGTGTACATGCTATCGTATCCAGCTACATCGGGAGGCTGAGGCAGGAGAAATTGCTTGAAACCCA GGAGGCAGAGCTTGCACTGAGGCAAGATCACACCACTGCACCTTACAGCTGGGTGACACAGTGGAGA CTCTGTCTCAA
ESTD- D3S11	--	--	--	---	---	AACTGATTAGAACCTGAAATACATATTTTATCTGAAAAAGTCGAGTTATTGGCTCATCACATTGG AATTTTTCATCATTAATAAATCCAAATAAGTACACTGTAATAAGAAATTTAACAGAAATATCATTGT TTATTCAAACTATTATCAGCTTATTTATTGGTAAGCCATACATAAATCTAAAGCATGTTTCTGAAAG TTTA
ESTD- D3S12	--	--	--	---	---	AGGTTCCACATTATTGCTGATGTTTGTGATGTTTCCAGGAGCCTTGATGTCTATCTCTCTCAG GTATCCCACTTGAGACGTACTTTTCAAAAGCTCTCTACAGCCGTTGTGTTATTAAATCAAGGTTGA ACATAAAGTA
ESTD- D3S2	--	--	--	---	---	GATCATGTGGCCCAAGTGGCAGAGCTACTTATACCATGACCCAGACCTGCTAGCAGAACATTCTGCG TGAGTCTTATTCAAACCTGACAGCCATTTATGCCACCTGAAATATGGTCAGGTTACAGCTGTATCCCG AGAGTGAAACATACTGCTCTAGAGCCAGAGTCATACTGGATGTTCTGTTTCGGTCTTCACGATGG CAGGTATGAAATATAATAATCTGTCTTTATTGGGAAGGATGCCGGTATGT
ESTD- D4S338	--	--	--	---	---	TTTTCTGTTACCTTGTTCAGATCCTTCAGAGGAATCCCTATATATGGCAGGTATATGAATGATTT CTTAACAATAAACTTGAAAGTCCAAATTTACTCCTTGATCCATGGACTGCAGATAAATGTTATTT TAGCTGTCAGAAACAATACTATCTTGCATATGTTTCATCAGAGCCCTTGGGTGACCAGGTGATT GCCAATAAGCAGTAATATTTGAGAGGAATCTGTTTCAATGCAGTAG
ESTD- D4S95	--	--	--	---	---	CTTTTCATGCAGATAGGCTTTCTCTACTAATCACAGAAATTTTGAGAGAGCAAAACAACTTCAAGG ATAATGGGGCAATCAGCTTTCTTCTCTTCTAGAGTCTACCGG



ESTD- D7S399	--	--	--	--	--	TGAATCTTAATTGCTATCTCTACAAAATGTATAATCCTGAATCTGACATCTAGCCACCTCCATAGAT AACTGCTAGAGACCCAGTCTCCTACATCATCTTTTTCAGAAACATTTTCATCCATGGACTCCATAG AATATTGAAGAAACAACATGACAAACATTTTC
ESTD-DM	--	--	--	--	--	GTGGGACACCGAGGGCTOCAGGCTGGGGCTTGACGTGTGGCTCAAGCAGCTGCTGGCTCCACT TCCATGGGTGTGGGGCTGGGACCTCACTGTCCCTGGGAGAGGAGGAGGTGGGAGGAGACA GATGCTGATTATCTGTGTGAGAACCAAGAACTTCTGGCTGTGGTGGGAGGAGCTGCTTCCAAGACC TCCTGATTTGAGGAAGGGGAGCAGCAGAGCGGAAGAGAACAGAGT
ESTD- DRD1	--	--	--	--	--	TCCCAGCCCTATCGGTCTATTTGGACTATGACACTGACGTCTCTCTGGAGAAAGATCCAAACCATCAC ACAAAACGGTCAAGCACCCCAACCTGAACCTGCGAGATGAATCCTGCCACACATGCTCATCCCAAAGCT AGAGGAGATTGCTCTGGGGCTCGCTATTAGAAACTAAGGTAC
ESTD- DRD2	--	--	--	--	--	TCTGCTTTGGTGCAGGAGGCTGCCGGCGAGCCAGGAGCTGGAGATGGAGATGCTCTCCAGCACCA GCCAACCCGAGAGACCCGGTACAGCCCATCCACCCAGCCACCCAGCTGACTCTCCCGGACCCCG TCCACACGGTCTCCACAGCACTCCGACAGCCCGCCAAACAGAGAAATGGGCATGCCAAAG ACCACCCCAAGATTGCCAAGATCTTTGAGATCCAGACCATGCCCAATG
ESTD- DRD3	--	--	--	--	--	AAGACGATGCCAGGATGAGCGCGCAGTAGGAGAGGGCATAGTAGGCATGTGGCGGGCTGGCTGG CACCTGTGAGTTCTCTGCCCCACAGGTGTAGTTCAAGTGGCCACTCAGCTGGCTCAGAGATGCCATA GCCAGAGGGAGGTGCGTGATGCCAAGGGCTTCTGTGAGGAGA
ESTD- ERBB2	--	--	--	--	--	TCTTCAGGATCCGATCTGCGCTGTGGTGGCATCGCTCCGCTAGGTGTACGGCTCCACAGCTGG GGTGAGGGGTGTGGTCACTGTCGGGGGGCGGTGCAGACCCAGCGGGCTGGAGGACTTCAACCG CGCTCACCTCCGTTCTGTCAGCAGTCTCCGCTCGTACT
ESTD- ETS2	--	--	--	--	--	ACTCACAGTGCTTTAAGTGAAATGGTCGAGAAAGAGGACCCAGGAAGCCGCTCTGGCGCTGGCA GTCCGTGGACGGGATGGTCTGGCTGTTGAGATTCTCAAAGGAGCGAGCATGTCTGTGACACACAC AGACTATTTTGAATTTCTTTTGGCTTTTGCACCCAGGAACAGCAATGCAAAACTCTTTGAGAGG GTAGGAGGTGGGAAGGAACAACCATGTCTCAGAAAGTTAGTTG
ESTD-F2	--	--	--	--	--	GATAAGTACACTGAGGCCCCAGGAGGTTATTCCTAGTAGCCCAACTGTGCTGCAAGCTTAACCTCT GCACCAATGGCTCCAGGCCCGTAGGGGAACCTGGGGATCTAGGGGATGGGTGAGGAATGGCCC AGCCAGTCCCGCGGTGCTGGGTCCCAACAGAGGAGGCGGTGGAGGAGACAGGAGATGGGC TGGATGAG
ESTD-F9	--	--	--	--	--	AGATCCTGATGATTTTTCCTATTTTCTAAATGTTTACAGTTTGAAGTTTAGATTTATGCCCA TGCTCCATTTGAGTTAATATTTGTGTAAAGTATGATGTTTAAAGTCAAACTTCATTTTTTTTCCATA GGTATGTCCCAATTTATCCAGCACAAATTTGTTAAACAAAC



ESTD- G0DH	--	--	--	--	---	---	CGCAGAACGGTCAGTGTGGGTGCGGAGTGTGGAGGGAAGGAGGAGGAACTGGGGTTTAGGGACT TTCCGGGGTGACTTTCCCGTTCTGTGCTTCAGAGAAAGCGGGAGAAACACAGAGCCAACTGGCTAA GTGTAAGGGAACCTCTGTGTCGACCGTGTGTCTGCTGCCCCCTGTTACGCTGTCTGTCTGCCGAGTCGA CTCTGTCCCGGAAATTCGGAGAGCT
ESTD-GCK	--	--	--	--	---	---	GTTTTATGCATGGCAGCTCTAATGACAGGATGGTCAGCCCTGCTGAGGCCACTCCTGGTCAACCATGAC AACACAGGCCCTCTCAGGAACACAGTAAGCCCTGGCAGGAGAATCCCCACCCACACACCTGGCTGG AGCAGGAAATGCCAGCGCGGCTGAGCCCCAGGGAAGCAGGCTAGGATGTGAGAGACACAGTCAACC TGCAGCCTAATTACTCAAAGCTGTCCCCAGGTACAG
ESTD- GNAT2	--	--	--	--	---	---	GACCTGAGTACCTCCTAGTGAGCAAGATGTGCTCCGATCCAGGTCACAAACCACAGGCATCATTTG AAACCAAGTTTCCGTCAAAGACTTGAAATTCAGGTAAGTGCATGGTTCCTAGG
ESTD- GPK2L	--	--	--	--	---	---	AGTCTTCATCTGCGGTGTCCAGGTAGATCCCTTTCACCCCGGAGAACTGCTCGATATC
ESTD- HRAS	--	--	--	--	---	---	CTGGGCTGCCCGCAGCAGCTGCTGGCACTGAGAGCGCGCGCCAGGCTCACTCTATAGTGGGGTGG TATTCGTCCACAAATGCATCTGGATCAGCT
ESTD- HSD3B1	--	--	--	--	---	---	TTGAAAGTTCTCCACTGTTAACCCAGTCTATGTTGGCAATGTGGCCTGGGCCACATTCTGGCCTTG AGGCCCTGCAGGACCCCAAGAGGCCCAAGCATCCGAGGACAGTTCTACTATATCTCAGATGACA CGCCTCACCAAGCTATGATAACCTTAATTACACCCTGAGCAAGAGTTCCGCCCTCCGGCTTGATTCC AGATGGAGCTTTCCTTTATCCCTGATGTATGGATTGGCTTCCTGCTG
ESTD-HT2	--	--	--	--	---	---	GGGCTAAATTTCCGAGCACTTTGCATAGACTGTTTTATTGACTTGACAGGATTGCTAGAGATAGG CAGGAGAGGAAGATGTGTACAGTTTGTTCAGAGAGAATAAAGGATAACCTGGGGTTTCTGTGC TTTGCTTCTTCACATCCCTGGGAGTTAATAGCTGCAATTTTCAAGAACGGTATACAGGGACAGCA AAGCGCAGTCGTGAAGTTTCAACAAGACACACCTT
ESTD-HT4	--	--	--	--	---	---	ACCAACGAGCCGCGATACAGACACTCTTAAGTTTGCCCTAAGGCTCATTCAAATCATTAGGCATTTT CTGATAAACTAGGTTCTTGGGTGCTTCTATCGGCAAGAAATGCGTACTTATTTGAATAGTAGAGGTAA ACCACACGCCCAAGAGTCAGTACAGTGGCAGCTTCTGCAGCAGGCGTGAACCCCGTAGCCTAAA TGACAGCCGAAGAGCGCCGAAGACATGCAGATGTGC
ESTD-HT5	--	--	--	--	---	---	AACACACAAGCCCCAGCGAGAATTGAACCTCGCACCCCTGGTTTACAAGACCAGTGTCTTAACCCCT GAGCTATGGAGCCCTCGTCTGTGTGGTTTCTTCCTTTTCATCTTATAGATTGATGTTATGCTCCTA GCATTCGGGCTACCGAATAGGATGTTAGCTTGAGTAAATCCAGGATATTCTCCTACAAAATGAAA ACATTTTCGTGCTCTGTAATCCCTCGAAAAGGTTCT
ESTD- IGFBP1	--	--	--	--	---	---	ACCCAGTGGAGCCCGCTCATTCACGGTCTTGGCAGGAGGTGCCCTGGGAGAAAGGAAGATGTTTC CAGGGCACACATAGCTTAGTGGAGACTC

ESTD- IGHV4-6	--	--	--	--	---	---	TTTACTATTCAATGGATACAGAAATTGTGGGAGTCACTATATTCCTATGAACAAAATTCAGATTT CAGTGTTAAGTAATGTGCTACATTTGTGTAGTGACGGGAGTGGTGATCGAGAGTGTGGTGGG TGCACGGACATAATGATTCAGAAAGCAATATGGAAGATGAGTATCTATGGATACGAACACTGAAAGT ATGTAATACTTCACAAATACTAATAAACGGAGTTGAATATAAACCCA
ESTD-IL1A	--	--	--	--	---	---	CAAAGTAAGCACCCCAATAATGTTAGCTATTACTATCATATTATTATTATTTATTTTGTG AGATGGAGTCTGGCTCTGTCAACCAGGCTGGAGTGCAGTGGCACAATCTGGCTCACTGCAAGCTCTG CCTCCTGGGTTTCATGCCATTCTCCTGCCCTCAGCCTCCCGAGTAGCTGGGAATACAGGCACCCGCCACT GTTCCCGGCTAAATTTTGTATTTTGTAGTAGAGACGGAGTTTACCGT
ESTD-IL1B	--	--	--	--	---	---	CCACTTACAGATGGATAAATGGGTACAATGAAGGGCCAATAGCCCTCCCTGTCTGTATTGAGGGTGT GGGTCTCTACCTTGGGTGCTGTCTCTGCTCAGGAGCTCTGTGTCATTCAGG
ESTD- KRT10	--	--	--	--	---	---	CCAAAGTTAATAGTATTGGAGTTATCTGAGAAATTTTCCATGTCAGTGTACCTTTTGGCAATATT AAAGGAAGAAATGCAATTTTAAAGTAAGTCTAAGGTTTTTCCATTAAACCCTATTACTTCTAAG AGAACTGTACATGACAAATATTGCCATTACATGAGATCAACTATGTAGCTGCTTTTAAATAGTCTC TGCCCAGATACATCTCCCTATATAAGTTATAACCAGTATTGATA
ESTD- KRT18	--	--	--	--	---	---	ACCTCACCCCTCCCTTAGCCCGTGGGAAGCAGGAAATCTCTCTCCAATCCATGAATACACATCGG ATTGGACACCTTGAGAGTCTTAACAGCAGGCGCTGACATGAGACCTCAGACAGAACTTTCTAGAGTT TGCTAGAGGTCAAGGTCAAGACTAAAGAGGGGCCAGAAATGTTAAGTACAAAAGTGAGGCCCATAG GCTGCCTATCTCTCCGTCTCAGGTTTACCACGTCAACATTGACACA
ESTD- LF79	--	--	--	--	---	---	GGGTGATTTTGAGGCTCAGTTAATATTCAAAATTGTACCGTAGCAAAACTGCATTGTTATTAGA AAATAAAAATTTCCAATATGTAGTGCTGTGTTATACCTGCTCTGCCATGCAGCATCATAGCCTGT GGGAACCGAGGGCTTCCCTTACCACCCAGA
ESTD- LMP2	--	--	--	--	---	---	TACACACTTTCCTTACCCTTCACTGAAACGACTCGCAAACTGGAGCCTTGTAGGAATGGAGTTGA CCTTCCCAAAAGCCACTATGATAAGCTATTGGTG
ESTD-LPL	--	--	--	--	---	---	TGTCAGTGTCCTTAGGGGCACTCAACACTCCAGCTTCTTCAGCTCTGGCCTGTCTGCTGCTGCA AGGGTTTGCTTAATCTCAATTCAATGTCTCTTCACTTTTAGCAGCTGTGGGTTTGTGTTGTTTC TTCTGTTTTCCTTAGTATCTGACTACTTTTAAATTATAAAAGAGATGTATCTAAACAAAATAGAG ATTGTTATCAGAAGTTCACAACATTTATTAAAATTTTTCACCTG
ESTD-MCC	--	--	--	--	---	---	TTGTCAGGAGTGTGCTGATGCTGCTCCCGCTCTGTCCCTAGCCGAACTTCAGGACAACGTGCAG
ESTD- METH	--	--	--	--	---	---	CATCCATGTAGGAGAGCCTTAGTCAAGTGAATGCTGAGGAAGCAGTAACAGCATGCCATCCCGAA TCTCAGGAAGTCTGTCTTCCAAAGGGTTGGTCTAAGTTGCTGATTACCCGGATTTTCTGACGATC TTTCAACTGCTAGAGCATCTGTTCTCTGTTTAGCATGG
ESTD-NF1	--	--	--	--	---	---	ATTATCCAGATGAATTTACAAAACATATACCAGATCCACAGACTGATATGGCTGGT



ESTD- NFKB1	--	--	--	---	---	AACATGGACTTGATATTTGTACAAAAGTTTTATTTTCTAAAAAGAAAAGAAAGAA AAATTTAAAGGGTGACTTATATCCACTGCACACTGCCTAGCCCAAACGTCTTATTGTGGTAGG ATCAGCCCTCATTTGTTGCTTTGTGAACCTTTTGTAGGGGACGAGAAAGATCATTTGAAATTTCTGAG AAACTTCTTTTAAACCTCACCTTTGTGGGGTTTTTGAGAAAGGTTATCA
ESTD- NPPA	--	--	--	---	---	TGTCCCTAGGCCAGCCCTGCTTGTCTCCCTGGCTGTTATCTTCAGTACTGCAAGAGAACACAGAC AT
ESTD- NRAMP	--	--	--	---	---	GGAGGCAGGAGTGGGGAGGGGCTGTCTGCTCCAGGTCCACAGACAGAGAGGGCCCTCAGTG TATCCCCACCCCAATGTGGGCGCTGGGAGATGAAGAGAGTTGATGCAGGT
ESTD- NRAS	--	--	--	---	---	GTGTTTTCTTAATCTTTCCAGGAACACAGTGAACCATATTTCTTCTGCAGGCATATAGAATTTGGT GGGTTTTCTTTATGTAGGTGATATTGGATACTTTTGTGTTGATTATATATTAGCAATTTGAGGG ACAAACCAGATAGGCAGAAATGGGCTTGAATAGTAGATGCTTATTTAACCTTGGCAATAGCATTGC ATTCCCTGTGGTTTTAATAAAAT
ESTD-OTC	--	--	--	---	---	GTGACCTTCTCACTTTAAAAAATTTACCGGAGAGAAATTAATATATGCTATGGCTATCAGCAGA TCTGAAATTTAGGATAAACACAGAAAGGAGAGGTATGTAAACA
ESTD-PAH1	--	--	--	---	---	GCCACCAACCCACCCAGCACACCTCCACCTCAGCCAGACAAGTTGTTGACACAGAGAGGCC TCAGGGCACAGAGAGTCTGGACACAGTGGGGAGTCAGCCGTGTATCATCGGAGCGCGGGGCAC ATGGCAGGGATGAGGGAAGACCAAGAGTCTCTGTGGGCCCAAGTCTAGACAGACAAACCTAG ACAATCACGTGGCTGGCT
ESTD-PAR	--	--	--	---	---	CTCTTCAGGAACCAACAGTCTTCTTACCAACACGACTTATTGCTGCCGAGAGGTACAACCCGTAGA ACTTCTTCTTAACCTGTAATTTAGTTAAAGGAATCGAACTGCTCTGAAGACATGGAGATACTGCCT AATCGACTGGCTTTTATTAGCTCTGTGAGTGTCTTCTTCTTCTTCTGTTCTAGAACGTTTCTTAG GACTGGCAGTTTAAGCTTTCACCTTAGGCTTTCTGTATACCCATGCC
ESTD- PBDA	--	--	--	---	---	CCTTCTCATGCCAGATGGAATTCAGTCCCTTCAGGATCTGCCCTAACCTGTGACAGTCTAAAGAGT CTGAGCCGTGGCTGGGAAGGCGAGGACTAATCCAAATCTCTACCCGAGCTTGCTGCATACAGACG GACAGTGTGGTGCAACATTGAAGCCTCGTACC
ESTD-PS-1	--	--	--	---	---	GGGAGTAAACTTGGATTGGGAGATTTCATTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACA GCCAGTGGAGACTGGACACAAACCATAGCCTATTTCGTAGCCATATTAATTGGTTTGTGCTTACATT ATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT CTACTTTGCCACAGATTATCTTGTA
ESTD- PXMP1	--	--	--	---	---	ATGAAACATGGTTCTTTAATTTATGATATGTTGTTATAGCTATCTTAAAGGGCTTCTTTTTTAA ATGCAGAAAGAGGGGAAAGAGCGAGCTGTGGTGACAAAGGTGTTTTTCTCAAGGCTCATACAGA TTCTGAAATCATGGTCCCTAGAACATTTTGTAAAGAGGTAGTCTTATGAAATTATAATCTT
ESTD- Per/RDS	--	--	--	---	---	ACCTACAGACGTGCTGGATGGTGTGTCCAAACCCGAGGAATCTGAGAGCGAGAGCGGCTGGCTG CTGGAGAGAGCGTGCCGAGACCTGGAAGGCT



ESTD-RDS	--	--	--	---	---	CCCGAGGAATCTGAGAGGAGAGGGCTGGCTGCTGGAGAAGAGCGTCCCGGAGACCTGGAAGG CCTTTCTGGAGAGTGTGAAGAAGCTGGCAAGGGCAACAGGTGGAGAGCGAGGGCGCAGACGACGG CCAGGCCCCAGAGGCTGGCTGAGGGCCCTGGGGCCCTCCCTCCGAACTGAGAAATAGTGCACT CCAAGAAACGTGGATCTCCCCCTCATCCAACTCCGAAAGTCTGAA
ESTD- FYR1	--	--	--	---	---	CTTCGTGACGGAGGTACGTCCTCCGCTCTTTCATGGACATATGGATGAGTGTCTGACCATTTCC CTGCTGACAGTGTGATGACGAGCGAGACTTGTCTACTATGAGAGGGAGCTGTGTGCACTCATGCCCGC TCCCTCTGAGGCTGGAGCCACTGAGAAATCAGCTGGAGTGGAGCCACCTGCGCTGGGGCCAGCCACT CCGAGTCCGGCATGTCACTACCGGGCAGTACCTAGCGCTCACCGAGG
ESTD- SPTB	--	--	--	---	---	TGAAACACCCTGTGTCCGGAGCCAGGTGTGTTCTCTCTGGGAGCCTGAGGAGTTTGTGTCTGTGTG CAGTCCCCCGCCACCTGCTGTTGAGCTGGACATACACCTTCACCTCTTGGCCCGGAGAAAGAC ATTTACCCACCTGGCCATGTCCCTGCTGTTGTGTGACACCCCTCTGTGAAGACCCCAACCCCTGCTCC CCCCCAAGCCAGTTTCTAGCAAGGGCAGGAC
ESTD- SSA1	--	--	--	---	---	TTCACTTTGTGGATTGTTCTTTTGTGTGTCAGCACCTTTTCAACATGATGTGATCCCATTTGTCCAAG TTTGCTTTGGCTGCTGTGTTGGGATATTTGAAGAGATCTTTGCCAGTCCAATGTCTAGAGAG TTTCCCAATGTTTCTTGTAATAGTTTCATAGTTTGAGGCCCTTAGATTTAAGTCTTTAATCCATTTTG ATTTGATTTCTGTA
ESTD-TAT	--	--	--	---	---	AAATGGTCAGGACCCTGATCCACAAGAGTGGTACCATTTCATCAGGGCCATCAGTTTCATTCAGCTC CCATGACTGGGATGCTAAGTCAGCAACTGAGTTTCATTCATCTTAAATGACTTGTGGACAGGATCA ATTTCTCTCACCTAGAACGTTTGTTTACAACCTTTCTCCAGTATGATGGGATTATGATGGGGGG GAGAAAGCAATTTTAAATAGGACCCATGAGACACATCA
ESTD- THPB	--	--	--	---	---	TGCGGCTTTCTCCGGCAGGTAGACTTCTTACTTGGCTGTGATTTCCAAGAGAAAGAGTCCCAAG CACACGAAACAGAGTTGCAGATCCCATGAGGCCAGTCTCAATCACACAGGATCACTTCATCCA CACTGGATTGGCCCAACAAGTCTGAGTGCCAGCCAGGACTCAACGGTCCCTGTAGATGGG
ESTD- TNFA	--	--	--	---	---	TTCTGTCATCCTGTCTGGAAGTTAGAAGGAACAGACAGACCTGGTCCCAAAAGAAATGGAGG CAATAGGTTTGGGGGCATGAGGACGGGTTTCAGCTCCAGGTTCTACACACAAATCAGTCAGTG GCCCAGAGACCCCCCTCAGAAATCGGAGCAGGAGGATGGGAGTGTGAGGGGTATCCTTGATGCTT GTGTGTCCCAACTTTCCAATCCCGCCCGCGATGG
ESTD-TYR	--	--	--	---	---	TAGTGAAGTTTTCATCTCTCTGTCAGCTTCTGGAATTTCTTGTCCACCGCAACAAGAGTCTATGC CAAGGCAGAAAGCTGGTGTCTCATGGCAAAATCAATGTCTCTCCAGATTTCCAGATCCCCCAAGCA GTGCATCCATTGACACATAATAATGCATCCAGACAAAGAGGTCAATAATATTGATGTGCTTAACAT GGGTGTTGATCCATTTTTCATTTGGCCATAGGTCCCTATGGGGATGACA

ESTD- TYRP1	--	--	--	---	---	---	AGTAGTGATGAAGCTAACAGCCTCTCCTCACTGATCAGTATCAATGCTATGCTGAAGAATATGAA AACTCCAGAAATCCTAATCAGTCTGTGGTCTAACAAATGCCCTACTCTCTTATGCATTAGTATCACAA AACCACTGGTTGAATATAATAGATTGAGTTAATTAAGTATTTCTTTCACCTTATTAACCTTCTTCT
ESTD- VB12	--	--	--	---	---	---	AATACAAGCATATGTTAGAATTAAAGTCTAGGCATACTT TTCCCAAGGCCTCAATACAAAGTCTTTTCTTGGGATTACAACATCAGGGTCTGTGTTTCTATTACA GGACACATGGATGCTGGAATCACCCAGAGCCCAAGACACAAAGGTACAGACAGGAACACACAGTG ACTCTGAGATGTCACCACTGAGAACCCGTTATATGTACTGTATCGACAAAGACCCGGGGCATG GGCTGAGGCTGATCCATTACTCATAT AGGTAGGAAAGCAAGAGTTGATTAGTGAAGGAGAGAAATGGACCTACCTCCACACTGTCTTTTGG
ESTD-VWF	--	--	--	---	---	---	TCCCTAGAGTCTG AAGACCTACGTGAATGTTACATGTGCTTAAAGCCTCCCTTCTCTTACTCTCTGCTGCAGGATGTG CGACGTGTGCTGGAGTAGCCCGACTCTTGTACGGTCGGCATCTGAGACCAGTGAGAAACGCCCTT CATGTGTGCTTACCCAGGCTGCAA TTGGGAAGTTAGAGCCTATATTAAATTACGGAATTACTAAGCAGGACACAGAGGCTTAATTGAAAA TATCCCAAAGTTGAATGTCTCAGTTCGCTGTGTGGTTAGATGCAGGATTTATATGATCCGTTAACC TCT
ESTD- s14544	--	--	--	---	---	---	AGCACCACTCTCACGTCAAGCCTCAGCACAGATGCTGTCTTCTATAAGGATGACGTGCTGTTTACAA CATCTCCTCCATGAAGAGCACAGAGATTATTTATCCTGAAGTCCGGATCTATGACTCAGGGACAT ATAAATGTAGTGTGATTGTGAACAACAAGAGAAACCACTGCAGAGTACCAGCTGTTGGTGAAGG AGTGCCAGTCCCAGGTGACACTGGACAAGAAAGAGGCCATCCAAGG
EST71770 6	--	--	--	---	---	---	CAAATTACAGGGTCAACTGCTATGATGTGTTGGAGCCAGTCACCTTTGGTGGCTACAAGATGTGCG GGGAGTGGCCGGAGTTGGCGAGTACGGGCTGCAGGCATACACTAAAGTGAAACTGTGAGTGTGG OCCACTCTATTGCCCAGCCCCAGGGACAGAGCTGATCCTTTGAAGTCTTAAGTTCCACATTGCCAGGA CCAGTGAGCAGCAACAGGGCCAGGGCTGGCTTATCAGGCTCCAGCCAGACCCCTGGCTGCAGACAT AAATAGGCCCTGCAAGAGCTGGCTGCTTAGAGACTGCGAGAAGGAGGTGCTGCTGCTGCTGCCCCG GTCACTC
EST13586 3	--	--	--	---	---	---	AGGCAGAACTGGGCCCCCATGCGGGGGACGTGGAAAGGCCACTTGAGCTTCTGGAGAAAGCACTGA GGGACAAAGGTCAACTCTTCTTTCAGCACCTTCAAGGAGAAAGAGAGCCAGGACAAAGACTCTCCCT CCCTGAGCTGGAGCAACAGCAGGAACAGCAGGAGGAGCAGCAGGAGGAGGATGCTGGGC CCTTTGGAGAGCTGAGCTGCCCCCTGGTGC
EST51976 7	--	--	--	---	---	---	



EST11458 6	--	--	--	---	---	CCACTTTGGTAGTGCCAGTGTGACTCATCCACAATGATTTCTCCAGTGCTCATCTTGTCTCGAGTTT CTCTGCCATGTTGCTATTGCAGGACGACCTGTCCAGCCAGATGATTTACCATTTTCCACAGTGGT CCCATTAACAACATTCTATGAGCCAGGAGAAGATTACGTATTCCTGCAAGCCGGGCTATGTGTCC CGAGGAGGGATGAGAAAGTTTATCTGCCCTCTCACAGGACTGTGGCC
EST39852 8	--	--	--	---	---	CGGTCTTCTCCAGGTATTGTTGCAGAAAGCCGAGATGACCTCTATGTCTCAGATGCATTCCTAAG GCATTCTTGAGGTGAGTACACCTTCCCACTCTCTACGGTACAGAAAGGAGATGCATGAACAGCA GGAACACGTGGAAAGGCCTGTTTCCAGTGTAAAGGCATGCAAAAGGCCTCCACAGGCTGCTATAAT ACAGCCCT
EST62448 0	--	--	--	---	---	ACCTGGTGTGCTGGTGTGGTGAACCTGGTCTCTTGGCATTGCGGCGCTCTGGGGCGCGTGG TCTCTGGTGTGGTGTGGTGTGGTGAACCTGGTCTCTTGGCATTGCGGCGCTCTGGGGCGCGTGG CTGGGAACGATGGTCCCGCAGGTGGGATGGTCAACCGGACACAAGGGAGAGCGCGTTAOCCTGG CAATAT
EST38027 2	--	--	--	---	---	AGTGACTTCCAAGGAATGGCTACCCAACCTTGCCTTATGCGCTGTGGCCAACATATGCCTCTCAGA ACATCACCTACCCTGCAAGAACAGCATTGCATACATGATGAGGAGACTGGAAACCTGAAAAGG CTGTCACTTCTACAGGGCTCTAATGATGTTGAACCTTGTGCTGAGGGCAACAGCAGGTTCACTTACACT GTTCTTGTAGATGGCTGCTCTAAAAGACAAATGAATGGGGAAGACAA
EST12274 0	--	--	--	---	---	CCCCAGTTGACAGCCACTGCTAGACTAAGTTTCTTGTCCAAATAGAGCCTTACCAAAGTGTAT TACATAAAGAAAGTCAAGTGGTTTACTCTCATGACCAATATTCTTCCCTCTTAGGATGAGGTGA TAGTAAATGACCGATGGGGTCAGAACTGTTCTCTGTCACCATGGAGGATACTATACTGTGAAGATAA ATTCAAGCCACAGAGCTTGCCAGATC
EST76807 7	--	--	--	---	---	ATGCTAAGGGGATCGGACATGAAGGACCTGTGAGCCGATTGTCTATCTCCAGCGGCCCTGTCTATC CAGCTCACTCATCAATGGGGCCAGTCAAGGCCAGGCACTGGGCTCCGGAGGACTCACCACTGCCCCCT GCTGCCATGTGGACTGGTGAAGTTGAGGACTTCTTG
EST44438 7	--	--	--	---	---	GCAGCCAGGAGCCGCTGCACCATGCCCGCATAGATGGGACCTCAAGCTCGACTTCAAGGACGTCCT GCTCCGACCTAAGCGGAGCAGCCTCAAGAGCCGAGCGGTGGG
EST12839 3	--	--	--	---	---	TGCAAAACACACAAAATCTTCTCCAGATGCCCTATGGCTGTGGAGAGCAGAATATGGTCTCTTTGCT CCTAACATCTATGTACTGGATTATCTAAATGAACACAGCAGCTTACTCCAGAGATCAAGTCCAAGG CCATTGGCTATCTCAACACTGGTGAAGTATTACTTGAAGTAAGGGAACCTTGAATGTTATTCAACTGG ATTTCCAGTAGGTTTCAGTTACTTATGAATATTATGATACTTAGCTTAG
EST54419 8	--	--	--	---	---	CTTCTGCCATAATTGAATGATATTGTGCTGTGGACCTGAGCACTTTTATGGCACAATGATCACTA TTTTCTTGACCCCTACTTACAATCCTGGGAGATGATTGGGTTAGCGTGGTGTGTTGTTGTTACTA TAGTCCAAGTGAA



EST10398 2	--	--	--	--	---	---	TGCCTGGGTGGCAAGGCTGCAACAAGGAGGCAACCAGGAGGCTTTTATGAAGCGGGCCATGGTA AGATGCTGCCACCTCTTATCTACTTGTATGATGATGTTACATTTGGGGCTTGACTTCCAACACGGAGAAG CATTGTTTCTCGGGCCAAGAAGGTATCTACCAATAGTGCTATTAGGCAATTG
EST36751 7	--	--	--	--	---	---	CCAAGTCGTTCAATTTAGCTTTGCAGGTTTAACTCGATTACTTTTCTATTCAAATCTCTGTAAAA TTGAAATATGAACCTAGTTTCTGATCTATGGTTCAAGTTAAACAG
EST40562	--	--	--	--	---	---	CACGTGGAAGGAGCTATTTTGGAGGCTTAAAGAGTAAGAATCTGTCCCAAACTTGTGGCTGAC TTTATGGCTAAGAAGTTTCACTGGATGCATTAATAACAAATATTTACCTTTTGAAAAAATAATG AAGGATTGACCTGCTTCGCTCTGGAAGAGTATCCGTACCGTCTGACGTTTGAACAATACAGAT GCCTTCCCTGTAGCAGTTTTCAGCCTCCTCTACCTA
EST18288 3	--	--	--	--	---	---	GCTCTCTATACCCCTGTGTCTCTCCACGCTCTCTGGACTTCACAGAACTGGATGTTGCTGTGAGAA GATTGACAGGTTTCAGGCTGTGACAGGATGGAAGACTGGCTGCTCCTGACGGGAGCCAGTGTGG ACAGCACCTGGCTTTCACACACCTACGTCCACTTCCAAGGTAAAGCAAACTCTCTGCTGCTGCTGCGC CCTAGGACTTAGTATCC
EST70523 3	--	--	--	--	---	---	TTCCGCGAGCCCCCATCTTGGCACTGCTGCTCCCTCAGGGGCCACCCCGGCACTCACCGCTCT CGCTCTCGGTAAACATCGGGCGGCGCTCTTGACACATAGCCTGGACCGTTTCCGTATAGGAGG ACCGTGTAGGCTTCTGCTCCCGGCTTGCAGGGGCCAGCCCTGCAGAGAGGGGTTCCCTGTGTGT TGAGCTGAACACACAGCTGTGGAGTGTCTCCACGTG
EST58707 7	--	--	--	--	---	---	CAGTGTATCTGGAAGCCTACAGGACACCAAAATAACCTTAATCATCAATTGGTTACAGGAGGCTTT AAGTTCAGCATCTTTGGCTCACATGAAGGCCAAATCCGAGAGACCCTAGAAGATACACGAGACCGA ATGTATCAATGACATTACAGCAGGAACCTTCAACGATACCTGTCTGTAGGCCAGGTTTATAGCA CACTTGTACCTACATTTCTGATTGTTGGACTCTTGTCTAAGAACCTT
EST74167 6	--	--	--	--	---	---	AGACCATGAAGGAGTTGAAGGCTACAAATCGGAATCGGAACTGGAGGAACAACACTGACCCCGGTGGCGAGG AGACGGGGCACGGCTGTCCAGGAGCTGACGGCGCGCAGGCCGCGGCTGGCGGACATGGAGGA CGTGGGGCGGCTGTGTGAGTACCGCGGAGGTGCAGGCCATGCTGGCCAGAGCACCGAGGAGG TGCGGGTGGCTCGCTCCCACTGGCAAGCTGGTAAGCGGCTCTC
EST43211 8	--	--	--	--	---	---	CGCTGTGTCAGTACCGCGGAGGTGCAGGCCATGCTGGCCAGAGCACCGAGGAGTGGGGTGG CCTCGCTCCACCTGCGCAAGCTGCGTAAGCGGCTCTCCGGATGCCGATGACCTGCAGAACGGCC TGGCAGTGTACAGGCGGGCGGCGGAGGGCGGCGGCTCAGCGCCATCCGGAGGCGCTG GGGCGCTGTGTGAACAGGGCGGCTGGGGCGCGCAGCTGTGGCTC
EST36770 4	--	--	--	--	---	---	TGTAGCCAAAGTCACCTGCATCATCTTTGGCTGCTGGCAGGCTTGGCCAGTTTGGCAGCTATAATCC ATCGAAATGTATTTTCATTGAGAACACCAATATTACAGTTTGTGCTTTCATTATGAGTCCCAAAAT TCAACCTCCCGATAGGCTGGGCTGACCAAAATATACTGGGTTTCTGTTCTCTTCTGATCAT TCTTACAAGTTACTCTTATTGGAAGGCCCTAAGAGGCTTATG

EST26021 1	--	--	--	---	---	TAATGTAAGCTCATCCACCAAGAAGCCTGCACCATGTTTGGAGTTGAGTGACATGTTGCGAAACCTGT CCATAAAGTAATTTGTGAAGAAGGAGCAAGAGAACAATTCCTCTGCAGCACTTCACTACCAAATGA GCATTAGCTACTTTTCAGAAATTGAAGGAGAAATGCATTATGTGGACTGAACCGACTTTTCTAAAGC TCTGAACAAAGCTTTTCTTTCCCTTTTGCAACAAGACAAGCAAAGCC
EST51212 0	--	--	--	---	---	ATCCTGAGCTCGCCAATAAGCTTCTTGGTTCTACTTCTCTTCTCCACAAGCCCAATTCACCTTTCTCA GAGGAATCCCAAGCTTAGGAGCCCTGGAGCCCTTTGTGCTCCACTCAATACAAAAGGCCCTCTCTCT ACATCT
EST20118 2	--	--	--	---	---	GTTCGGAATCCTCCTCTGAAAGTGGCCGGTTAATCTGCTCATGACGCTGCGGCTGTGGTCCAGCT GAGGTAGGGGCCCTTGAAGCTGGAGTGGGTTTAGGGACGCGGGTCTCTGCGTGCATCCTAAGCTCT GAGAGCAAACCTCCCTTGAAGCTGGGAGTGGGTTTAGGGACGCGGGTCTCTGCGTGCACTCCTAAGCT CTGAGA
EST53018 6	--	--	--	---	---	ACAATCCAGGTCACACATTCAGAAAGAGGAGGGTGTGTCAGTGAGCCTGGGTAGGTCCAGTAATCCA AGGATTCAGGAAGGAGGCCACGAGGATCGAAGTTAGTGAAGTC
EST68787 5	--	--	--	---	---	CTTCCTATGGGATTGACTTTATTTCTCCATTGCTTACCTTTTACAGGTGTTAATATAGTGAAAAG GAAGCTTGAGCTCATGACAAATTTGAAGCTGACAAATTACACAAGAGGAAATAAATTCACAGTCAA AGAAATCAAGCACTTTTCGAAACATTGAAGTTGTTTTGAACCTTGTGTCACTTTAATTACAACCTAG CAGACGGAACCTGAACCTCAGGGTAAGAAAT
EST34088 2	--	--	--	---	---	GTGGGGGCAACAGTGGGAGAGAAGGGGCCAGGGTATAAAGGGGCCACACAAGAGACCGGCTCAAGG ATCCCAAGGCCAACTCCCGGAACCACTCAGGGTCTGTGGACAGCTCACTAGCTGCAATGGCTACA GGTAAG
EST37382 5	--	--	--	---	---	CTGAGAAACAATTGGCAAAATAAAGGAATTTGGCACTCCCAACCCCTCTTTCTCTCTCCCTTGGGA CTTTGAGTCAAAATTGGCCTGGACTTGAGTCCCTGAACCAGCAAGAGAAAGAACGCCAGAAAT CACAGTGGGCACGTGCGTCTACCGCCATCTCCCTTCTCACGGGAATTTTCAGGGTAAACT
EST74082	--	--	--	---	---	TCAGGGTGGTGGAACCCAGGCCCACTCTGTGACGAGGAGGACGTGGCTGGCTGTGGAAGCATG TGGGGGTAGCCCAAGGGCCCCAAGGCAGGGCACTGGCTTCAGCTGCTCAGCCCTGCTGTGCAC CCAGATCACTGTCTTCTGCCATGGCCCTGTGGATGCGCCTCTGCCCCCTGCTGGCGCTGCTGEOCCTC TGGGGACCTGACCCAGCCGACGCTTTGTGAACCAACACCTGTGCG
EST45311 0	--	--	--	---	---	GCCCTCCTCTCTTCCAATTCTGTCCCTATAGTTTCTCTATTAAAGTGAACATACATGCACTCTTTTAGT GGATAGATGCACACAAACACACAAGCCATTATGGGGAAGGATCCACGTGTGTGGCCATATTGTAACA CATTTTCTGCAAAATCACCTCTTTTCATTTAACAGCCCTTATTCAATGGCCTTTTCTTTTCAGTAGTA CATACACATCTGTGTCAATTTGTTGAAT



EST65258 8	--	--	---	---	TGCCCATCACGCGCGGAGACATGGCTTGCCACAGCTCTTGAGGATGTACCAATTAACCAGAAAT CCAGTTATTTCCACCCTCAAAATGACAGCCATGGCCGGGCTTCTGGGGCTGCTGGGGGGG ACAGTCCACTCTGACTGGCACAGTCTTTGCATGGAGACTTGAGGAGGGGCTTGAGGTTGGTGAG GTTAGGTGCGTGTTCTCTGTGCAAGTCAGGACATCAGTCTGATTAA
EST38216 3	--	--	---	---	ATGCAGGATGAAGGTGGACAGGGAGGAGAGGGGCCAACCTGTTCATCCAGGGCTGCAGATGTGCTG GACTATGGGTTTGTGACCCCACTGACCTCCATGAGCATCAGGG
EST62782	--	--	---	---	ATACTAGTACAAGTGGTAATTTTGTACATTACACTAAATTATTAGCATTTGTTTAGCATTACCTAA TTTTTTTCTGCTCCATGCAGACTGTAGCTTTTACCTTAAATGCTTATTTTAAATGACAGTGGAAG TTTTTTTTCTCGAAGTGCCAGTATTCGCCAGAGTTTGGTTTTTGAACCTAGCAATGCCTGTGAAAAA GAACTGAATACCTAAGATTCTGTCTTGGGGTTTTTGGTGCAATGCA
EST35879 9	--	--	---	---	GAGATCGGTGTGTGAGTTATTAGGCATGGTTACCTGTGATTCTCCCAATCTTGTGCGTCCACCGATG GAACTGCCGGCAATCCTGACACGTGTGCAOCCAGGCTGTACCCAAATTAGGTGAACATGGCTTCGAG AGAGTTGAACAGATTCTCTGGAAGACAGCAGCGGGGATGGGGCAGGAGAGAGCTGCCTGGATGAA
EST68308 5	--	--	---	---	GGAAAGAGATTTAAGAAGCTTGATTGGACAATTCTGGTCTTTGAGTGTGGAAGAGTTTCATGTCTCT GCCTGAGTTACAAACAGAAATCCTTTAGTACAGCGAGTAATAGATATATTCGACACAGATGGGAATGGA GAAGTAGACTTTAAAGGTAAGAAAGTAGTTATTTTTTA
EST54045 6	--	--	---	---	GGAAATTAATAAATAATTTAAATACCTCCATTTTGCTTATCCTTTTAGTGAAGATGATACCTGCAA AAGACATGGCTAAGTTATGATTGTCATGTTGGCAATTTGTTTTCTTACAAATCGGATGGGAATCT GTTAAGTAAGTACTGTTTGCCCTTGGAAATGGATTTTAAATGTGACTTTATCAT
EST52908 0	--	--	---	---	ATCACAGGTCTCTGGTCTCTGGCCATCATTTCTCTGGAGAGATGGATGGTGTGCTGCAAGCCCTTGG CAATGTGAGATTGATG
EST19590	--	--	---	---	AGGAGAAGCTGAGGAGGGGAAGAGAGACAGAAGATGACATTGATGAGTGAAGATGTGCGCTCAGGAT GCCGGAAATGAC
EST76136	--	--	---	---	TGAAGCTTCTGCCAGCTTGCTGCTTCTAGGAGAACCCGGCTCATACCTTTATCTATAGCCTTCCCC TAGGTCTT
EST58607 0	--	--	---	---	CTCTGGATGGGTTACAGGTGGCAGGCACAAGCCAGTCCATCCTGTAGTCATCATAGTTGTGGCTCC CAAGTTGCTCTCCTCACTGGAGAACAGGACAGCCACATGGCGGGATGGCCGGGAGTTCTTGGT TGCGGCCACGGCTGTGGCTCGTTGTGAACGGTAGCCTTTGGCGTTGCGATGCCTAAACCTTTGTTCT TGGCCAAGGAGGGGGGTGCCATGCCCTGAGATGTAGATGCGGCC
Legend: 1=Marker 2=PM Position 3=Reference Allele 4=Altered Allele 5=SNP Forward Primer 6=SNP Reverse Primer 7=Sequence					



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## EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that  
5 various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will recognize or be able to ascertain using no more than routine experimentation, many equivalents to the  
10 specific embodiments of the invention described specifically herein. Such equivalents are intended to be encompassed in the scope of the claims.

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## CLAIMS

WE CLAIM:

1. A nucleic acid segment shown in column 7 of the Table,  
or a portion thereof which includes a polymorphic site,  
5 or the complement of the segment or portion thereof.
2. The nucleic acid segment of claim 1 that is DNA.
3. The nucleic acid segment of claim 1 that is RNA.
4. The segment of claim 1 that is less than 100 bases.
5. The segment of claim 1 that is less than 50 bases.
- 10 6. The segment of claim 1 that is less than 20 bases.
7. The segment of claim 1, wherein the polymorphic site is  
biallelic.
8. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is the reference base  
15 for the fragment listed in the Table, column 3.
9. The segment of claim 1, wherein the polymorphic form  
occupying the polymorphic site is an alternative form  
for the fragment listed in the Table, column 4.
10. An allele-specific oligonucleotide that hybridizes to a  
20 segment of a fragment shown in the Table, column 7 or  
its complement.
11. The allele-specific oligonucleotide of claim 10 that is  
a probe.

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12. The allele-specific oligonucleotide of claim 10,  
wherein a central position of the probe aligns with the  
polymorphic site of the fragment.
13. The allele-specific oligonucleotide of claim 10 that is  
5 a primer.
14. The allele-specific oligonucleotide of claim 13,  
wherein the 3' end of the primer aligns with the  
polymorphic site of the fragment.
15. The allele-specific oligonucleotide of Claim 10, which  
10 is selected from the group consisting of the nucleotide  
sequences of the Table, column 5.
16. The allele-specific oligonucleotide of Claim 10, which  
is selected from the group consisting of the nucleotide  
sequences of the Table, column 6.
- 15 17. An isolated nucleic acid comprising a sequence of the  
Table, column 7 or the complement thereof, wherein the  
polymorphic site within the sequence or complement is  
occupied by a base other than the reference base shown  
in the Table, column 3.
- 20 18. A method of analyzing a nucleic acid, comprising  
obtaining the nucleic acid from an individual; and  
determining a base occupying any one of the polymorphic  
sites shown in the Table.
- 25 19. The method of claim 18, wherein the determining  
comprises determining a set of bases occupying a set of  
the polymorphic sites shown in the Table.



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20. The method of claim 18, wherein the nucleic acid is obtained from a plurality of individuals, and a base occupying one of the polymorphic positions is determined in each of the individuals, and the method  
5 further comprising testing each individual for the presence of a disease phenotype, and correlating the presence of the disease phenotype with the base.



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>6</sup> :</b> <b>C12Q 1/68, C12N 15/11</b>	<b>A3</b>	<b>(11) International Publication Number:</b> <b>WO 98/20165</b> <b>(43) International Publication Date:</b> 14 May 1998 (14.05.98)
<b>(21) International Application Number:</b> PCT/US97/20313 <b>(22) International Filing Date:</b> 5 November 1997 (05.11.97)  <b>(30) Priority Data:</b> 60/030,455                      6 November 1996 (06.11.96)                      US  <b>(71) Applicant (for all designated States except US):</b> WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH [US/US]; Nine Cambridge Center, Cambridge, MA 02142 (US).  <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only):</b> LANDER, Eric, S. [US/US]; 151 Bishop Allen Drive, Cambridge, MA 02138 (US). WANG, David [CN/US]; Apartment 314, 276 Mass- achusetts Avenue, Arlington, MA 02173 (US). HUDSON, Thomas [CA/US]; 361 Metcalfe Avenue, Westmount, Quebec H3Z 2J2 (CA).  <b>(74) Agents:</b> GRANAHAH, Patricia et al.; Hamilton, Brook, Smith & Reynolds, Two Militia Drive, Lexington, MA 02173 (US).		<b>(81) Designated States:</b> JP, US, European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).  <b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims</i> <i>and to be republished in the event of the receipt of amendments.</i>  <b>(88) Date of publication of the international search report:</b> 12 November 1998 (12.11.98)
<b>(54) Title:</b> BIALLELIC MARKERS  <b>(57) Abstract</b>  The invention provides nucleic acid segments of the human genome including polymorphic sites. Allele-specific primers and probes hybridizing to regions flanking these sites are also provided. The nucleic acids, primers and probes are used in applications such as forensics, paternity testing, medicine and genetic analysis.		

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# INTERNATIONAL SEARCH REPORT

International Application No

PLI/US 97/20313

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12Q1/68 C12N15/11

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 12607 A (MOLECULAR TOOL INC) 11 May 1995 see the whole document ---	1-20
X	WANG D ET AL: "TOWARD A THIRD GENERATION GENETIC MAP OF THE HUMAN GENOME BASED ON BI-ALLELIC POLYMORPHISMS" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 59, no. 4, October 1996, page A03 XP002050641 see abstract --- -/--	1-20

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

### \* Special categories of cited documents :

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Date of the actual completion of the international search

17 June 1998

Date of mailing of the international search report

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## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBL10 emb1 Accession number: hst27766, 12 January 1995 ADAMS M D ET AL.: "Initial assessment of human gene diversity and expression patterns based upon 52 million basepairs of cDNA sequence" XP002067789 * Sequence *</p>	1-3,10, 11
X	<p>--- SYVANEN A -CH ET AL: "IDENTIFICATION OF INDIVIDUALS BY ANALYSIS OF BIALLELIC DNA MARKERS, USING PCR AND SOLID-PHASE MINISEQUENCING" AMERICAN JOURNAL OF HUMAN GENETICS, vol. 52, no. 1, January 1993, pages 46-59, XP002050638 see abstract see page 47, column 1, paragraph 3 - page 50, column 1, paragraph 1 see page 51, column 1, paragraph 3; figure 1; table 1</p>	1-3, 7-10,13, 14,17-20
X	<p>--- FR 2 722 295 A (ROUSSY INST GUSTAVE) 12 January 1996 see abstract see page 1, line 5 - page 2, line 17 see page 9, line 9 - page 10, line 15; tables 2,3</p>	1-3,7-9, 17-20
X	<p>--- HRUBAN R H ET AL: "K-RAS ONCOGENE ACTIVATION IN ADENOCARCINOMA OF THE HUMAN PANCREAS A STUDY OF 82 CARCINOMAS USING A COMBINATION OF MUTANT-ENRICHED POLYMERASE CHAIN REACTION ANALYSIS AND ALLELE-SPECIFIC OLIGONUCLEOTIDE HYBRIDIZATION" AMERICAN JOURNAL OF PATHOLOGY, vol. 143, no. 2, 1 August 1993, pages 545-554, XP000572114 see the whole document</p>	10-16, 18-20
X	<p>--- GROMPE M: "THE RAPID DETECTION OF UNKNOWN MUTATIONS IN NUCLEIC ACIDS" NATURE GENETICS, vol. 5, no. 2, October 1993, pages 111-117, XP000615290 see the whole document</p> <p>--- -/--</p>	18-20

# INTERNATIONAL SEARCH REPORT

International Application No

PC1/US 97/20313

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>NIKIFOROV T T ET AL: "GENETIC BIT ANALYSIS: A SOLID PHASE METHOD FOR TYPING SINGLE NUCLEOTIDE POLYMORPHISMS" NUCLEIC ACIDS RESEARCH, vol. 22, no. 20, October 1994, pages 4167-4175, XP002015765 see the whole document</p> <p>-----</p>	18-20



# INTERNATIONAL SEARCH REPORT

I. International application No.  
PCT/US 97/20313

## Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-20 (partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: 1-20 (partially)

INVENTION 1: An isolated nucleic acid segment including a polymorphic site having the nucleotide sequence of SEQ ID NO:1149, or the complement of that segment or portions thereof, an allele-specific oligonucleotide probe or primer hybridizing to such a segment or its complement, and a method of analyzing such a nucleic acid by determining the bases occupying the polymorphic site(s).

2. Claims: 1-20 (partially)

INVENTION 2 to INVENTION 2669:

-Idem as invention 1 but limited to the sequences having SEQ ID Nos. 1150 to 3817. (Invention 2 is limited to SEQ ID NO:1150, invention 3 is limited to SEQ ID NO:1151, ..., invention 2269 is limited to SEQ ID NO:3817).

For the sake of conciseness, the first group is explicitly defined, the other groups are defined by analogy hereto.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PC 1/US 97/20313

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9512607 A	11-05-95	AU 8132194 A CA 2175695 A EP 0726905 A US 5762876 A	23-05-95 11-05-95 21-08-96 09-06-98
FR 2722295 A	12-01-96	NONE	